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RESULT 8
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                                                                                                          Q9XE89
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                          Veau B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Hamdi S., "Genes encoding glycine-rich Catharanthus roseus proteins with RNA-
                                                                          Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Veau B., Oudin A., Courtois M., Chenieux J.-C., Hamdi S., Rideau M.,
Clastre M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Iracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Gentianales, Apocynaceae, Rauvolfioideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of two cDNAs encoding crGRP2 and crGRP3 (Accession Nos. AF200323 and AF200322), the first members of the RRM-GRP family in Plant Physical. 122:1459-1459(2000).
EMBL: AF200323: AAF31404.1;
                                                                                                                                                                                                                                                                                                                                                                                  í
O
                                                                                                                                                                                                                                                                                                                                               34.7%; Score 66; DB 10; Length 137; 50.0%; Pred. No. 1.8; tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 66; DB 10; Length 160; 50.0%; Pred. No. 2.1; tive 4; Mismatches 7; Indels
                                                                                                                                                                                                            Submitted (007-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AP200221; AAF31402.1; -
HSSP; AP200321; HAA1.
INCEPTCO; IPR000504; RRW.
Ffam; PP00076; rrm: 1.
SWART; SW00360; RRW; 1.
PROSITE, PS030102; RRW; 1.
PROSITE, PS030102; RRW; 1.
SROUENCE 137 AA; 14162 WW; 4FABADB9C7A989FC CRC64;
          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 160 AA; 16264 MW; DCDC9F63C983F5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA-BINDING PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           80 TVNEAQSRGSGGGGGGGFRGP 101
                                                                                                                                                                                                                                                                                                                                                                                           5 TLRQCLAARAGGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P09651; 1HA1
InterPro; IPR002952; Eggshell.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.0
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00076; rrm; 1
PRINTS; PR01228; EGGSHELL.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0%
hes 11; Conservative
                                                                                                                           Vinceae; Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vinceae; Catharanthus.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4058;
    Q9M6A1;
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                 Matches
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Q9M699
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Gaps

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Matches

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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 13, Last annotation update)
11-NOV-1999 (TrEMBLrel. 13, Last annotation update)
11-NOV-19FICAL 39-1 KDA PROTEIN.
Sorghum bicolor (Sorghum) (Sorghum vilgare).
Sorghum bicolor (Sorghum) (Sorghum vilgare).
Spermatophyta; Magnoliophyta; Liliopsida; Embryophyta; Tracheophyta;
Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                Liaca V., Lou A., Messing J.W.;
"Microsynteny analysis of 22-kDa zein cluster in maize and sorghum.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF061282; AAD22156.1;
Hypothetical protein.
SEQUENCE 369 AA; 39080 MW; DAA3C6508BF106CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0708G02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.7%; Score 66; DB 10; Length 369; 40.0%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.7%; Score 66; DB 10; Length 413; 64.7%; Pred. No. 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP001539; BAA92912.1; -.
Hypothetical protein.
SEQUENCE 413 AA; 45035 MW; 4FEC2A4C5D1271CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 PAKKASISASVGGGGGGGGGGGGGTWRRRGPCSGSRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLRQCLAARAGGGGGGGGIEGPTLRQ--CLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5;
2; Mismatches
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                              80 TVNEAQSRGSGGGGGGGFRGP 101
5 TLRQCLAARAGGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryzeae; Oryza.
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 RRCAGLLAGGGGGGGV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RQCLAARAGGGGGGGI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                      Q9XE89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09LI26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09LI26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096802
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome."; Mnol. Microbiol. 21:77-96(1996).

EMBL; AL512667; CAC21636.2; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                             Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Sudo H., Nasai K., Sudo H., Suzuki T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Matanashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanashi M., Chiba Y., Ishida S., Murakawa K., Masuho Y., Namamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; Namamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.

Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.

SEQUENCE 474 AA: 51313 MW; OBCA301518F20DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacteridae; Actinobacteridae; Actinomycetales; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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46.2%; Pred. No. 6;
tive 2; Mismatches 9; Indels
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ14713 FIS, CLONE NT2RP3000845, MODERATELY SIMILAR TO
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           34.7%; Score 66; DB 4; Length 474; 45.0%; Pred. No. 5.8; ative 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam: PF02687; DUF214; 1.
SEQUENCE 496 AA; 49548 MW; 54E110C4F86231A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GPTLR-----QCLAARAGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTATIVE INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003838; DUF214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 45.09 tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Seeger K.J., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                NCBI_TaxID=9606;
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Conservative

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Kato T., Satoh S., Okabe H., Kitahara O., Ono K., Kihara C.,
Rato T., Satoh S., Okabe H., Kitahara O., Ono K., Kihara C.,
Tanaka T., Taunoda T., Yamaoka Y., Nakamura Y., Furukawa Y.;
Tanaka T., Taunoda T., Yamaoka Y., MARKLI, homologous to MARK3 and its
insolation of a novel human gene, MARKLI, homologous to MARK3 and its
involvement in hepatocellular carcinogenesis.";
Neoplasta 3: 49(2001).
-- SIMILARIY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-- SIMILARIY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-- HSSP; 063450; 1A06.
Interpro: IPRO0290; Ser_thr_pkinase.
Interpro: IPRO01245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.78; Score 66; DB 5; Length 500; 56.5%; Pred. No. 6.1; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                          Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Serine protease.
SEQUENCE 500 AA; 53946 MW; 1416327086FE7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAP/MICROTUBULE AFFINITY-REGULATING KINASE LIKE 1.
                                                                                                                                 01.NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
                 4 PTLRQCLAARAGGGG------GGGGIEGPTLRQCLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         688 AA.
                                                                                                       500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       investigating blology.";
Science 282:2012-2018(1998).
BEBL; ZRO13; CABO1420.1;
Interpro; IPRO11554; Trypsin.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPTLRQCLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 56.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                         F15B9.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                               Percy C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BYD8
                                                                                                              Q19476
Q19476;
                                                                                                                                                                                                          F15B9.
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                                                                                   RESULT 12
Q19476
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                                                                                                                              ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 688 AA; 75261 MW; A03B5A7943ACD086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muş.
                                                                                                                                                                                                                   6;
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                                                                                                                                                                              Score 66; DB 4; Length 688;
Pred. No. 8.2;
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                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            689 AA; 75449 MW; 439B11FD33D78B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIAA1860 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) KERATIN 2 EPIDERMIS.
                                                                                                                                                                                                                                                Print Pro0069; pkinase; 1.

PRINTS; PR00109; TYRINASE.
SWART; SM00120; S_TKC; 1.
SWART; SM00109; TYRC; 1.
SWART; SM00107; PYRC; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
                                                                                                                                                                                                                               3 GPTLR-----QCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1:1
| 563 GSTIRSTFHGGQVRDRRAGGGGGGVQNGPPASPTLAHEA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLR-----QCLAARAGGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 707 AA.
                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21245130; PubMed=11347906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for large Proteins in vitro.";
DNA Res. 8:85-95(2001).
EMBL: AB058763; BAB47489.1;
                                                                                                                                                                              34.78;
                                                                                                                                                                                            45.08;
InterPro; IPR000449; UBA.
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                         Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN
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                                                                                                                                                                            Query Match
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Herzog F., Winter H., Schweizer J.;

"The large type II 70-kDa keratin of mouse epidermis is the ortholog
J. Invest. Dermach. 102:165-170(1994).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

"THE LANGE TO THE INTERMEDIATE FILAMENT FAMILY.

"THE LANGE TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drewes G., Ebneth A., Preuss U., Mandelkow E.M., Mandelkow E.;
"MARK, a novel family of protein kinases that phosphorylate
microtubule associated proteins and trigger microtubule disruption.";
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                       34.7%; Score 66; DB 11; Length 707; 64.7%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.7%; Score 66; DB 4; Length 752;
45.0%; Pred. No. 8.9;
tive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drewes G., Mandelkow E.M.; "MARK2 and MARK3."; "MARK4, homologue of MARK1, MARK2 and MARK3."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     Colled coil; Intermediate filament.
SEQUENCE 707 AA; 70977 MW; D58FA5E6E30BBB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinase; Serine/threonine-protein kinase.
SEQUENCE 752 AA; 82519 MW; 4B430FFD2B150E7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                   752 AA
                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARK4 SERINE/THREONINE PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequel-DEC-2001 (TrEMBLrel. 19, Last semnel-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                          MGD; MGI:96699; K+t2-17.
InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97262070; PubMed=9108484;
                                                                                                                                                                                                                                                                        1;
                                                                                                                                         Pfam, PF00038; filament; 1.
PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last HOMEOTIC PROTEIN HB9 (FRAGMENT).
                                                                                                                                                                                                                                                                                                   9 CLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                             7 CRSRRGGGGGGGGFRG 23
                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 45.0° Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 89:297-308(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                      Local Similarity
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01-DEC-2001
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7

Gaps

6;

Indels

3; Mismatches 34.5%; Score 65.5; I 43.2%; Pred. No. 10;

2 EGPTLRQCLAARAGGGGGGG-----GIEGPTLRQC 31

DB 5; Length 770;

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SEQUENCE 770 AA; 82032 MW; 5C6D2A2D8C9CDD58 CRC64;
                                                                                  0.0ery Match
Best Local Similarity 43.23
Matches 16; Conservative
                                                                                                                                                                                                                  δλ
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                                                                                                                                                    MEDLINE-99263496; PubMed=10329000; McDLINE-99263496; PubMed=10329000); McL., Hing A., Baren M.Jvan, Joosse M., Breedveld G., Wang J.C., Burgess A., Donnis-Keller H., Berglund C., Scherer S.W., Rommens J.M.,
                                                                                                                                                                                                                                                             DOUGHESS A., Houtink P.;

"A physical and transcriptional map of the preaxial polydactyly locus on chromosome 7436.";

"I physical and transcriptional map of the preaxial polydactyly locus on chromosome 7436.";

"I subscribility in the price of the preaxial polydactyly locus on chromosome 7436.";

"I subscribility NUCLEAR (BY SIMILARITY).

"I SUBCELDILAR INCATION: NUCLEAR (BY SIMILARITY).

"I STAINTARITY: WITH OTHER HOMEOBOX PROTEINS.

"EMBL, ARIOT453; AAD41467.1;

"INTERPORT STAINTARIANT.1."

InterPro; IPR001355; Eggshell.

InterPro; IPR001355; Homeobox.
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34.5%; Score 65.5; DB 4; Length 355;
Best Local Similarity 57.1%; Pred. No. 5;
Matches 16; Conservative 0; Mismatches 9; Indels
                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AA; 35587 MW; CD41D18CC811F0E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NON_TER 355 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 LAAAASGTGGGGGGGGASGGTSGSCSPA 61
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ATP-binding; Helicase; Zinc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000047; HTH_repressr.
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InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR001878; Znf_CCHC.
Pfam: PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS: PR01228; EGGSHELL.
PRINTS: PR00024; HOMEOBOX.
PRINTS: PR000031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSDEAD1B(CSVHB).
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                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciona savignyi
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
STRAIN-CV. MATSUMOTO T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0499C11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sosaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Pred. No. 6.1;
tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfant: PF00153; mito_carr; 3.
PRINTS: PR00926; MITOCARRIER; 2.
PROSITE; PS00215; MITOCALCARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 381 AA; 40761 MW; F3A0E3CEBD950778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 452 AA.
                                             381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 65; 48.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTLRQCLAARAGGGGGGGGGTEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 PHARRALALRVGGGGGGPAFASLTVRE 49
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:P0453A06."
                                                                                                                                                                           01-JUN-2001 (T
ESTS AU068633.
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                                                                                          Q9LD54;
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                                                          09LD54
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RESULT 19
                                   09LD54
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Fabburer M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nalson C.R., Miklos G.L.G,
RA Abrill S.P., Agbapani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M. Basu A., Baxendal J., Bayraktarold L., Beasley E.M.,
RA Borkova D., Botchman M.R., Bouck J. Brokatein P., Brottier P.,
RA Borkova D., Botchman M.R., Bouck J., Brokatein P., Brottier P.,
RA Borkova D., McChand M.R., Bouck J., Brokatein P., Brottier P.,
RA Borkova D., McChand W.R., Bouck J., Brokatein P., Brottier P.,
RA Borkova D., WcChand W.R., Bouck J., Brokatein P., Brottier P.,
RA Geblos B., Delcher A., Deng J., Mass A.D., Davis S.,
RA Borbin K.J., Evangellsta C.C., Ferrac C., Ferrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.2%; Score 65; DB 5; Length 452; 73.3%; Pred. No. 7.1; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 AA.
                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 ARAGGGGGGGGIEGP 26
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
    NCBI_TaxID=7227;
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                                                           STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Dros
NCBI_TaxID=7227;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amantides P.G., Scherer S.E., LiP.W., Hoskins R.A., Galle R.F.,
Amantides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
B. George R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,
R.A., Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A., Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Basaley E.M.,
Bescon K.Y., Benos P.V., Berman B.P., Bhandari D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
R.A., Bortona M.R., Bouck J., Brokstein P., Brottler P.,
R.A., Bortona M.R., Bouck J., Brokstein P., Brottler P.,
R.A., Chenson D.A., Buller H., Cadieu E., Center A., Chandra I.,
R.A., Chenson D.A., Buller H., Cadieu E., Center A., Chandra I.,
R.A., Bablos M., Delder A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R.A., Bouch R. J., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R.A., Bouch R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R.A., Bouch R., Delcher A., Boulland R.J., Harris M.,
R.A., Harris N.L., Harvey D., Heimen T.J., Herrandez J.R., Houck J.,
R.A., Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalli M., Mattei B., McIntosh T.C., McIratz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McIratz S., Kulp D., Lai Z.,
Mount S.M., Molson K.A., Molyand T.C., Morris J., Moshrefi A.,
Ralazzolo M., Pitlman G.S., Panders R.D.C., Scheeler F., Santh H.,
Ralazzolo M., Pullshina N.V., Mobarry C., Morris J., Moshrefi R.,
Ralazzolo M., Pullshina N.V., Molazy K.C., Wu D., Santh T.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Santh H.,
Ranger E., Spradling A.C., Stapleton M., Skupski M.P., Santh H.,
Ranger R.M., Wassaraman D.A., Wenter E., Wang G., Zhang C.,
R.M., The genome sequence of Drosophila melanogaster ".,
R. The genome sequence of Drosophila mel
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NCBI_TaxID=1772;
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 AA; 15131 MW; 7A065C21C1376079 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SINGLE-STRANDED DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%; Score 64.5; DI 51.6%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR001545; Glyco_hormone_beta.
InterPro; IPR002172; LDL_recept_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TLRQCL-----AARAGGGGGGGGIEGP 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003592; AAF51656.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0037034; CG13257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00057; ldl_recept_a; I
SMART; SM00192; LDLa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01209; LDLRA_1; 1. PROSITE; PS50068; LDLRA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; Q07954; 1CR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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δλ
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REPURESTREENT NOT NOT THE NATION OF SEQUENCE FROM NATA Address FROM NATA Address FROM NATA Address FROM NATA Address NATA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
             Reddy M.S., Muniyappa K.; Biochemical properties of single-stranded DNA-binding proteins from Mycobacteria.";
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                          33.9%; Score 64.5; DB 2; Length 165; 48.5%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF349434; AAK30583.1;
                                                                                                                                                                                                                      165 AA; 17401 MW; 8786415C16F26F39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AA
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                            107 GPSLRYATAKVNKASRSGGGGGGGGGGGGGGGGG 139
                                                                                                                                                                                                                                                                                                                                                   3 GPTLRQCL----AARAGGGGGGGGGEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                        InterPro; IPR000424; SSB.
Pfam; PF00436; SSB; 1.
DNA-binding.
                                                                                                                                                                                                                                                                                          Best Local Similarity 48.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                 HSSP; P02339; 1EYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
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Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL, ABO03528; ARF49521.1; ..
RIYBase: FBGn0036583; CG13055.
SEQUENCE 309 AA; 33224 MW; 9DAEB67784852A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 64; DB 5; Length 331; 76.9%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                               Length 309;
                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Steward C.A.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; rrva...; PRLZ; 1. PRART; SMO0338; BRLZ; 1. PROSITE; PSO0036; BZIP_BASIC; 1. DNA-binding; Nuclear Protein. A414C19D4ADCC91E CRC64; DNA-binding; Nuclear Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
V41C4A.4B PROTEIN.
                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.7%; Score 64; DB 5;
57.9%; Pred. No. 6.5;
Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                     331 AA.
                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99069613; PubMed=9851916;
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94 SRSGGGGGGGGVAGVTLQE 112
                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 19,
                                                                                                                                                                   12 ARAGGGGGGGGIEGPTLRO 30
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                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 GGGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                 Y41C4A.4A.
Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Y41C4A.4A PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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Caenorhabditis elegans.

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karabinos A., Riemer D., Erber A., Weber K.; "Homologues of vertebrate type I, II and III intermediate filament (IF) proteins in an invertebrate: the IF multigene family of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERNEDIATE FILAMENT PROTEIN El.
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
6
                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                Query Match
33.7%; Score 64; DB 5; Length 333;
Best Local Similarity 76.9%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 5; Length 422;
Pred. No. 8.7;
                                                                     Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 AA; 44892 MW; 85FE742F07751B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cephalochordate Branchiostoma.";
FEBS Lett. 437:15-18(1998).
EMBL; AJ010294; CAR09068 1;
InterPro; IPR002592; Eggshell.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin...
InterPro; IPR003895; Ribosomal.S30.
Pfam; PP00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                           MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99019308; PubMed=9804163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00038; filament; 1
PRINTS; PR01228; EGGSHELL.
PRINTS; PR01248; TYPEIKERATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.7%;
61.9%;
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     169 GGGGGGGVPGPS 181
                                                                                                                                                                                                                                                                                                                                                               15 GGGGGGGGIEGPT 27
                                              SEQUENCE FROM N.A.
                                                                                             SEQUENCE FROM N.A.
                         NCBI_TaxID=6239;
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                                                             Steward C.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Targeted Gene Disruption of the avermectin O-methyltransferase gene and polyketide synthase gene from Streptomyces avermitilis."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF275943; AAG09812.1; InterPro; IPR001227; Acyltransf_domain.

InterPro; IPR001227; Acyltransf_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVERMECTIN POLYKETIDE SYNTHASE (FRAGMENT).
Streptomyces avermitilis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                 STRAIN=CV. NIPPONBARE;
STRAIN=CV. NIPPONBARE;
STRAIN=T. MATSUMOTO T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                 3626 AA; 380557 MW; 6272F5F088C1A8D0 CRC64;
                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00698; Acyl_transf; 3.
Pfam; PF00109; Retcacyl_synt, 2.
Pfam; PF02801; Retcacyl_synt, 2.
PROSITE; PS50075; ACP_DOMAIN; 2.
                               529 AA.
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                             33.7%; Score 64;
51.7%; Pred. No.
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                                                      Created)
                            PRT;
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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                                               01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17,
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 51.79
Matches 15; Conservative
                         PRELIMINARY;
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                                                                                   P0456F08.14 PROTEIN.
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                                                                                                              Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC31271;
Hong Y.-S., Lee J.J.;
                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                  NCBI_TaxID=4530;
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RESULT 27
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Matches
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R. Ikeda H., Monomiya T., Usami M., Ohta T., Omura S.;

R. Torganization of the biosynthetic gene cluster for the polyketide

R. Torganization of the biosynthetic gene cluster for the polyketide

R. Torganization of the biosynthetic gene cluster for the polyketide

R. Torganization of the biosynthetic gene cluster for the polyketide

R. Torganization of the biosynthetic gene cluster

R. R. Babel, ABO31367; BAB4474.1; -

R. R. MELE, ABO3137; BAB4474.1; -

R. InterPro; IPR000794; Ketoacyl-synt.

R. InterPro; IPR000380; Phosphopant_attach.

R. Ffam, PF00698; Acyl_transf; 3.

R. Ffam, PF00698; Acyl_transf; 3.

R. Ffam, PF00699; Acyl_transf; 3.

R. Ffam, PF006907; Ketoacyl-synt. 2.

R. Ffam, PF006907; Ketoacyl-synt. 2.

R. Ffam, PF00550; Pp-binding; 3.

R. Rosite; PS00606; B_KET0ACKL_SYNTHASE; 2.

R. ROSITE; PS00013; CARBOXYPEPT_ZN.2; UKNOWN_2.

R. PROSITE; PS00013; CARBOXYPEPT_ZN.2; UKNOWN_2.

R. PROSITE; PS00012; PADSPHOPANTETHEINE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                  Streptomyces avermitilis.
Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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STRAIN-CY. MIPPONBARE:
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Susaki T., PAC
Susaki FEB-2011, to the EMBL/GenBank/DDBJ databases.
BNBL; AR003272; BAB67948.1;
SEQUENCE 113 AA: 11708 MW; 26D982C86935BCOB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 2; Length 3972;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphopantetheine; Transferase.
SEQUENCE 3972 AA; 416852 MW; 2A293695B032B1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P0506E04.26 PROTEIN.
                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                    PRT; 3972 AA
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MEDLINE-99380548; PubMed-10449723;
                                                                                                                                                                                              TYPE I POLYKETIDE SYNTHASE AVES 1.
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33.7%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.5
Matches 12; Conservative
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                                                                                                             PRELIMINARY;
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(without alignments)
247.023 Million cell updates/sec
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/SIDSI/gcddata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
/SIDSI/gcddata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
/SIDSI/gcddata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
/SIDSI/gcddata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
/GIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
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              Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36
GenCore version 5.1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           747574 segs, 111073796 residues
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_032802:*
                                                                                                                                                                                                                                                           US-09-422-838C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                              Run on:
```

21: /SIDSI/gcgdata/hold-geneseg/geneseqp-embl/AA2000.DAT:* 22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		TPO-mimetic peptid TPO-mimetic peptid Cyclic or linear transposic TPO-mimetic peptid Linear thrombopoie TPO-mimetic peptid TPO-mimetic peptid Thrombopoietin mim Thrombopoietin mim TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid
SUMMARIES	ID	AAB17298 AAB17299 AAY6521 AAB13300 AAY6522 AAB17293 AAB17293 AAY96528 AAY96528 AAY17281
	DB	21 21 21 21 21 21 21 21 21
	Length	36 36 36 36 36 36 36 44 42 42
æ	Query e Match Length DB	100.0 100.0 100.0 90.5 90.5 88.4 88.4 88.4 88.4 88.4
	Score	190 190 172 172 168 168 168 168
	Result No.	1 2 3 3 4 4 4 10 10 11

Synthetic TMP-TMP Thrombopoietin mim Synthetic TMP-TMP- TWP-TMP-For protein Human 1961 For TMP FC-TMP-TMP protein TPO-mimetic peptid Thrombopoietin mim TPO-mimetic peptid Thrombopoietin mim TPO-mimetic peptid	c pepti c pepti c pepti c pepti
173 1173 1173 1173 172 173 173 173 173 173 173 173 173 173 173	
168 88.4 168 88.4 168 88.4 168 88.4 168 88.4 169 88.2 160 84.2 160 84.2 159 83.7 159 83.7 159 83.7 159 82.6 156 82.1 156 82.1 156 82.1 156 82.1 156 82.1 156 82.1 156 82.1 157 92.5 118 62.1 118 62.1 118 62.1 118 62.1	5 2 2 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5
112 113 1143 115 115 116 117 117 118 118 118 118 118 118 118 118	444 45

ALIGNMENTS

RESULT 1

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TWF; antagonist; Oxfotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. TPO-mimetic peptide sequence SEQ ID NO:354. Feige U, Liu C, Cheetham J, Boone TC; AAB17298 standard; Peptide; 36 AA. 99WO-US25044. 98US-0105371. 99US-0428082. 31-OCT-2000 (first entry) WPI; 2000-350702/30. (AMGE-) AMGEN INC. WO200024782-A2. 25-0CT-1999; 22-OCT-1999; 04-MAY-2000. 23-OCT-1998; AAB17298; Synthetic.

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Novel composition of matter comprising an Fc domain and
                                                                                                                                                                               1 IEGPTLROCLAARAGGGGGGGGGGTEGPTLROCLAARA 36
                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                        Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                        AAB17299 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                     99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                98US-0105371
                                                                                                                                                                                                                                                                                                                                                                       99US-0428082
                                                                                                                                                                                                                                               31-OCT-2000 (first entry)
                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
               autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                36 AA;
                                                                                                                                                                                                                                                                                                                               WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                           04-MAY-2000.
                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                      AAB17299;
                                                                                                                                                  Sequence
                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                               g
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The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L2)d-P2-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L2)d-P2-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L2)d-P2-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)f-P4 (L1)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L4)c-F1-(L3)a-P3-(L4)c-F1-(L4)c-F1-(L4)c-F1-(L4)c-F1-(L4)c-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclic or linear thrombopoietin mimetic peptide compound 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 190; DB 21; 100.0%; Pred. No. 3.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                              Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96521 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= linker
23.36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                 autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY9652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                         The present invention describes composition of matter (I) comprising an FC comain, pharmacologically active peptides, and linkers. Where (I) is: FC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P2-(L3)e-P3-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L3)d-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunoSuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoieth; thrombopoietin; interleukin 1; vacytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 190; DB 21;
100.0%; Pred. No. 3.8e-16;
tive 0; Mismatches 0;
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Gaps

. 0

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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                          A compound which binds to an mpl receptor comprising a thrombopoietin
                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; inmunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                      Length 36;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                              100.0%; Score 190; DB 21;
100.0%; Pred. No. 3.8e-16;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J, Boone TC;
                                                                       Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                             AAB17300 standard; Peptide; 36 AA.
  Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                   WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30
                                                                                                                                                                                                                                                            36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 AAB17300;
  Liu C,
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                      AAB17300
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The present invention describes composition of matter (I) comprising an (XI) are domain, pharmacologically active peptides, and linkers. Where (I) is: (XI) a-FI (XI)b, where: FI = an Fc domain; XI and X2 = are each independently selected from -(II) c-F1, (II) d-F2, (I3) d-F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin; mimetic; TMP: TPO: platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%; Score 172; DB 21; Length 36; 94.4%; Pred. No. 5.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear thrombopoietin mimetic peptide compound 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQCLAARAGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                             Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96522 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0105348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                A compound which binds to an mpl receptor comprising a thrombopoietin commetted peptide (TWP) dimer joined by a linker [TWP_1-(L_1)_nTWP_2], commetted peptide (TWP_2 are amino acid sequences varying from at least comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, cc. 10 to 14 residues in length comprising x_2-x_1_0, x_1-x_1_2, x_1-x_1_2, x_1-x_1_2, cc. 10 to 14 residues in length comprising x_2-x_1_0, x_1-x_1_1, x_2-x_1_2, cc. 1.2 to 1.2 t
                                                                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; vyctocoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothedial growth factor; matrix metalloproteinase; sathma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 172; DB 21;
94.4%; Pred. No. 5.5e-14;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheetham J, Boone TC;
                                                                                                                                 diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB16963 standard; Protein; 36 AA.
                                                                                                                                                                              Claim 16; Page 61; 91pp; English
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99US-0428082
               Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%
Query Match
Best Local Similarity 94.4%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C,
                                                            WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16963;
                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; amutoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; mumunosuppressive; EPO, TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%; Score 168; DB 21; Length 36; 94.4%; Pred. No. 1.6e-13; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                        Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17293 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 94.4 tes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17293;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The present invention describes composition of matter (I) comprising an (X1)4—FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each (X1)5—FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each (X1)5—FI-(Z2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A binding, complement fixation, and possibly placental transfer. AAA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-anemic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatologica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.4%; Score 168; DB 21; Length 36; 94.4%; Pred. No. 1.6e-13; Ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQCLAARAGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 6.
                                                                                                               Example 1; Page 318; 608pp; English.
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'label= linker
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                                               autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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Modified-site
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   ACCOMMENTATION OF THE PROPERTY OF THE PROPERTY
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A compound which binds to an mpl receptor comprising a thrombopoietin is new. TWP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_-2 \times 1_-1, X_-1 \times 1_-1, X_-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin mimetic peptide compound 9.
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                                                                                                                                                                                                                Claim 16; Page 62; 91pp; English.
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  Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20..27
/label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24834.
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                                                    WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
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     Liu C,
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                                                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17281 standard; Peptide; 42 AA.
                                                                                                                                                                                         Claim 16; Page 65; 91pp; English.
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                                                  Liu C, Feige U, Cheetham J;
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Best Local Similarity 94.4
Matches 34; Conservative
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                                                                                      WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AA;
                (AMGE-) AMGEN INC.
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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently scleeted from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 are each independently scleeted from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 are each independently schere P1, P2, P3, and P4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and b, c, d, e, and f = are each independently inkers; and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention and custivities. DNAs, vectors and host cells from the present invention and halfoly complement fixation, and possibly placental transfer. AAA69443 conformation, and possibly placental transfer AAA69443 conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; autoimmunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:338.
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                                                                                                                                                                            Disclosure; Page 313; 608pp; English.
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99US-0428082.
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                                                                                                                             autoimmune diseases -
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WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present invention describes composition of matter (I) comprising an (XI)a-FI-(X2)b, where: FI = an FC domain, XI and X2 = are each independently selected from - (LI)c-FI-(LI)a-FI-(LI)d-F2-(LI)e-F3, or - (LI)c-FI-(LI)d-F2-(LI)e-F3.

(C (LI)C-FI-(LI)d-F2-(LI)e-F3, or - (LI)c-FI-(LI)d-F2-(LI)e-F3-(LI)e-F3 (C (LI)c-FI-(LI)d-F2-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F3-(LI)e-F
                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 168; DB 21; Length 42; 94.4%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQCLAARAGGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                             Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17308 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 94.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17308
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The present invention describes composition of matter (I) comprising an (XI)=-1-(XI)b, where: FI = an Fc domain, XI and X2 = are each (XI)=-FI-(X2)b, where: FI = an Fc domain, XI and X2 = are each independently selected from -(LI)C-FI-(LI)C-FI-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(LI)d-FD-(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; IgG1; FC; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.4%; Score 168; DB 21; Length 42; 94.4%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                              Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96530 standard; Protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2A; Page 48; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105348,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA29225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96530
δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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coverlapping oligonucleotides were used to construct a synthetic construct and coding a thrombopoietin minetic peptide (TMF), which was then closed in frame to the Fc region of the human 1gGl chain (see AAY96529). A compound which binds to an mpl receptor comprising a TMP compound which binds to an mpl receptor comprising a TMP command of the compression of the comprision of the compression of the compounds bind to and activate the compounds the compounds bind to and activate the compounds the production of platelet compounds the production of platelet of the compounds bind to and activate the compounds the production of platelets of the precursors (e.g. megakaryocytes) in a mammanl, which is useful for increasing the production of platelets or platelet compounds thrombocytopenia, which is useful for compound of platelets or precursors (e.g. megakaryocytes) in a mammanl, which is useful for compound of platelets or platelet compounds thrombocytopenia, which is useful for compound of the compounds of platelets or precursors (e.g. megakaryocytes) in a mammanl, which is useful for compound of platelets or platelet compounds and activate the compounds of platelets or platelet compounds and compounds of platelets or precursors (e.g. megakaryocytes) in a mammand, which is useful for compounds (ITP), human immunodeficiency virus ansemba, immune thrombocytopenia (ITP), human immunodeficiency virus consociated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; 1L-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 88.4%; Score 168; DB 21; Length 42; Local Similarity 94.4%; Pred. No. 1.9e-13; local Single 94.4%; Pred. No. 1.9e-13; locals les 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17311 standard; Peptide; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -[L1]c-P1-(L2)d-P2-(L3)a-P3.

CC (L1]c-P1-(L2)d-P2-(L3)a-P3.

CC (L1]c-P1-(L2)d-P2-(L3)a-P3.

CC (where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, C, d, e, and f = are each independently linkers; and a, b, C, d, e, and f = are each independently contains and base of the present invention can activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present inventions are be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC be used for producing pharmaceutical compositions. The compositions are neglul for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC he used for producing pharmaceutical compositions. The compositions are neglul for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC he used for producing pharmaceutical compositions. The composition are beinding, complement fixation, and possibly placental transfer. AAA69443

CC banks0926 and AAB16955 to AAB18003 represent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic, antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin i, cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                          88.4%; Score 168; DB 21; Length 60; 94.4%; Pred. No. 2.7e-13; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16960 standard; Protein; 269 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 94.4%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA69446
                                                                                                                                                                                                                                                                                                                                                                                                          60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB16960
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0; Gaps

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The present invention describes composition of matter (I) comprising an (X13-F1-K2)b, where: F1 = an Fc domain; X1 and X2 = are each (X13-F1-K2)b, where: F1 = an Fc domain; X1 and X2 = are each (X13-F1-K2)b, where (I) is: C2 independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2. (L3)d-P2. (L3)d-P2-(L3)d-P2) or -(L1)c-P1, (L3)d-P2-(L3)d-P2-(L3)d-P2) or -(L1)c-P1, (L3)d-P2-(L3)d-P2-(L3)d-P2) or -(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin; IgG1; FC; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 168; DB 21; Length 269; 94.4%; Pred. No. 1.2e-12; Live 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96531 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human 1961 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Feige U, Cheetham J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA29229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY9653
× 399999999999988
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X_1-X_1-4. X_1 = 1, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, L, F, G, Q = W, Y or F; X_1 = L, I, V, A, F, M, or K; X_1 = A, I, V, Y, Y, Y, V, V, Q or G; X_1 = X_1 = A, I, V, L, F, G, S, or Q; X_1 = R, K, A, Comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and thrombopotetin. The TWDs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombotopropropressing the production of is useful for treatment of diseases which involve thombotypeans.
                                                                                                                                                                                                                                                                                                                         aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For domain, pharmacologically active peptides, and linkers. Where (I) independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2.

where P1, P2, P3, and P4 = are each independently sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; cytotoxic retribopoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.4%; Score 168; DB 21; Length 269; 94.4%; Pred. No. 1.2e-12; Live 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 IEGPTLROWLAARAGGGGGGGGGEGFTLROWLAARA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB16959 standard; Protein; 268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA69445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB16959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB16959
                8.*.6666666666668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_TMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_2, X_1-X_1_3, X_2-X_1_3, X_1-X_1_3, X_1-X
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Where (I) is:

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                                                                                                                                                                                                                                                                     useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17301 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.3
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
oor I, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP.1-(L.1)_nTMP.2], is new. TMP.1 and TMP.2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "optionally modified by bromoacetyl or PEG"
                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                     Score 160; DB 21; Length 36; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    1 IEGPTLRQCLAARAGGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                      Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               AAY96523 standard; peptide; 36 AA
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/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= TMP_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= TMP_1
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                                                                                                                                                                                                               84.2%;
91.7%;
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                                                                                                                                                                                                                               Best Local Similarity 91.79
Matches 33; Conservative
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                                                                                                                                                                                       36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96523;
                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                       RESULT 19
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CC X_1 = X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vascular cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 160; DB 21; Length 36;
Pred. No. 1.5e-12;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17303 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.28;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can useful for preating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein to AAA69526 and AAB18955 to AAB18003 represent nucleotide and anino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-T1-(X2)b., where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)a-P2-(A3)a-P3-(L1)c-P1-(L2)d-P2-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L3)a-P3-(L4)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; official inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 159; DB 21; Length 36; 91.7%; Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e-12;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQCLAARAGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17307 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17307:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
            55555555555555<del>x</del>8
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Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69226 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1]^-(L_1) nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note" "optionally linked to an Fc molecule"
                                                                                                                                                                                                                       Score 159; DB 21; Length 36;
                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                            Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                            1 IEGPTLROCLAARAGGGGGGGGGGEGPTLROCLAARA 36
                                                                                                                                                                                                                                                                                                                            1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                               AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24834.
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                                                                                                                                                                                                                                83.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.78
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96524;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pept1de
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
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is:
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0
                                                                                                                                                                                                                                                                     thrombopoietin. The TMPs are useful for increasing the production of thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
10 to 14 residues in length comprising X_{-2} \cdot X_{-1} = 0, X_{-2} \cdot X_{-1} = 1, X_{-2} \cdot X_{-1} = 2, X_{-1} \cdot X_{-1} = 1, X_{-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) i (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, where P1, P2, P3, and P4 = are each independently sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; autoimmunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%; Score 159; DB 21; Length 36; 91.7%; Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLROCLAARAGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17294 standard; Peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17294
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                                             55555555555555<del>×</del>8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
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pharmacologically active peptides; Ll, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or l, provided that at least l of a and b is l. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive extivities. DNAs, vectors and host cells from the present invention can useful for producing pharmaceutical compositions. The compositions are buseful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-rP1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P3. or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)FP4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropietin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                 DB 21; Length 37;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                       82.9%; Score 157.5; DB 21;
91.9%; Pred. No. 3.1e-12;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQCLAARA-GGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO;351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17295 standard; Peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                       Local Similarity 91.9 nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                    37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                       Matches
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AAB17295
   8555555555555x8
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O or 1, provided that at least 1 of a and b is 1. The composition can activities. Substance, antiasthmatic, thrombolytic and immunosuppressive activities. DNBA. vectors and host cells from the present invention can used for producing pharmaceutical compositions. The compositions are require useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FG domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69526 and AAB16055 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes composition of matter (I) comprising an (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of independently linkers; and a, b, c, d, e, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO: TPO: CTLA4; minetic; IL-1; TNF; antagonist; MNF; inhibitor; erythropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; escular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                          82.6%; Score 157; DB 21; Length 38;
                                                                                                                                                                                                                                               1 IEGPTLRQCLAARA--GGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17304 standard; Peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                               89.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases -
                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                           38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                              34;
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                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17304;
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1 -(L2)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3, ind P4 = are each independently sequences of hidspendently sequences of the are last 1, b, c, d, e, and f = are each independently inhers; and ab, b, c, d, e, and b is 1. The composition can or 1, provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, such as Fc receptor binding, protein balf-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                         DB 21; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                       82.4%; Score 156.5; DB 21;
87.2%; Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQCLAARAGGG---GGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17305 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                34; Conservative
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                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                39 AA;
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                                                                                                                                                                                                                    Sednence
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                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                       Matches
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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (Fc domain, pharmacologically active peptides, and M2 = are each (M1) = F1 - (X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (M2) = F2 - (M3) = F2 -
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                       Gaps
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M
                                                                                                                                                                                                                                                  DB 21; Length 39;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                    82.4%; Score 156.5; DB 21;
87.2%; Pred. No. 4.2e-12;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGG---GGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17306 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases
                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17306;
                                                                                                                                                                                                                                                                        Query Match
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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_IIMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least x_2-x_{-1}, x_{-1}, and x_{-1}, x_{-1}, x_{-1}, x_{-1}, x_{-1}, x_{-1}, x_{-1}, and x_{-1}, and x_{-1}, x_{-1},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "optionally linked to an Fc molecule"
                                                                                                                                                            82.1%; Score 156; DB 21; Length 36; 88.9%; Pred. No. 4.5e-12; live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                         Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2000 (first entry)
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-365108/31.
                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000.
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96526;
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                          RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                          SXSSSS
                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                          g
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)4-FL'(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from '(L1)C-P1'(L2)d-P2'(L3)e-P3'(L4)F-P4 (L2)d-P2'(L3)e-P3'(L4)F-P4 (L2)d-P2'(L3)e-P3'(L3)e-P3', or '(L1)C-P1'(L2)d-P2'(L3)e-P3'(L4)F-P4 (L3)e-P1'(L2)d-P2'(L3)e-P3'(L4)F-P4 (L3)e-P3', or '(L3)e-P3'(L4)F-P4 (L3)e-P3'(L4)E-P4 (L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-P3'(L3)e-
activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                        Length 36;
                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                         82.1%; Score 156; DB 21;
88.9%; Pred. No. 4.5e-12;
                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17296 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                          Local Similarity 88.9 hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                  36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000.
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17296;
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
        SSSSSSXS
                                                                                                                                                                                                                                                                                                                                                                                                                QQ
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SSSSSXS

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The present invention describes composition of matter (I) comprising an Fe domain, pharmacologically active peptides, and linkers. Where (I) is:
Fe domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a *F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3.

(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 = are each independently sequences of where P1, P2, P3, and P4 = are each independently independently linkers; and a prince of a not bis 1. The composition can one of the present invention can activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are be used for producing pharmaceutical compositions are compared in the present invention can be used for producing pharmaceutical compositions are compared in the present invention are compared for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer of the present invention in the present invention and possibly placental transfer. AAA69443 and binding, complement fixation, and possibly placental transfer. AAA694443
                                                                                                                                                                                                      ij
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, minetic; IL-1; TNF; antagonist; mMNF; inhibitor; erythropoietin; thrombopoietin; interleukin 1, cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                      ;
9
                                                                                                                                                         Score 155; DB 21; Length 42; Pred: No. 6.9e-12; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                  1 IEGPTLRQCLAARA-----GGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                            TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                            AAB17292 standard; Peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371.
                                                                                                                                                                       81.6%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                 Best Local Similarity 81.03
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17292;
                                                                                                                                    Seguence
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                AAB17292
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to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                               1; Gaps
                                                                     DB 21; Length 35;
                                                            Score 151.5; DB 21, --
ored. No. 1.5e-11;
                                                                                                                         1 IEGPTLRQCLAARAGGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                       0; Mismatches
                                                                                                                                                                                      Search completed: October 9, 2002, 08:58:57
Job time : 17.1874 secs
                                                                          79.78;
                                                                                                     33; Conservative
                                                                            Query Match
Best Local Similarity
                                                   Sequence 35 AA;
                                                                                                          Matches
                                                                                                                                                           g
                  22 X 8
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October 9, 2002, 08:55:27; Search time 5.98595 Seconds (without alignments) 146.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                        231628
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/Aa_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/fB_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                   1 IEGPTLRQCLAARAGGGGGGGGGTEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                              US-09-422-838C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                    Run on:
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Description	Sequence 27, Appl Sequence 27, Appl Sequence 31, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 13, Appli Sequence 13, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 18, Appl Sequence 11, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 11, Appl
SUMMARIES . ID	US-09-352-159-27 US-09-352-159-27 US-09-352-158-31 US-08-352-168-31 US-08-987-466-4 US-09-240-359-4 US-09-100-664A-4 US-09-100-664A-4 US-09-100-664A-4 US-08-100-664A-4 US-08-100-664A-4 US-08-100-664A-4 US-08-100-664A-4 US-08-100-664A-4 US-08-100-664A-4 US-08-100-64A-4 US-08-100-133 US-09-244-298A-193 US-09-244-298A-193 US-09-516-704-193 US-09-516-704-193 US-09-516-704-185 US-08-764-640-17 US-08-764-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-17 US-09-244-298A-185 US-09-516-704-185 US-09-516-704-18
Length DB	99911 111966 5884 5884 6440 7884 7440 7440 7440 7440 7440 7440 7
% Query Match Le	33.0 34.0 35.0
Score	2444 4444 7 • • • • • • • • • • • • • • • • • • •
Result . No.	100 100 100 100 100 100 100 100 100 100

Sequence 232, App Sequence 18, Appl Sequence 194, Appl Sequence 220, App Sequence 194, Appl Sequence 194, Appl Sequence 232, Appl Sequence 232, Appl Sequence 57, Appl Sequence 27, Appl Sequenc	Polypeptides and Methods of Use	4; Length 991; 7; Indels 1; Gaps 1; Polypeptides and Methods of Use
2 US-08-764-640-232 3 US-08-973-225-18 3 US-08-973-225-194 3 US-08-973-225-220 3 US-09-244-298A-194 3 US-09-244-298A-194 3 US-09-244-298A-194 3 US-09-516-704-194 4 US-09-516-704-194 4 US-09-516-704-194 5 US-08-424-826A-57 2 US-08-424-826A-57 2 US-08-424-826A-57 2 US-08-224-936-57 2 US-08-244-941-2 2 US-08-447-642-2 4 US-08-244-941-2	ALIGNMENTS 59A Amine Oxidase es and Related /352,159A 2,936 5,391 sion 3.0	smatches; smatches occupance of the control occupance oc
28 60 31.6 16 30 60 31.6 16 31 60 31.6 16 32 60 31.6 16 33 60 31.6 16 34 60 31.6 16 35 60 31.6 16 37 60 31.6 16 38 59.5 31.3 126 40 59.5 31.3 126 44 59.5 31.3 969	7, Application 6211434 6211434 1 Duvick, Jourse, Joursell, J	Query Match Best Local Similarity 54.2%; pred Matches 13; Conservative 3; Mi OY 3 GPLLRQCL-ARRAGGGGGGGIEG 25 Db 503 GPSIPPCADGAKAGGGGSGGGGSG 526 RESULT 2 US-09-352-168-27 Sequence 27, Application US/09352168A; Patch No. 6211435. APPLICANT: Crasta, Oswald R. APPLICANT: Crasta, Oswald R. APPLICANT: Crasta, Oswald R. APPLICANT: Gliliam, Jacob T. APPLICANT: Gliliam, Jacob T. APPLICANT: Gliliam, Jacob T. APPLICANT: Gliliam, Jacob T. APPLICANT: AINEWATION: AMINO POLYON AMILE OF INVENTION: AMINO POLYON AMILE OF INVENTION: AMINO POLYON AMILE SEFERENCE: 0875

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7; Indels 1; Gaps
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31.9%; Score 64.5; DB 4; Length 1196;
31 Similarity 54.2%; Pred. No. 6.1;
13; Conservative 3; Mismatches 7; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fisher, Douglas A. APPLICANT: Gooding, Doug APPLICANT: Streeter, Dave TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3114 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS Windows Version 2.0 SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/987,466 FILLING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                     108 GPSIPPCADGAKAGGGGSGGSGG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08987466 ; Sequence 4, Application US/08987466 ; Patent No. 5922595 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 ALRAGGGGGGGGGMAPRTGGC 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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CLONE: 829179
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                               TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-987-466-4
                                                                                                   SEQ ID NO 31
LENGTH: 1196
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                                                                                                                                                                                          US-09-352-168-31
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US-08-987-466-4
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GENERAL INFORMATION:
APPLICANT: DUVLCK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Joyce R.
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polyoucleotides and Methods of Use
FILE REFERENCE: 1999-07-12
CURRENT FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
SAFLIER PILING DATE: 1999-05-21
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Crasta, Oswald R.
APPLICANT: Davick, Jonathan P.
APPLICANT: BULLORY: Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
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                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.2%; Pred. No. 5.1; Matches 13; Conservative 3; Mismatchon
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                                  CURRENT APPLICATION NUMBER: US/09/352,168A
                                                  CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 991
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; Sequence 31, Application US/09352159A
; Patent No. 6211434
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; LOCATION: (1)...(24)
US-09-352-168-27
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                                                                                                                                                                                                                                           ORGANISM: Unknown
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUGSTIN
APPLICANT: BLCB, JUGSTIN
APPLICANT: PICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
            Sequence 4, Application US/09240359; Patent No. 6255456; GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A. APPLICANT: Gooding, Doug APPLICANT: Streeter, Dave TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,466
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Patent No. 6057129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AARAGGGGGGGGIEGPTLRQC 31
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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CLONE: 829179
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                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                    94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
JS-09-240-359-4
                                                                                                                                                                                                                                                                    COUNTRY:
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0; Gaps
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Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: PICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.6%; Score 62; DB 3; Length 440; 55.0%; Pred. No. 4.4; 7; Indels tive 2; Mismatches 7; Indels
                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Vers CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/100,664A FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JGACKSON ESQ., DAVIG A. REGISTRATION NUMBER: 26,742
REPERBUCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26,742
RRR: 600-1-221
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19-JUN-1998
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 201-5...
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 PERRPSIRMRQGGGGGGGV 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
Hackensack
New Jersey
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CLASSIFICATION:
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                                   COUNTRY:
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US-09-100-664A-3
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US-08-764-640-13
                                                                                           US-08-764-640-13
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APPLICANT:
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                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLOSS, BRIAN
APPLICANT: BRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                             32.6%; Score 62; DB 3; Length 440; 55.0%; Pred. No. 4.4; 7; Indels tive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 43.3
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/CDCKET NUMBER: 600-1-221
RELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-580
TELEX: 201-487-580
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFINAL APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/100,664A
FILLING DATE: 19-JUN-1998
CINCATTORION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09100664A Patent No. 6057129
                  TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                                                           403 PERRPSIRMROGGGGGGG 422
                                                                                                                                                                                                                                                                                                                        4 PTLRQCLAARAGGGGGGGI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 440 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.0v
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                           Best Local Similarity 55.0 Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Jersey
: USA
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                                                                                                                                  amino acid
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                                                                                                                                    TYPE:
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Gaps
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 2; Length 14;
Pred. No. 0.25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                        Schatz, Peter J.
Balasubramanian, Palaniappan
Bagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 193, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; Sequence 13, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                                                                                                                                                                                Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                            Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.6%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T
REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.9
Watches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1
                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Matches
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                              TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 60; DB 2; Length 14; 92.9%; Pred. No. 0.25; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/764,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSES:
GLACO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                             STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERRECE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                         Deprince, Randolph B.
Podduturi, Surekha
Gates, Christian
                                                                                                                                                                                                                                 Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-764-640-193
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                   Yin, Qun
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                              27709
                                                                                                                                                                                                                               ADDRESSEE:
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-973-225-13
                                    APPLICANT:
                                                                       APPLICANT:
                                                                                         APPLICANT:
                                                                                                             APPLICANT:
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                        STATE:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.6%; Score 60; DB 3; Length 14; Best Local Similarity 92.9%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                     ATORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/COCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 193, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLROCLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NC
  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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0; Mismatches

Matches 13; Conservative

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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gates, Christian
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Schatz, Peter J.
APPLICANT: Schatz, Peter J.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 3; Length 14; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-08-973-225-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: HIUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09244298A Patent No. 6121238
TELECOMMUNICATION INFORMATION:
                                    INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Five Moore Drive, P. CITY: Research Triangle Park
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92.9%;
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Best Local Similarity 92.9%;
Matches 13; Conservative C
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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Best Local Similarity
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COUNTRY: US!
ZIP: 27709
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CORRESPONDENCE ADDRESS:
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APPLICANT: Barrett, Ronald W.
APPLICANT: CWirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendien, Richard W.
                                                                                                                                       ; Sequence 193, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REPERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
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Best Local Similarity 92.9
Matches 13; Conservative
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                                     1 IEGPTLROWLAARA 14
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                                                                                                                            US-09-244-298A-193
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Deprince, Randolph B.
Podduturi, Suresha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 60; DB 4; Length 14; 92.9%; Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                   ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                     Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
RERERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ. ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
TOPOLOGY: linear
WOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                         CITY: Research Triangle Park
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Podduturi, Surekha
                                                                                                   Hendren, Richard W.
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Patent No. 6251864
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Cwirla, Steven E.
                    Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                              NUMBER OF SEQUENCES: 244
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                    USA
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 60; DB 4; Length 14; 92.9%; Pred. No. 0.25; tive 0; Mismatches 1; Indels
                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <unreselected to the control of the control
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-516-704-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
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Balasubramanian, Palaniappan
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.

    Sequence 17, Application US/08764640
    Patent No. 5869451
    Patent No. 5869451

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STRANDEDNESS: <Unknown>
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research Triangle Park
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Cwirla, Steven E.
Gates, Christian
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Five Moore Drive,
                                                                                                                                                       COMPUTER READABLE FORM:
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Best Local Similarity 92.99
Matches 13; Conservative
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MEDIUM TYPE: Floppy of
                                                                                USA
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                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
US-08-764-640-17
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APPLICANT:
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 185, Application US/08973225A
                                                                                                                                                                                                                                                                                                                     APPLICANT: Dower, William J.
APPLICANT: Dower, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                           ; Sequence 17, Application US/08973225A; Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                           Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
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, MOLECULE TYPE: peptide US-08-764-640-185
                                                                                                                                  1 IEGPTLROCLAARA 14
                                                                                                                                                                      2 IEGPTLROWLAARA 15
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APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                   31.6%; Score 60; DB 2; Length 15; 92.9%; Pred. No. 0.27;
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Research Triangle Park

 Mismatches

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Balasubramanian, Palaniappan
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                                                         NAME: Hrubiec, Robert T.
REGESTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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ZIP: 27709

COMPUTER READABLE FORM:
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LENGTH: 15 amino acids
                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                     linear
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APPLICANT: DOWER,
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
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31.6%; Score 60; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.27;
Matches 13; Conservative 0; Mismatches 1; Indels
31.6%; Score 60; DB 2; Length 15; 92.9%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                          Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOLETIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-08-973-225-185
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Balasubramanian, Palaniappan
                                                                                                                                                                           Schatz, Peter J. Magstrom, Christopher R.
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                    Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                               APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwila, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
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LENGTH: 15 amino acids
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 232
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Best Local Similarity 92.99
Matches 13; Conservative
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              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              STATE: NC
Patent No. 6083913
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Gaps
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 3; Length 15;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                     ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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               E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/244,298A
FILLING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HINDIEC, RODERT T
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wagstrom, Christopher R. Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 185, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deprince, Randolph B.
Podduturi, Surekha
                                                     Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%;
92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                             USA
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                   ADDRESSEE:
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APPLICANT:
                                                                                             COUNTRY:
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                                   STREET:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.6%; Score 60; DB 4; Length 15; 92.9%; Pred. No. 0.27;
                                                                              31.6%; Score 60; DB 4; Length 15; 92.9%; Pred. No. 0.27;
                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
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                                                                                                                          0; Mismatches
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3281 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                 Sequence 185, Application US/09516704; Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 244
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COMPUTER READABLE FORM:
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hes 13; Conservative
                                                                                                                               Conservative
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                                                                                    Query Match
Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                  US-09-516-704-185
                                          US-09-516-704-17
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

FILING DATE: 01.Mar-2000

CLASSIFICATION - CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 60; DB 3; Length 15; 92.9%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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NAME: HUDLAC, ROBERT T.
REGISTRATION NUMBER: 36,332
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
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Hendren, Richard W.
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    APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                   PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                       NAME: Hrubiec, Robert T
REGISTRATION UNDRER: 36,392
REPERENCE/DOCKET UNDRER: PK328
TELECOMMUNICATION INFORMATION:
TELEHONE: 919-248 1.000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
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                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-244-298A-185
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                          linear
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US-09-516-704-17
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Schatz, Peter J.
Balasubramanian, Palaniappan
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APPLICANT:
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APPLICANT:
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                APPLICANT
                                     APPLICANT
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                                                                                                                                                                                                                                                                    APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 2; Length 16; Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUBICC, NUMBER: 9K,392
RECISTATION NUMBER: 9K,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 15
; OTHER INFORMATION: /product= "Beta-ala"
US-08-764-640-18
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                                                                                                                                                              Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
         Sequence 18, Application US/08764640
Patent No. 5869451
Patent No. 5869451
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Cwilla, Steven E.
APPLICANT: Cwilla, Steven E.
APPLICANT: Cwilla, Steven E.
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palania
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Patent No. 5869451
Patent No. 5869451 5837683
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.(
CITY: Research Triangle Park
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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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US-08-764-640-18
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.6%; Score 60; DB 2; Length 16; 92.9%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                       ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dower, William J.

Barrett, Ronald W.

CWilla, Steven E.

Gates, Christian
Schatz, Peter J.

Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
Hendren, Richard W.
Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 233, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451
                 Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                     Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-194
                                                                                                                                                                                                                                                                                                                  ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IEGPTLRQWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROCLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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REFERENCE/DOCKET NUMBER: PK3065USW
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                 NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Curla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                        LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 232
                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                       LOCATION: 15
OTHER INFORMATION:
                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
US-08-973-225-194
                                                                                                                                                                                                                                                                                                                   US-08-973-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagstrom, Christopher R. Wrighton, Nicholas C. Wrighton, Nicholas C. TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%; Score 60; 92.9%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08973225A
Patent No. 6083913
CENERAL INFORMATION:
APPLICANT: DOWER, William J.
Barrett, Ronald W.
CWILLA, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheapkis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HTUDIGC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/POCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHORE: 919-248 1-000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.6
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQCLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IEGPTLROWLAARA 15
                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-764-640-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
US-08-973-225-18
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Gaps
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                    31.6%; Score 60; DB 3; Length 16; 92.9%; Pred. No. 0.29;
                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
/product= "Beta-ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEFENDEN: 319-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      0; Mismatches
                          SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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0;

0; Gaps

Search completed: October 9, 2002, 09:06:32 Job time : 6.98595 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:54:17; Search time 8.09368 Seconds (without alignments) 427.397 Million cell updates/sec Run on:

Perfect score:

US-09-422-838C-28 190 1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* 3 8 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	laccase (EC 1.10.3	(EC 1.10	tical		homeotic protein H	insulin precursor	insulin precursor	hypothetical 20.2K	probable nuclear a	hypothetical prote		١.	hypothetical prote	`	hflx protein - Myc		5			×	protocadherin 68 -	probable HflX - My	glycine-rich RNA-b	probable membrane	transforming prote	hdc protein - frui	-		ij
SUMMAKIES	ΙD	KSNCLO	KSNCLT	T48099	T20961	A53662	INSH	IPBO	JQ1094	B45344	T26807	T26808	S65543	T47772	G87033	S72938	T13690	MWAXIC	T06612	T49792	S57795	T09055	D70505	S71779	869312	S20099	S58064	T13386	E96495	B39490
	DB	7	٦	7	7	7	-	-	7	_	7	7	~	7	7	~	7	Н	7	7	7	7	7	7	7	7	7	7	7	7
	Length	619	619	199	200	403	11	105	201	1733	331	333	777	434	488	518	806	1168	339	201	867	889	495	167	285	323	649	1325	443	487
ф	Query Match	38.4	38.4	35.8		34.5	34.2	34.2	34.2	33.9	33.7	33.7	33.7	33.4	33.2	33.2		33.2	32.9	32.6	32.6	32.6	32.1	31.6	31.6			31.6		31.3
	Score	73	73	89	S	65.5	65	65	O	64.5	64	64	64	63.5			63	63	62.5	62		62	61	09	9	9	9	09	59.5	59.5
	Result No.	1	2	m	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain TS) N;Alternate names: urishiol oxidase

7 RQCLAARAGGGGGGGGIEGPTLRQC 31

q Qγ

RESULT 2 KSNCLT

subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	subtilisin-like pr	hypothetical prote	qlycine-rich RNA-b	RNA-binding glycin	hypothetical prote	unknown protein F2	heterogeneous ribo	helix-loop-helix t	qlycine-rich prote	hypothetical prote	hypothetical prote	نب	
JC2191	JC55/I	A39490	JC5570	H95992	S41773	S59529	н85067	C36690	835500	JC6087	T49109	B71260	F96624	KRHU0	T13926
- - σ	7	-	C)	7	7	~	~	~	-	~	7	7	7	Н	~
652	706	696	975	102	165	165	250	298	346	367	396	517	543	593	1428
31.3	34.3	31.3	31.3	31.1	31.1	31.1	31.1	31,1	31.1	31.1	31.1	31.1	31.1	31.1	31.1
	n.	9.5	59.5	59	29	29	59	59	59	59	59	59	29	59	29
59.5	0	S	٠.												

ALIGNMENTS

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A; Introns: 86/3
C; Superfamily: laccase
C; Seupords: cooper; all voprotein; oxidoreductase
C; Seupords: cooper; all voprotein; oxidoreductase
C; Seupords: cooper; all vopertide *status predicted <PRO>
F; 22-49/Domain: signal sequence *status predicted <PRO>
F; 22-49/Domain: propeptide *status predicted <PRO>
F; 31-500 main: mindle beta-barrel *status predicted <BB1>
F; 316-372/Domain: middle beta-barrel *status predicted <BB2>
F; 318-500 main: carboxyl-terminal beta-barrel *status predicted <BB3>
F; 319-500 main: carboxyl-terminal beta-barrel *status predicted <BB3>
F; 319-500 main: carboxyl-terminal beta-barrel *status predicted <BB3>
F; 319-500 main: carboxyl-terminal beta-barrel *status predicted <BB3>
F; 3144-480/Binding site: copper (His) (type 2) *status predicted F; 146,189,191,482,548,550/Binding site: Coulo cluster (His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (type 1) *status predicted *B; 477,549,554/Binding site: copper (His, Cys, His) (ty
                                                                                                                                                                                                                                                                                                  C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999 C;Accession: A28523; A29762 R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K. J. Blol. Chem. 263, 885-896, 1988 A;Tile: Characterization of two allelic forms of Neurospora crassa laccase. Amino- a A;Reference number: A28523; MUID:88087214 A;Accession: A28523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 379-619 <GE2>
A;Cross-references: GB:M14554; NID:g168823; PIDN:AAA33590.1; PID:g168824
C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:M14554
R;Germann, U.A.; Lerch, K.
R;Germann, U.A.; Lerch, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A;Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospor A;Reference number: A29762; MUID:87067412
A;Accession: A29762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                      laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                    C; Species: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-619 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
RESULT 1
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A; Molecule type: protein
A; Residues: 1-30;57-77 <BRO>
R; Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4871, 197
A; Title: Determination of the amino acid sequence of the monkey, sheep, and dog proin
A; Reference number: A32111; MUID:72258016
A; Accession: S16431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 1-403 <HBA.
A,Cross-references: GB:U07663
A,Note: the nucleotide sequence and conceptual translation as given are self-consiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A; Title: A novel human homeobox gene distantly related to proboscipedia is expressed
A; Reference number: A53662; MUID: 94327547
                                                                                                                                                                     A;Cross-references: EMBL:278013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5 A;Experimental source: clone F15B9 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Ovis Orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: A53662
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A;Map position: 1q41-1q42.1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

34.7%; Score 66; DB 2; Length 500;
Best Local Similarity 56.5%; Pred. No. 5.5;
Matches 13; Conservative 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                        A.Gene: CESP:F15B9.5
A.Map position: 5
A.Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
                               A;Accession: T20961
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: S16430; S16431
R;Brown, H.; Sanger, F.; Kitai, R.
Biochem. J. 60, 556-565, 1955
A;Title: The structure of pig and sheep insulins. A;Reference number: A90344
A;Accession: S16430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LAARA---GGGGGGGGGIEGPTLRQCLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPTLRQCLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homeotic protein HB9 - human
   A; Reference number: Z19351
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                                                                                                                      A; Molecule type: DNA
A; Residues: 1-500 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A53662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: HLXB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 30-Sep-191 #sequence_revision 30-Sep-1991 #text_change ll-Jun-1999
C;Accession: B28523; Muller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A;Reference number: A28523; MulD:88087214
A;Accession: B2853
A;Accession: B28533
A;Accession: B2853
A;Accession: B28533
A;Accession: B2853
B;Accession: B28533
A;Accession: B28533
A;Accession: B28533
B;Accession: B28533
B;Accession: B285334
A;Accession: B28534
B;Accession: B28524
B;Accession:
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Orapr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C; Accession: T48099
R; Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24484
A; Accession: T48099
A; Accession: Preliminary
A; Residues: 1-199 cobs>
A; Residues: 1-199 cobs>
A; Residues: 1-199 cobs>
A; Cross-references: EMBL: Al163816
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20961
F;Percy, C.
Submitted to the EMBL Data Library, August 1996
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.8%; Score 68; DB 2; Length 199; Best Local Similarity 34.8%; Pred. No. 1.5; Matches 16; Conservative 3; Mismatches 11; Indels
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A; Map position: 3
A; Introns: 163/2
A; Note: T20010.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ROCLAARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 RODSOAERYGGGGGGGCCNSPINROC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.4'
Best Local Similarity 60.0'
Matches 15; Conservative
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A,Title: Existence of a molecular ruler in proteasomes suggested by analysis of degra A, Reference number: S46258; MUID:94326921
A; Accession: S46258
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A;Residues: 1-201 <ROT>
A;Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
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C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C.Accession: B45344
R.Vicology 179, 365-377, 1990
A.Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented
A.Reference number: A45344; MUID:91021039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191094
hypothetical 20.2K protein - tomato ringspot virus
C; Species: tomato ringspot virus
C; Species: tomato ringspot virus
C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C; Accession: J01094
R; Roctt, M.E.; Tremaine, J.H.; Rochon, D.M.
J; Gen. Virol. 72, 1505-1514, 1991
A; Title: Nucleotide sequence of tomato ringspot virus RNA-2.
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A; Residues: 25-54 <WEN>
C; Superfamily: insulin
C; Keywords: hormone; pancreas
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-54 Ownain: insulin chain B #status experimental <BCH>
F; 25-54 85-105/Product: insulin #status experimental <BCH>
F; 57-82/Domain: connecting peptide #status experimental <CREP>
F; 85-105/Domain: insulin chain A #status experimental <CREP
F; 31-91,43-104,90-95/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 34.2%; Score 65; DB 1; Length 105; Best Local Similarity 41.0%; Pred. No. 1.8; Matches 16; Conservative 4; Mismatches 11; Indels
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                                                                                                              A;Status: preliminary
A;Status: preliminary
A;Molecule type: protein
A;Residucs: 25-30, X',32-42, X',44-54 <CH2>
B;Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai, R.
Biochem. J. 60, 541-556, 1955
A:Title: The disulphide bonds of insulin.
A;Reference number: A90343
A;Contents: annotation; amides; disulfides
R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 VEGP---QVGALELAGGPGAGGLEGPPQKRGIVEQCCAS 93
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Best Local Similarity 61.58
Matches 16; Conservative
                                  A; Molecule type: protein
A; Residues: 85-105 <CHE>
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                                                                                              A; Accession: S48185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C;Accession: A40909; A92080; A92074; A91185; A90342; A90341; S48184; S48185; S46258; A01
R;D'Agostino, J.; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.
A;Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 85-105 <SAN>
R;Sanger. F.; Tuppy, H.
Biochem. J. 49, 481-490, 1951
A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigat
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Blochem. J. 53, 366-374, 1953
A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of
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Bur. J. Biochem. 20, 183-189, 1971
A;Title: Bovine proinsulin: amino acid sequence of the C peptide isolated from pancreas.
A;Reference number: A91185; MUID:71257721
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Bur. J. Biochem. 223, 759-764, 1994
A:Title: Site-specific oxidation of histidine residues in glycated insulin mediated by
A;Reference number: S48184; MUID:9433378
A;Accession: S48184
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A.Residues: 25-105 <NOL>
R.Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
J. Biol. Chem. 246, 1365-1374, 1971
A.Fitle: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A.Reference number: A92074; MUID:71116409
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                        F.1-30,57-77/Product: insulin #status experimental <MAT>
F.31-56/Domain: connecting peptide #status experimental <CPEP>
F.57-77/Domain: insulin chain A #status experimental <ACH>
F.57-77/Domain: insulin chain Estatus experimental <ACH>
F.7-63,19-76,62-67/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                      34.2%; Score 65; DB 1; Length 77; 44.4%; Pred. No. 1.4; tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                  C;Keywords: hormone; pancreas
F;1-30/Domain: insulin chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson, J.D.; Steiner, D.F.
                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQCLAARAGGGGGGGGGEGP---TLRQCLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                 32 VEGP---QVGALELAGGPGAGGLEGPPQGIVEQCCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The structure of bovine proinsulin. A;Reference number: A92080; MUID:71166442 A;Accession: A92080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Nolan, C.; Margoliash, E.; Petersc
J. Biol. Chem. 246, 2780-2795, 1971
                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin precursor - bovine
                                                                                                                                                                                                                                                                                                  Best Local Similarity
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A; Residues: 57-82 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 57-82 <SAL>
A; Residues: 31-56 <PET>
                         C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-105 <DAA>
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                                                                                                                                                                                                                                                                   Query Match
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Matches
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Y41C4A.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
R;Steward, C.
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                                                                                                                                                                                                                              Gaps
                                                      A;Molecule type: DNA
A;Residues: 1-1733 <-VLC>
A;Crostdues: 1-1734 <-VLC>
A;Cross-references: GB:M34651; NID:g334070; PIDN:AAA47471.1; PID:g334072
C;Superfamily: pseudorabies virus 1 nuclear antigen
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rostdues: 1-331 < WILD-
A;Cross-references: EMBL:AL032627; PIDN:CAB54381.1; CESP:Y41C4A.4a
A;Experimental source: clone Y41C4A
                                                                                                                                                                    Score 64.5; DB 1; Length 1733; Pred. No. 23;
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33.7%; Score 64; DB 2; Length 333;
Best Local Similarity 76.9%; Pred. No. 6.3;
Matches 10; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Db 1645 GPSPRGCRGAGRAGGGGRGGCGGGRAPGAAGGPGLCRCECCR 1686
                                                                                                                                                                                                                                                                                 3 GPTLRQCL-AARAGGGGGG-----GGIEGPTLRQCLAAR 35
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A;Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C;Superfamily: fos/jun DNA-binding domain homology
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A;Gene: CESP:Y41C4A.4a
A;Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C;Superfamily: fos/jun DNA-binding domain homology
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                                                                                                                                                                               33.9%;
Best Local Similarity 42.9%;
Matches 18; Conservative
                    A; Status: translation not shown
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A; Accession: B45344
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hypothetical protein F2413.200 - Arabidopsis thaliana (Sispecies: Arabidopsis thaliana (mouse-ear cress) (Sispecies: Arabidopsis thaliana (mouse-ear cress) (Sispecies: Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (Sispecies: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 Sispecies: 20: Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M. Submitted to the Protein Sequence Database, February 2000 A; Reference number: 224475
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A;Gene: Flyasae:Hggn0000479
A;Cross-references: FlyBase:FBgn0000479
A;Cross-references: FlyBase:FBgn0000479
A;Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3
A;Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 262/3; 294/1; 407/3; 496/2; 534/2; 588/3
A;Introns: 93/2; 125/3; 152/2; 165/2; 200/2; 200/2; 204/1; 407/3; 496/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 534/2; 
3/5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form I 3/5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form III N; contains: 3',5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form III C; Species: Drosophila melanogaster C; Date: 28-oct-1995 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000 C; Date: 28-oct-1995 #sequence_revision 19-Jul-1996 #text_change 17-Nov-2000 C; Accession: S65543; S19662; S65542; S65544; A26651 R; Oiu, Y; Chen, C.N.; Malone, T.; Richter, L.; Beckendorf, S.K.; Davis, R.L. J. Mol. Biol. 222, 553-565, 1991 memory gene dunce of Drosophila melanogaster. A; Areference number: S19662; MuID:92085274
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Proc. Natl. Acad. Sci. U.S.A. 83, 9313-9317, 1986
A;Title: Molecular analysis of cDNA clones and the corresponding genomic coding seque A;Reference number: A26651; MUID:87092243
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A;Residues: 416-777 <CHE>
A;Cross-references: GB:M14982; NID:9157278; PIDN:AAC34201.1; PID:9157280
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A;Cross references: EMBL:X55174
A;Molecule type: DNA
A;Residues: 137-77 <012>
A;Crossion: S6542
A;Accession: S6554
A;Accession: S6542
A;Molecule type: DNA
A;Molecule 
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                                                   A; Experimental source: cultivar Columbia; BAC clone F2413
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A; Residues: 'MVCSFCCCCINFRN', 4, 'P', 6, 'S', 94-777 <Q14>
A; Cross-references: EMEL: X55174
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A; Cross-references: EMBL: AL138655
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A; Residues: 1-434 <NYA>
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A; Residues: 1-777 <QIU>
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Gaps

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Nicontains: myosin ATPase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Datcis: 30-68p-1990 #sequence_revision 30-Sep-1990 #text_change 19-Jan-2001
C;Accession: A33891; A24448; A24146
R;Jung, G; Korn, E.D.; Hammer III, J.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 6720-6724, 1987
A;Title: The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like and non a;Reference number: A33891; MUID:88016163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: this gene and protein are called WiB in this paper. Fib. 31.000.
R; Brzeska, H; Lynch, T.J.; Martin, B.; Korn, E.D.
J. Biol. Chem. 264, 19340-19348, 1989
A; Title: The localization and sequence of the phosphorylation sites of Acanthamoeba m A; Reference number: A34448; MUID:90037074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: protein
A; Residues: 308-314, 'x', 316-329 <BRZ>
C; Comment: In this protein, the coiled-coil rod-like region found in many myosin heav
he protein is globular and does not self-associate into filaments.
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-806 <MOR>
A;Cross-references: EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA21318.1
                         A;Residues: 1-1168 <JUN>
A;Cross-references: GB:J02974; NID:9155624; PIDN:AAA27707.1; PID:9155625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;983-1030/Domain: SH3 homology <br/>SH3><br/>F:1034-1168/Region: alanine/glycine/proline-rich<br/>F:107/Binding site: ATP (Lys) #status predicted<br/>F:311/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                       33.2%; Score 63; DB 2; Length 806; 54.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1168;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myosin heavy chain IC - Acanthamoeba castellanii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:923-978/Region: alanine/glycine/proline-rich
                                                                                                                                                                                                                                                                                               A;Cross-references: FlyBase:FBgn0025833
                                                                                                                                                                                                                                                                                                                    A:Introns: 37/3; 448/3; 611/2; 690/3
A:Note: EG:EG0003.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 GGGGGGGGGASITQAIAQAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920 QILGAKGGGGGGGGRGRGGPS 939
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                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 54.59
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                     probable ATP/GTP-binding protein [imported] - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Accession: G87031
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Devlin, K.M.
R; Davies, R.M.; Novin, R.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schife: Massive gene decay in the leprosy bacillus.
A; Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Start codon: GTG
C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-448 <STO>
A; Cross references: GB:AL450380; NID:913093026; PIDN:CAC31378.1; GSPDB:GN00147
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N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                   Gaps
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Residues: 1-518 <SMI>
Cross-references: EMBL:U00019; NID:9467079; PIDN:AAA17274.1; PID:9467091
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                  DB 2; Length 434;
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                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.2%; Score 63; DB 2; Length 488; 45.8%; Pred. No. 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B2235.
A:Reference number: $72587
A:Referencession: $772938
A:Status: preliminary
                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                       Pred. No. 9;
             33.4%; Score 63.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.2%; Score 63; DB 45.8%; Pred. No. 12;
                                                                                                                                      161 RVGGGGGGGDHIYLVYEYVNGASLADCL 189
                                                                                          13 RAGGGGGGG-----IEGPTLRQCL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                44.88;
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Best Local Similarity 45.00,
Thes 11; Conservative
                                                     Conservative
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R; Smith, D.R.; Robison, K.
Query Match
Best Local Similarity
Matches 13; Conserv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: G87033
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: ML0997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                RESULT 14
G87033
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C;Genetics;
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Gaps

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Gaps

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Length 867; 9; Indels

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A;Molecule type: mRNA
A;Residues: 1-867 <SMW>
A;Cross-references: EMBL:L07561; NID:g945420; PIDN:AAC37438.1; PID:g945421
                                                                                                                                                                                  A;Gene: CPH1
A;Introns: 34/3; 159/2; 210/3; 265/3; 329/3; 406/1; 837/3
C;Keywords: carbon-carbon lyase; photoreceptor
                                                                                                                                                                                                                                                                                                                 32.6%; Score 62; DB 2; 50.0%; Pred. No. 24; atlive 2; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPTLRQCLAARAGGGGGGGGGIEGP 26
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Neurospora crassa
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Accession: T49792
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A; Reference number: Z25022
A; Accession: T49792
                                                                                                                                              Tybols translated protein F16J13.120 - Arabidopsis thaliana hypothetical protein F16J13.120 - Arabidopsis thaliana (G. Species: Arabidopsis thaliana (Mouse-ear cress) C. Species: Arabidopsis thaliana (Mouse-ear cress) C. Species: Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000 C. Accession: To6612 A. Reference Toff C. A. C. Species: A. Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, Submitted to the Protein Sequence Database, April 1999 A. Reference number: 215789 A. Reference number: 215789 A. Reference number: 215789 A. Residues: 1-339 < REW. A. A. C. Species: 215789 A. Residues: 1-339 < REW. A. C. C. Species: EMBL:ALO49638; GSPDB:GNO0062; ATSP:F16J13.120 A. Residues: 1-339 < REW. A. C. C. Species: C. C. Conerios: EMBL:ALO49638; GSPDB:GNO0062; ATSP:F16J13.120 A. REPS:F16J13.120 A. REPS:F16J1
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A; Residues: 1-201 <SCH>
A; Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.6%; Score 62; DB 2; Length 201; 76.9%; Pred. No. 6.7; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 62.5; DB 2;
52.0%; Pred. No. 9.3;
Live 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11111111: 1: :1:11 | 282 GGGGGGGGGGGPPMMGQQQAMAAMA 306
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 RAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 RGGGGGGGGGVNG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-867 <SMA>
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                                                                                                                       RESULT 18
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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Ateference number: A70500; MuID:98295987
A; Accession: D70505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-495 <CCL>
A;Cross-references: GB:298209; GB:AL123456; NID:g3261838; PIDN:CAB10901.1; PID:e33228
A;Cross-references: GB:298209; GB:AL123456; NID:g3261838; PIDN:CAB10901.1; PID:e33228
A;Csenctics:
A;Genetics:
A;Gene: hflX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable HflX - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
C;Accession: D70505
Cipecians for a special series (man)
Cipacians for a special series (man)
Cipacession: T09055
Ridin, P.; Xu, H.; Israel, D.
Ridin, P.; Xu, H.; Israel, D.
Ridin, P.; Xu, H.; Israel, D.
A; Reference number: 216540
A; Reference number: 216540
A; Recession: T09055
A; Accession: T09055
A; Accession: T09055
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1889 <JINA
A; Residues: EMBL: AF029343; NID: 92599501; PID: 92599502
C; Genetics: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 62; DB 2; Length 889;
57.9%; Pred. No. 24;
tive 1; Mismatches 7; Indels
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R;Weaver, T.A.; White, R.A.
Submitted to the EMBL Data Library, July 1995
A;Description: hdc, an imaginal specific gene required for adult'morphogenesis in Dro
A;Reference number: S58064
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A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: EMBL:AL031581; NID:e1320978; PID:e1320992; PIDN:CAA20886.1
B;Voelker, R.A.; Gibson, W.; Graves, J.P.; Sterling, J.F.; Eisenberg, M.T.
Mol. Cell. Biol. 11, 894-905, 1991
A;Title: The Drosophila suppressor of sable gene encodes a polypeptide with regions salectence number: A39612; MUID:91117256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, D. submitted to the EMBL Data Library, May 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217665
                                                                           A Molecule Lype: DNA
A.Residues: 1-323 < HRA>,
A.Cross-references: EMBL:X60063; NID:962927; PIDN:CAA42665.1; PID:962928
C.Superfamily: Jun transforming protein; fos/jun DNA-binding domain homology
C.Keywords: DNA binding; nucleus; transcription regulation
F:237-277/Domain: fos/jun DNA-binding domain homology <FJD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Drosophila melanogaster
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1998
C;Accession: S58064
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13386; A39612
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                                                                                                                                                                                                                                                                                 DB 2; Length 323;
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                                                                                                                                                                                                                                                                                                                                      5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: 250097; NID: 9902623; PID: 9902624
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C;Genetics:
A;Gene: FlyBase:su(s)
                                                                                                                                                                                                                                                        31.6%; Sco. 72.2%; Pred. No. 10, 72.2%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hdc protein - fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                            151 AAAAGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                             11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.2%
Matches 13; Conservative
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A Molecule type: DNA
A Residues: 1-719,723-1325 <VOE>
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A;Molecule type: mRNA
A;Residues: 1-649 <WEA>
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Matches 10; Conserv
                                                          A; Status: preliminary
                                    A; Accession: S20099
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                                                                                                                       Glycine-rich RNA-binding protein GRP1 - wheat
C.Specios: Triticum aestivum (common wheat)
C.Specios: Triticum aestivum (common wheat)
C.Accession: 571779
C.Accession: 571779
R.Guiltinan, M.J.; Niu, X.
Plant Mol. Biol. 30, 1301-1306, 1996
A.Title: cDNA encoding a wheat (Triticum aestivum cv. Chinese spring) glycine-rich RNA-hAccession: 571779
A.Schoresion: 571779
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-167 <GUID
A.COSS-references: EMBL: U32310; NID: 9974604; PIDN: AAA75104.1; PID: 9974605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U19028; NID:9609380; PID:92340034; GSPDB:GN00012; MIPS:YLR338w
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology F;7-74/Domain: ribonucleoprotein repeat homology <RRM4>
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N;Alternate names: hypothetical protein L8300.13-a
C;Species: Saccharomyces cerevisiae
C;Date: 20-Jul_1996 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transforming protein junD - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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31.6%; Score 60; DB 2; Length 285;
Best Local Similarity 57.9%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 7: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, January 1994
A:Description: The sequence of S. cerevisiae cosmid 8300.
A:Reference number: S69312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Keywords: transmembrane protein
F:142-158/Domain: transmembrane #status predicted <TM1>
F:201-217/Domain: transmembrane #status predicted <TM2>
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R'Hartl, M.; Hutchins, J.T.; Vogt, P.K.
Oncogene 6, 1623-1631, 1991
A; Title: The chicken junb gene and its product.
A; Reference number: S20099; MUID:92019832
205 GESMSRQAGGRAGGSGGGVGLRGP 228
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55.6%;
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236 LPPNAGGGGGGGGAGAPAI 254
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A:Molecule type: DNA
A:Residues: 1-285 <DUZ>
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Substilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form C substilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form C N.Alternate names: kexin-like protease isoform C.Species: Homo sapiens (man) C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000 C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000 C.Accession: JC2191 R.; Hine C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y. R.; Tsuji, A.; Higashine, K.; Hine C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y. R.; Tsuji, A.; Higashine, K.; Hine C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y. R.; Tsuji, A.; Higashine, C.; Mori, C.; Nagamune, H.; Matsuda, Y.; Reference number: JC2191; MUID:94235049 Manna kexin-like proteins of novel CDNAs encoding human kexin-like proteins of a signal peptide, a propeptide, a substilisin-lik C.; Comment: This protein cleaves precursor proteins at dibasic amino acid residues. C.; Genetics: A; Genetics: B; Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 652;
DB 2; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.3%; Score 59.5; D
60.0%; Pred. No. 34;
tive 0; Mismatches
   Match 31.3%; Score 59.5; Di Local Similarity 60.0%; Pred. No. 27; ess. 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 9, 2002, 09:05:07 Job time : 9.09368 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AAGAGGAGGAGGAGFRP-LAPR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AARAGGGGGGGGIEGPTLRQCLAAR 35
                                                                                                                                                      11 AARAGGGGGGGGIEGPTLRQCLAAR 35
                                                                                                                                                                                                                             24 AAGAGGAGGAGGPGFRP-LAPR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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                       Query Match
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                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                               RESULT 30
                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein FBD11.2 [imported] - Arabidopsis thaliana hypothetical protein FBD11.2 [imported] - Arabidopsis thaliana (C.Species Arabidopsis thaliana (Mouse-ear cress) C.Species Arabidopsis Labilana (Mouse-ear cress) C.Species 20-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001 C.Saccession: E96495 M. Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Theologis, B.; Huizar, L. Nature 408, 816-820, 2000 M. E.; Huizar, L. Nature 408, 816-820, 2000 M. S., Liu, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziall, Rizzo, M.; Mu. D.; Yu, G.; Fraser, C.M.; Verter, J.C.; Davis, R.W. Sun, H.; Tallon, A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form B - hum N.Alternate names: subtilisin homolog precursor, short splice form C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-487 <KIE>
A;Note: the lack of a domain necessary for correct folding and activity of other serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J. DNA Cell Biol. 10, 757-769, 1991
A;Tile: Identification of a second human subtilisin-like protease gene in the fes/fps A;Reference number: A39490; MUID:92075167
A;Accession: B39490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE005173; NID: 910092398; PIDN: AAG12804.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
E;196-434/Domain: subtilisin homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
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                                                                                                                                                                             DB 2; Length 1325;
56;
                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: barley pathogen resistance protein Mlo
                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:131390; OMIM:167405
                                                                                                                                                                                             Score 60;
Pred. No.
                                                   A;Map position: X
A;Introns: 92/1; 170/3; 603/2; 645/1
A;Note: EG:115C2.3
                                                                                                                                                                                                     31.6%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1162 GGGGGGGVVLPNLSQ 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                       15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AGGGGGGGG-EGP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A: Residues: 1-443 <STO>
                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: B39490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: E96495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: F8D11.2
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                                                                                                                                                                                                                                                                                        Matches
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100

Gaps

1;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein . protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds Run on:

(without alignments)
324.181 Million cell updates/sec

1 IEGPTLRQCLAARAGGGGGGGGGTEGPTLRQCLAARA 36 US-09-422-838C-28 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 segs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	i neurospor			tomat		was n	P33485 pseudorabie	P01318 ovis aries			acanthe		Q39610 chlamydomon	P93527 sorahim hic		Of1374 ceratitie	drosonhila	2 6			mesoc		O83933 treponema p		m	_	P46390 mycobacteri	_	homo	homo	m sum	rati		
SUMMARIES		O .	LAC1 NEUCR	LAC2 NEITOR	INS BOUTN	YR21 TRCVP		CVV2	MATTA PRINTS	THO CHEES	TNS_SHEEP	CNAL DROME	FXD3_CHICK	MYSC_ACACA	DCO_DROME	DYHA_CHLRE	PHYB_SORBI	JUND_CHICK	SXL_CERCA	SUS_DROME	SOX1 MOUSE	PAC4 HIMAN	BET3 MESAII	EVAN CANA	VORT TARA	7007 INDER	ATCO_DOMAN	TODE THOUSE	ECK_LUCCU	SSB MYCLE	HH3R_HUMAN	EVX2_HUMAN	ONC2_HUMAN	BRN1_MOUSE	BRN1_RAT	BRN1_HUMAN	K1CJ_MOUSE
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æ	Query	Match	38.4	œ	34.2	34.2	4	4	0.00		٠,		2 0	•	,	4.75	ψ,	31.6	_;	Ξ.		31.3				31.1	31 1	31 1	100	0.00	0.00	0.0	0.00	30.5	30.5	30.5	30.5
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Pfam; PF00394; Cu-oxidase; 3. PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.

P54865 cellulomona O54839 wus musculu O55165 rattus norv P25764 oryza sativ Q15911 homo sapien P49842 homo sapien P49842 mus musculu P17656 caenorhabdi P23091 avian muscu P91705 drosophila Q98937 gallus gall	
XYND_CELFI EOMD_MOUSE KF3C_RAT PHYB_ORYSA ABFI_LUMAN ST19, HUMAN CANS_MOUSE CCO_CAREL TMAF_AVISA PER_DROSC FXGA_CHICK	
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644 688 796 1171 3703 369 266 269 369 440	
58 57 57 57 57 57 57 57	
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                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88087214; PubMed=2961749;
MEDLINE=mann U.A., Mueller G., Hunzlker P.E., Lerch K.;
"Characterization of two allelic forms of Neurospora crassa laccase. Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-896(1988).
                                                                        01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFÁCTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
                                                                                                                                                        Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUIAR LOCATION: Secreted (Potential).
-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                 619 AA.
                                                                                                                                                                                     Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A28523; KSNCLO.
PIR; A29762; A29762.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; Multicu_oxidse2.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 379-619 FROM N.A. MEDLINE=87067412; PubMed=2947240;
                                                           01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M14554; AAA33590.1; -.
                             STANDARD;
                             LACL_NEUCR
                                            P06811;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Germann U.A., Mueller G., Hurziker P.E., Lerch K.; Characterization of two allelic forms of Neurospora crassa laccase. Amino- and carboxyl-terminal processing of a precursor."; J. Biol. Chem. 263:885-886(1988).
J. Biol. Chem. 263:885-886(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
  PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Secreted (Potential).
-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                  Score 73; DB 1; Length 619;
pred. No. 0.64;
                                                                                                                                    (TYPE 3) (PROBABLE).
(TYPE 3) (PROBABLE).
(TYPE 1) (PROBABLE).
(TYPE 2) (PROBABLE).
(TYPE 3) (PROBABLE).
(TYPE 3) (PROBABLE).
(TYPE 3) (PROBABLE).
(TYPE 3) (PROBABLE).
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                                                                                                                COPPER (TYPE 2) (PROBABLE)
COPPER (TYPE 3) (PROBABLE)
                                                                                                                                                                                                                                     (PROBABLE)
                                                                                                                                                                                                                                                                                                       LINKED (GLCNAC. . .) (PORDED6D78B65048E3 CRC64;
                                                                                PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                        (GLCNAC.
                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 619 AA.
                                                                                                                                                                                                                                      TYPE 1)
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Urishiol oxidase) (Laccase allele TS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                     COPPER
COPPER
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COPPER
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                                                                                                                                                                                                                                                                                                                                                                               7 RQCLAARAGGGGGGGGIEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                            39 RQDSQAERYGGGGGGGCNSPINRQC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88087214; PubMed-2961749;
                                                                                                                                                                                                                                                                                                                   68198 MW;
                                                                                                                                                                                                                                                                                                                                      38.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                  619 AA;
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                               Glycoprotein;
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P10574;
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the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                             pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                          COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
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COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
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Pred. No. 0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                       PLASTOCYANIN-LIKE 1. PLASTOCYANIN-LIKE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                              PIR; B28523; KSNCLT.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.4%;
60.0%;
                                                                                                                          EMBL; M18334; AAA33592.1; -.
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NCBI_TaxID=9913;
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SIGNAL 1
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619 AA;
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Best Local Similarity
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P01317;
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INS_BOVIN
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Sanger F., Tuppy H.;
"The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";
Biochem. J. 49:481-490(1951).
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MEDLINE-97285914; PubMed=9141131;
MEDLINE-97285914; PubMed=9141131;
Mended Jof London G.G., Edwards D.J., Holden P.H., Whittingham J.L.;
Mended Jof insulin fibrils derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin).";
Proteins 27:507-516(1997).
                                                                                                                                                                                                                                                       "Isolation and characterization of proinsulin C-peptide from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYMTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                Salokangas A., Smyth D.G., Markussen J., Sundby F.;
Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanger F., Thompson E.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";

Biochem. J. 53:366-374(1953).
                                                                                                                                                                                                                            Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D., Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDES, SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS. Ryle A.P., Sanger F., Smith L.F., Kitai R.; "The disulphide bonds of insulin."; Biochem. J. 60:541-556(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DATABASE: NAME-Protein Spotlight;
                            MEDLINE=71166442; PubMed=4928892;
Nolan C., Margoliash E., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The structure of des-Phe bl bovine insulin.";
Acta Crystallogr. B 38:3028-3032(1982).
                                                                                                                                                                                                                                                                                     Biol. Chem. 246:1365-1374(1971).
                                                                                                                                                                                                            MEDLINE=71116409; PubMed=5545080;
                                                                                                                                                                                                                                                                                                                                                                                             J. Biochem. 20:183-189(1971).
                                                                                                                                                                                                                                                                                                                                  MEDLINE=71257721; PubMed=5105368;
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               SEQUENCE OF 25-105.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 85-105.
                                                                                                                                                                                             SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 57-82.
                                                                                                      SEQUENCE OF 25-54
                                                                                                                                                                                                                                                                                                                                                                                from pancreas.";
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                                                                                                                                                                                                                                                                          pancreas.
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Query Match
SIGNAL
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STRAND
                                          PROPEP
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                                                                    CHAIN
                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M54979; AAA30722.1; -.
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PIR; A01585; IPBO.

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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                  Hormone; Glucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 20.2 kba protein in RNA2.
Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 65; DB 1; Length 105; 41.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                        0.96;
-rhes 11; Indels
                                                                                                                                                                                                                                                                                                                                       11393 MW; 75307CF78E61C06A CRC64;
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Rott M.E., Tremaine J.H., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQCLAARAGGGGGGGGIEGP----TLRQCLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN B CHAIN.
                                                                                                                                                                                                  INSULIN A CHAIN. INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 201 AA.
                                                    PDB; 1DPH; 31-CT-93.
PDB; 1PID; 07-DEC-96.
InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                         INTERCHAIN.
                                                                                                                                                                                       C PEPTIDE.
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POLY-GLY.
                                                                                                                          SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Gluc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D12477; BAA02044.1; -.
                                                                                                    PRINTS; PR00276; INSULINA. PRINTS; PR00277; INSULINB.
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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82
82
105
91
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90
             2INS; 31-MAY-84.
1APH; 31-OCT-93.
                               31-OCT-93.
                                            PDB; 1CPH; 31-OCT-93
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66
 A40909; A40909.
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                                                                                                                                                                                                                                                                                                                                       105 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=12281;
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57
31
32
33
33
                                   1BPH;
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BINDING
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                                                                                                                                                                                                                                                                                                         -i SUBCELLULAR LOCATION: Nuclear.
-i TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.
-i TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.
                                           Gaps
                                                                                                                                                                                                                                                          Homeobox; DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches 10; Indels
                       Query Match

34.2%; Score 65; DB 1; Length 201;
Best Local Similarity 61.5%; Pred. No. 1.7;
Matches 16; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0006AEAD71D594FE CRC64;
144 148 POLY-GLY.
201 AA: 20194 MW: 9038506E18D7B450 CRC64;
                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                             401 AA
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POLY-ALA.
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                                                               13 RAGGGGGGGGIE----GPTLRQCLAA 34
                                                                                13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
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EMBL; U07663; AAB60647.1; JOINED.
HSSP; P14653; 1B72.
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                                                                                                                                                                                                                                                  TISSUE-Placenta;
MEDLINE-94327547; PubMed-7914194;
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242 301 HOI
316 325 POI
401 AA; 40932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%;
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                                                                                                                               STANDARD;
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                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                          Homeobox protein HB9
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                HB9_HUMAN
P50219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00986; TRNASYNTHVAL.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYV2_MOUSE STANDARD; PRT; 1263 AA.
092109; 090UN2;
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
16-00T-2001 (Rel. 40, Last annotation valy1-tRNA synthetase 2 (EC 6.1.1.9) (Valine--tRNA ligase 2) (VALRS)
                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                     Rowen L., Madan A., Qin S., Shaffer T., Ratcliffe A., Abbasi N., Dickhoff R., James R., Loretz C., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=BALB/C, AND C57BL/RIJ; TISSUE-Brain;
MEDLINE-99216447; PubMed-10199925;
PRT; 1263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IPR001412; tRNA-synt_I.; IPR002303; tRNA-synt_val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004046; GST_C.
InterPro; IPR004045; GST_N.
InterPro; IPR002300; tRNA-synt_la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF109906; AAC84172.1; EMBL; AF087680; AAD26532.1; EMBL; AF087141; AAD26531.1; HSSP; P96142; 1GAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF109905; AAC84151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00043; GST_C; 1
Pfam; PF02798; GST_N; 1
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:90675; Vars2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTOR 1-GAMMA.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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864
959
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CHAIN
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                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                     MEDLINE=91021033; PubMed=2171211; Vicek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.; Pseudorabies virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1733;
                               Score 65; DB 1; Length 1263;
Pred. No. 7.9;
                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches 13; Indels
  1219 1219 E -> K (IN REF. 2).
1263 AA; 140214 MW; B510E73284FCE26D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OC8CD8BE475BB5E2 CRC64;
                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 1645 GPSPRGCRGAGRAGGGGGGRAPGAAGGPGLCRCECCR 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLRQCL-AARAGGGGGG-----GGIEGPTLRQCLAAR 35
                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                PRT; 1733 AA.
                                                  2; Mismatches
                                                                                                                                                                                                           Pseudorables virus (strain Kaplan) (PRV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64.5;
                                                                      4 PTLRQCLAARAGGGGGGGGGIEGPTLRQCL 32
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                                                                                         14 PSLRALIAARYGEAGDGPGWGGPHPRICL 42
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequ
01-FEB-1994 (Rel. 28, Last anno
Probable nuclear antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1733 AA; 172166 MW;
                              34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M34651; AAA47471.1; -.
                                                                                                                                                                                                                                                                                                                 enhancer regions.";
Virology 179:365-377(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.98;
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                                       Local Similarity 51.7 tes 15; Conservative
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B45344; B45344
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin precursor.
                                                                                                                                                                                                                                         NCBI_TaxID=33703;
                                                                                                                                            VNUA_PRVKA
P33485;
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INS_SHEEP
P01318;
CONFLICT
                              Query Match
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                                                Matches
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                                                                                                                                   VNUA_PRVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ************************************
                                                                                                                      Ohlsen S.M., Lugenbeel K.A., Wong E.A.; "Characterization of the linked ovine insulin and insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 57-82.

MEDLINE=72258016; PubMed=4626369;
Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.;
"Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. BIOL. Chem. 247:4866-4871(1972).
-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AA; 11235 MW; 8B27C7FB9922BC7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQCLAARAGGGGGGGGGIEGP----TLRQCLA 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C PEPTIDE.
INSULIN A CHAIN.
                                                                                                                                                                                                                                                                    Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Blochem. J. 60:556-565(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNAL_DROME STANDARD; PRT; 584 AA. P12252; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, PO1315, 91XNS.
HACFPED, 1PRODO739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINA.
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                                                                                                 MEDLINE=94280618; PubMed=8011164;
                                                                                                                                                                                             DNA Cell Biol. 13:377-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                             SEQUENCE OF 25-54 AND 85-105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00659; AAB60625.1; -.
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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105
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Best Local Similarity
Local 51milarity
                                                                       SEQUENCE FROM N.A.
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                          NCBI_TaxID=9940;
                                                                                                                                                                      factor-II genes.
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DOMAIN 305 310 TO MAMMALIAN REGULATORY SUBUNIT OF TYPE 2

CAMP DEPENDENT PROTEIN KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIFFERENT TRANSCRIPTION START SITES AND SPLICE PATTERNS.
-1- DISEASE: MUTATION OF DUNCE PRODUCES FEMALE FLIES THAT ARE STERILE.
-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLECTIDE PHOSPHODIESTERASE
15-JUL-1998 (Rel. 36, Last annotation update)
CAMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Learning/
memory process protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF
                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                              SEQUENCE OF 223-584 FROM N.A.
MEDLINE-87092243; PubMed-3025834;
Chen C.-N., Denome S., Davis R.L.;
"Molecular analysis of cDNA clones and the corresponding genomic coding sequences of the Drosophila dunce+ gene, the structural gene for CAMP phosphodiesterses.";
                                                                                                                                                                                                                                                                                                                                                            Qiu Y.H., Chen C.-N., Malone T., Richter L., Beckendorf S.K., Davis R.L.,
                                                                                                                                                                                                                    "Characterization of the memory gene dunce of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99239BE33C620501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY-RICH
                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                  SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X55173; CAA38960.1; JOINED.
X55174; CAA38960.1; JOINED.
X55175; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X55167; CAA38960.1; -.
EMBL; X55168; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X55170; CAA38960.1; JOINED. X55171; CAA38960.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X55172; CAA38960.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M14980; AAC34201.1; JOINED EMBL; M14981; AAC34201.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA38960.1; JOINED
                                                                                                                                                                              MEDLINE-92085274; PubMed-1660926;
                                                                                                                                                                                                                                         melanogaster.";
J. Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00387; PDIESTERASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003607; HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0000479; dnc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14982; AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00233; PDEase;
                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; A26651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 AA;
                                                                                                                                                                     STRAIN-CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X55169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M14979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A26651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                          ö
                                                                                                                                                                                                                                               Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged
                                                                                                                                                                                                                                                                                                        Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
MEDLINE-97141794; PubMed-8988052;
Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.;
Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.;
Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.;
Capcer Res. 57:123-129(1997).
Cancer Res. 57:123-129(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.2%; Score 63; DB 1; Length 394; 58.3%; Pred. No. 4.7;
DB 1; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear protein; Transcription regulation.
DOMAIN 67 70 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324A4B36B9E31899 CRC64;
                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
33.7%; Score 64; DB 1
61.9%; Pred. No. 5.2;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORK - HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 RGGGGGGGGEEGASGGGAAAAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00657; FORK_HEAD_1; 1. PROSITE; PS00658; FORK_HEAD_2; 1. PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 RAGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T02495; -.
InterPro; IPR001766; Fork_head.
pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40995 MW;
                                                                                    555 ALRAGGGGGGGGMAPRTGGC 575
                                                              31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U37274; AAC60066.1; -.
                                                                11 AARAGGGGGGGGIEGPTLRQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                  13; Conservative
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
106
211
                                                                                                                                                                                                                                                                      helix protein CWH-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
117 2
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00339; FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q63245; 2HFH.
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYSC_ACACA
ID MYSC_ACACA
                                                                                                                                                                        FXD3_CHICK P79772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                     FOXD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                            FXD3_CHICK
                                  Matches
                                                                                                                                                                                          δλ
                                                                                                 q
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*** MEDILINE-9003/074; Pubmed=2530230; A BTZESKA H., Lynch T.J., Martin B., Korn E.D.;

*** MEDILINE-9003/074; Pubmed=2530230; A BTZESKA H., Lynch T.J., Martin B., Korn E.D.;

*** Brzeska H., Lynch T.J., Martin B., Korn E.D.;

*** The localization and sequence of the phosphorylation sites of Acanthameeba myosins I. An improved method for locating the phosphorylated amino acid.";

*** The localization and sequence of the phosphorylation because the phosphorylated amino acid.";

*** The localization and sequence of the phosphorylation the Phosphorylation and science acid.";

*** The localization acid.";

*** The localization size a ProTein Har Binds To F-ACTIN. The ATPASE ACIVITY THAT IS ACTIVATED BY F-ACTIN.

*** The Nority THAT IS ACTIVATED BY F-ACTIN. THAN ENTR.

*** The Nority THAT IS ACTIVATED BY F-ACTIN. THAS ATPASE AND ALGENT AND ALGORITHE MEMBRANES.

*** THE NOCEOTIDE-SENSITY TO ANIONIC PHOSPHOLIPID MEMBRANES.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jung G., Korn E.D., Hammer J.A. III;
"The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           France.
Probom; PD000355; m.r.
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
SMART; SM00326; SH3; 1.
MYOSIN: PS50002; SH3; 1.
MYOSIN: AFP-binding; Phosphorylation; Multigene family; SH3 domain.
1 670 MYOSIN HEAD-LIKE.
1 670 TAIL HOMOLOGY REGION 1 (TH.1).
                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
MEDILINE-86259656; PubMed-3014500;
Hammer J.A. III, Jung G., Korn E.D.;
"Genetic evidence that Acanthamoceba myosin I is a true myosin.";
Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLY/PRO/ALA-RICH (TH.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE MYOSIN IB.
                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987)
P10569;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
                                                                                                                                              Acanthamoeba castellanii (Amoeba).
Eukaryota; Acanthamoebidae; Acanthamoeba.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88016163; PubMed=3477803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A33891; MWAXIC.
HSSP; PO8799; 1LVK.
InterPro; IPR001452; SH3.
InterPro; IPR01609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PD000355; MYOSIn_head; 1.
                                                                                                                                                                                                                                                                                                                                                      non-myosin-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00063; myosin_head; 1. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J02974; AAA27707.1; -.
                                                                                                     Myosin IC heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      975
1035
1168
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION SITE.
                                                                                                                                                                                                     NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTACENESIS, AND FUNCTION.
MEDLINE=98337187; PubMed=9674430;
Price J.L., Blau J., Rothenfluh A., Abodeely M., Kloss B., Young M.W.;
"Double-time is a novel Drosophila clock gene that regulates PERIOD protein accumulation.";
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: INVOLVED IN CIRCADIAN RHYTHMS, VIABILITY AND MOLECULAR OSCILLATIONS OF THE CLOCK GENES PERIOD (PER) AND TIMBLESS (TIM). DBT REDUCES THE STABILITY AND THUS THE ACCUMULATION OF MONOMERIC PER PROTEINS, PROBABLY THROUGH PHOSPHORYLATION. NO EVIDENT CIRCADIAN OSCILLATION IS DETECTED IN HEAD.
-i- SUBUNIT: FORMS A COMPLEX WITH PER.
-i- TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS OF THE EVES AS WELL AS IN THE REGION SITUATED BETWEEN THE OPTIC LOBE AND THE CENTRAL BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENTRAL BRAIN.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF CKI-EPSILON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kloss B., Price J.L., Saez L., Blau J., Rothenfluh A., Wesley C.S., Young M.W.;
                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Discs overgrown protein Kinase (EC 2.7.1.-) (Double-time protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Fram; PR00069; pkinase; I.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
BROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Biological rhythms; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Drosophila clock gene double-time encodes a protein closely related to human casein kinase I epsilon."; Cell 94:97-107(1998).
                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                         33.2%; Score 63; DB 1; Length 1168;
 311 311 PHOSPHORYLATION.
1168 AA; 127309 MW; D07084B373A37A32 CRC64;
                                                                                                    6; Indels
                                                                                                                                                                                                                                                                      440 AA
                                                                                                2; Mismatches
                                                                          Pred. No. 12;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98337188; PubMed=9674431;
                                                                                                                                                                                                                                                                                             15-Jul-1999 (Rel. 38, Created)
                                                                                                                                                                 920 QILGAKGGGGGGGRGRGGPS 939
                                                                                                                                8 QCLAARAGGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF055583; AAC39134.1; -.
                                               Query Match 33.2%
Best Local Similarity 60.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P40233; 1CSN.
FlyBase; FBgn0002413; dco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 94:83-95(1998)
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            DCO OR DBT.
                                                                                                                                                                                                                                                                DCO_DROME
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PROTEIN KINASE.

FT FT FT FT FT FT FT FT

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                                                                                                                                                                                   ö
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain genes.";
J. Cell SC1. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                M->1: IN DBTL; LENGTHENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas reinhardtii flagellar alpha
                                                                                            P->S: IN DBTS; SHORTENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYNEIN HAS AFPASE ACTIVITY.
--- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
--- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                   ;
0
                                                                                                                                                           Score 62; DB 1; Length 440;
Pred. No. 6.6;
                                                                                                                                                                                    7; Indels
                                                                                                                                        B875891D5747391D CRC64;
                                                                                                                                                                                                                                                                                                         07.NOV-1997 (Rel. 35, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Dynein alpha chain, flagellar outer arm (DHC alpha).
     ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                         PRT; 4499 AA.
                           BY SIMILARITY.
                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell Motil. Cytoskeleton 37:120-126(1997).
                                                                          POLY-GLY.
                                                   POLY-GLN
                                                              POLY-GLY
                                                                                     POLY-GLY
                                                                                                           PERIOD.
                                                                                                                                  PERIOD.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94274778; PubMed-8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97329535; PubMed-9186009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L26049; AAA57316.2; -.
Interpro; IPR003593; AAA.
Interpro; IPR001298; Filamin.
Interpro; IPR001798; Kelch.
Interpro; IPR001798; Kelch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1142-4499 FROM N.A.
                                                                                                                                             48073 MW;
                                                                                                                                                                                                                          | | : | ||||||||:
403 PERRPSIRMRQGGGGGGW 422
                                                                                                                                                                                                              4 PTLRQCLAARAGGGGGGGI 23
                                                                                                                                                                  32.6%;
55.0%;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                      80
        23
38
1128
333
333
335
426
437
                                                                                                  47
                                                                                                                                                                            Best_Local Similarity
Matches 11; Conserv
                                                                                                                                             440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dynein gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN~21GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-21GR
                                                                                                                                                                                                                                                                                           CHLRE
                               ACT_SITE
DOMAIN
                                                                                                                                               SEQUENCE
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                              DYHA_CHI
Q39610;
                                                                                                   MUTAGEN
                                                                                                                         MUTAGEN
         NP_BIND
                      BINDING
                                                                   DOMAIN
                                                       DOMAIN
                                                                             DOMAIN
                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                   DYHA_CHLRE
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plant Physiol. 113:611-619(1997).
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS AARIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE PER REGION. PHOTOCONVERSION OF PR IN PROCESS AN ARRAR OF MORPHOGENIC RESPONSES, WHEREAS PECONVERSION OF PROTOCHORESION OF A NUMBER OF WUCLEAR RESPONSES. PER COMPROLS THE EXPRESSION OF A NUMBER OF WUCLEAR GENES INCLUDING THE SMALL SUBBUIT OF REBULOSE-GENES INCOPING THE SMALL SUBBUIT OF REBULOSE-BROYOCHLOROPHYLLIDE REDUCTASE, CHLOROPHYLL A'B BINDING PROTEIN, EXPRESSION OF TIS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACC clade:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.; "The phytochrome gene family in tomato and the rapid differential evolution of this family in angiosperms."; Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. 58M;
MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Childs K.L., Millet J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 4499;
                                                                                                                                                      COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
                                                                       PROSITE; PS50194; FILAMIN_REPEAT; 1. Motor protein; Microtubules; Dynein; ATP-binding; Flagella; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
W; 319AC7FD30F1591A CRC64;
                                                                                                                                                                                                                                                COLLED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                            COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4194 GETLFKTVVEVAGGGGGGGGGGGGGGGTAVRQAL 4226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GPTLRQCLAARAGGGGGGGGIEG---PTLRQCL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panicoideae; Andropogoneae; Sorghum
                                                                                                                                           FILAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. 58M;
MEDLINE=20188796; Pubmed=10723737;
                                                                                                                                                                                                                                                                                                                                          ATP
                                                                                                                                                                                                                                                                                                                                                                                                      503606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 208-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%;
Pfam; PF00630; Filamin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                    Pfam; PF01344; Kelch; 3.
SMART; SM00382; AAA; 3.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                2688
3023
3262
3515
1723
                                                                                                                                                                      1334
1450
1864
                                                                                                                                                                                                                                                                                                                                                                                                      4499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4558;
                                                                                                                                                                        1261
1382
1836
2655
3003
3170
3486
1716
2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHYB_SORBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                 DOMAIN
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                          DOMAIN
                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYB_SORBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
              -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE. -!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY. -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS. -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1; Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 372 CHROMOPHORE (BY SIMILABITY).
1178 AA: 129136 MW; C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92019832; PubMed=1923529;
Hartl M., Hutchins J.T., Vogt P.K.;
"The chicken junD gene and its product.";
 SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                                                                                                            InterPro; IPR00318; GAF
InterPro; IPR00318; GAF
InterPro; IPR00318; GAF
InterPro; IPR003564; HATPase_C.
InterPro; IPR003564; HAS_KiN_A.
InterPro; IPR00159; HS_KiN_A.
InterPro; IPR001294; Phytochrome.
Pfam; PF00218; HATPase_C; 1.
Pfam; PF00218; HATPase_C; 1.
Pfam; PF00318; HATPase_C; 1.
Pfam; PF00318; HATPase_C; 1.
Pfam; PF00318; HATPASE_C; 1.
SMART; SM00051; Signal; 1.
SMART; SM00087; HATPASSE_C; 1.
SMART; SM000387; HATPASSE_C; 1.
SMART; SM00031; PAS; 2.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS501046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-HIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY
                                                                                                                                                                                                                 EMBL; AF182394; AAB41398.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription factor jun-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ARAGGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JUND_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS
A1, A2, A3, A4, AN EMBYO'S SPECIFIC ISOFORMS B1, E2 AND E3 (SHOWN
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYOS OF BOTH SEXES. ALSO
EXPRESSED IN THE PROCENTION OF THE GENELINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C., "The Ceratitis capitata homologue of the Drosophila sex-determining gene Sex-lethal is structurally conserved, but not sex-specifically regulated.",
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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                           -i - SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%; Score 60; DB 1; Length 323; 72.2%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A7F6D21A97DBB676 CRC64;
                 -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                      BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sex-lethal protein homolog (CCSXL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98171464; PubMed=9502730;
                                                                                                                                                                                                                                                                                  InterPro; IPR002112; Leuzip_Jun.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 125:1495-1500(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 323 AA; 33205 MW;
                                                                                                                                                                                                                                                                                                                               PRINTS; PR00043; LEUZIPPRJUN. SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                 EMBL; X60063; CAA42665.1; -.
 Oncogene 6:1623-1631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AAAAGGGGGGGGGGEL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                               Pfam; PF00170; bZIP;
                                                                                                                                                                                                                                  PIR; S20099; S20099.
                                                                                                                                                                                                                                               HSSP; P05412; 1FOS.
TRANSFAC; T02196; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 155
242
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SXL_CERCA
061374;
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- DEVELOPMENTAL STAGE: AT ALL STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDINE-91117256; PubMed-1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T.; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T.; Teglons salmilar to those of RNA binding proteins."; Mol. Cell. Biol. 11:894-905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                     protein; Alternative splicing. GLY/ASN-RICH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CABA3DA5C2C8874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM Al)
                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-BINDING (RRM) 1. RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                                                        InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 2.
PRINTS; PR00961; HUDSXLRNA.
SMART; SM0360; RRM; 2.
PR051TE; PS50102; RRM; 2.
PR051TE; PS50103; RRM; 1.
RNA-binding; Repeat; Nuclear Prot
                                                                                                                                                                                           EMBL; AF026145; AAC38968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 AA; 37188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last a
Suppressor of sable protein.
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es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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75
99
311
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                                                                                                                                                                                                                           HSSP; P19339; 1SXI
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AD SUS_D
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DT 01-A
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A comparison of the properties of Sox-3 with Sry and two related genes, Sox-1 and Sox-2.";
Development 122:509-520(1996).
-:- SUBCELLOLAR LOCATION: Noclear (Probable).
-:- TISSUE SPECIFICITY: MAINLY IN THE DEVELOPING CENTRAL NERVOUS SYSTEM. EXPRESSED IN DEVELOPING UROGENITAL RIDGE.
-:- SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M., Norris D., Rastan S., Stevanovic M., Goodfellow P.N., Lovell-Badge R.;
                                                                                                                                                                                                                                                                                                        31.6%; Score 60; DB 1; Length 1322; 68.8%; Pred. No. 27;
                                                                                                                                                                                                                                      46 474 GIN-RICH (OPA REPEAT).
1087 1162 RNA-BINDING (BY SIMILARITY).
1322 AA; 143555 MW; D5F334EB5702EA08 CRC64;
                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                          HIGHLY CHARGED DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-077-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                             Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:98357; SOX1.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00398; HMG; 1.
DNA-binding; Nuclear protein.
                                                                                                                                                             FIYERSE; FBGN0003575; su(s).
InterPro; IPR000571; Zf-CCCH.
Pfam; PF00642; Zf-CCCH; Z.
RNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X94126; CAA63846.1; -.
                                                                                                           EMBL; M57889; AAA28920.1; -.
EMBL; X59364; CAA42010.1; -.
PIR; A39612; A39612.
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                                                                                                                                                                                                                                                                                                                                                                                                              1159 GGGGGGGVVLPNLSQ 1174
                                                                                                                                                                                                                                                                                                                                                Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                             15 GGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOX-1 protein.
SOX1 OR SOX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOX1_MOUSE
P53783;
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SOX1_MOUSE
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                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                           PAC4_HUMAN STANDARD; PRT; 969 AA.

PAC4_HUMAN STANDARD; O9UEJ1; Q9UEJ7; Q9UEJ8; Q9UEJ9; Q9UEG7; Q9YG9; Q9Y4H0; Q9Y4H1; Q9UEG7; Q9YG9; Q9Y4H0; Q9Y4H1; Q01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a second human subtilisin-like protease gene in the fes/fps region of chromosome 15."; DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of novel cDNAs encoding human kexin-like protease, PACE4 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                  DB 1; Length 391;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                 9F81ED667F947C05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 204:1381-1382(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS PACE4A-1 AND PACE4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                  1; Mismatches
                                                                                                  31.3%; Score 59.5; 54.5%; Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                  Pred. No.
                                 POLY-ALA.
                                                  POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
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                                                                                                                                                                1 IEGPTLRQCLAARAGGGGGGG 22
                                                                                                                                                                                              22 LSGPA----GARGGGGGGGG 38
                                                                39237 MW;
                                                                                                                                  12; Conservative
 204
288
306
364
                                                                                                                                                                                                                                                                                                                                                                                                              convertase 4) (SPC4).
                                                                391 AA;
                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Placenta;
197
280
296
357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PACE4 isoforms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuda Y.;
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                                                                 SEQUENCE
                                                                                                  Query Match
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DOMAIN
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TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4-1: IS EXPRESSED IN HEART,
PLACEWRA, LUNG, SKELETAL WUSCLE, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4-1: IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
EXPRESSED IN PLACENTA. PACE4E-II IS EXPRESSED IN CERREBELLUM,
PLACEMTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT PROPERTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE. SUBCELLULAR LOCATION: PACE4A-I AND PACE4-AII ARE SECRETED. PACEACAND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
                                                             Tauli A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), Kexin-like processing endoprotease."; J. Biochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: LIKELY TO REPRESENT AN ENDOPROTEASE ACTIVITY WITHIN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TERMINUS. PACE4B MIGHT BE SECRETED.
ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,
Tsuji A., Matsuda Y.;
"Biosynthetic processing and quaternary interactions of proprotein
convertase SPG4 (PACE4).";
FEBS Lett. 434:155-159(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                       (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPROTEINS BY CLEAVAGE OF ARC.*AAA.YAA.*ARG.+L~ZAA BONDS,
WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
                                                                                                                                                                                                                                                                  Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Functional analysis of human PACE4-A and PACE4-C isoforms: identification of a new PACE4-CS isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
                                                                                                                                                                                                                  ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE=97064242; Pubmed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE=99233559; Pubmed=10215603;
               SEQUENCE FROM N.A. (ISOFORMS PACE
MEDLINE=98021085, Pubmed=9378725,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98408849; PubMed=9738469;
                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 396:31-36(1996),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBTILASE FAMILY.
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Gaps

1;

9; Indels

60.0%; Pred. No. 24; iive 0; Mismatches

11 AARAGGGGGGGIEGPTLRQCLAAR 35

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Conservative

Best Local Similarity Matches 15; Conserv

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entities requires a license agreement ( or send an email to license@lsb-sib.ch)
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                                                            BAA21620.1
                EMBL; M80482; AAA59998.1;
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Score 59.5; DB 1; Length 969;

31.3%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Nuclear (Potential).
-:- TISSUE SPECIFICITY: KIDNEY, LUNG, BRAIN AND PANCREAS (INSULINOMA).
-:- SIMILARITY: BELONGS TO THE BASIC HELIX LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TST M. -J;;

TST M. -J;

MOL -Cell. Biol. 16:626-633(1996).

-I - FUNCTION: INHIBITS DAM BINDING OF TCF3 (E47) HOMODIMERS AND TCF3

-I - FUNCTION: INHIBITS DAM BINDING OF TCF3 (E47) HOMODIMERS AND TCF3

(E47) / NEURODI HETERODIMERS AND ACTS AS A STRONG REPRESSOR OF

NEURODI AND MYOD-RESPONSIVE GENES, PROBABLY BY HETERODIMERIZATION

WITH CLASS A BASIC HELIX-LOOP-HELIX FACTORS. DESPITE THE PRESENCE

OF AN INTACT BASIC DOMAIN, DOES NOT BIND TO DNA.

-I - SUBGNIT: HETERODIMER WITH OTHER BILL PROTEINS, LIKE TCF3 (E47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S80870; AAB50691.1; -.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS00038; HELK_LOOP_HELIX; 1.
Nuclear protein; Transcription regulation; Repressor.
DOMAIN
11 14 POLY_ALA.
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                                                                          30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 1
Pred. No. 12;
1; Mismatches
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POLY-GLY.
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POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96140430; PubMed=8552091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35905 MW;
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61.1%;
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                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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229
241
311
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                              BETA3 protein.
                                                                                                                                                                                                                                                                                              Mesocricetus
                        BET3_MESAU
009029;
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BET3_MESAU
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                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D2 (Forkhead-related protein FKHL17) (Forkhead-related transcription factor 9) (FREAC-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                      Ernstsson S., Betz R., Lagercrantz S., Larsson C., Ericksson S., Gederberg A., Carlsson P., Enerbaeck S., Caloning and characterization of freac-9 (FKHL17), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34.";
                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.1%; Score 59; DB 1; Length 497; 66.7%; Pred. No. 15;
                                                                                                                                                                                                                                                               Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSTIE; PSO0657, En, I. PROK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAAF498D216BE019 CRC64;
                             497 AA.
                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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FORK-HEAD.
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POLY-GLY.
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                          PRT;
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                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98066765; PubMed=9403061;
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
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                                                                                               FOXD2 OR FKHL17 OR FREAC9.
                        STANDARD;
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                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                063245;
                     FXD2_HUMAN
060548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 602211;
                                                                                                                                                                                                                                                      REVISIONS
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DOMAIN
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             FXD2_HUMAN
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RESULT 21
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Y967_TREPA RESULT 22

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterbback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fulji C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of an orthologous mammalian cytokeratin gene. High degree of intron sequence conservation during evolution of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 59; DB 1; Length 517; 60.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                               Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN 152 161 POLY-GLY.
SEQUENCE 517 AA; 56597 MW; E224976333989DF6 CRC64;
                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome. DOMAIN 152 161 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                 STRAIN=NICHOLS;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89125611; Pubmed-2464696;
Rieger M., Franke W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88122104; PubMed=2448602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001264; AAC65925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biol. 204:841-856(1988).
                                                                                                   Hypothetical protein TP0967.
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    STANDARD;
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(atches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                               Treponema pallidum.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
Y967_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            spirochete.
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MEDLINE-92141228; PubMed-1371013; Mischke D., Steinert P.M.; Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides in the C-terminal v2 subdomain due to variable numbers and sizes of alvohne loops.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126. MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Gludice G., Pearson R., Fuchs E.; "Genetic mutations in the Kl and KlO genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v-Riants EHK PRO-156 AND SER-156.
MEDLINE-94117870; PubMed-7507152;
McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A., Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.; "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
Compton J.G., Bale S.J.;
Preferential sites in keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.; "prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                                                                                                "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
Darmon M.Y., Semat A., Darmon M.C., Vasseur M.; "Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheng J., Syder A.J., Yu Q.-C., Letai A., Paller A.S., Fuchs E.; The genetic basis of epidermolytic hyperkeratosis: a disorder of differentiation-specific epidermal keratin genes."; cell 70:811-819(1992).
                                                                                                                                                                     Kisselev L.L.; "Exons I and VII of the gene (Ker10) encoding human keratin 10 undergo structural rearrangements within repeats."; Gene 116:245-251(1992).
                                                                                                                                                                                                                                                                                                                 Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;
                                                                                                                                                 Tkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease severity.";
J. Clin. Invest. 93:1533–1542(1994).
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MEDLINE=92376531; PubMed=1380725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92386600; PubMed-1381287;
                                                                        expression.";
Mol. Biol. Rep. 12:277-283(1987).
                                                                                                                                                                                                                                                                                       TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed-1286667;
                                                                                                                    SEQUENCE OF 197-593 FROM N.A.
MEDLINE-92339897; PubMed-1378806;
                                                                                                                                                                                                                                                                     SEQUENCE OF 180-184 AND 577-589.
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                                                                                                                                                                                                                                                                                                                                                                                                            Arin M.J., Longley M.A., Anton-Lamprecht I., Kurze G., Huber M., Hohl D., Rothnagel J.A., Roop D.R.; "A novel substitution in keratin 10 in epidermolytic hyperkeratosis."; J. Invest. Dermatol. 112:506-508(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND III (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8] FILAMENT FAMILY.
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN POSITIONS 513 TO 555.
                                                                                    Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                                                                                                                                        "Genetic and clinical mosaicism in a type of epidermal nevus."; New Engl. J. Med. 331:1408-1415(1994).
"Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                        MEDLINE-99072665; PubMed=9856845; MEDLINE-99072665; PubMed=9856845; Suga Y., Duncan K.O., Heald P.W., Roop D.R.; A novel helix termination mutation in keratin 10 in annular epidermolytric ichthyosis, a variant of bullous congenital ichthyosiform erychroderma."; J. Invest. Dermatol. 111:1220-1223(1998).
                                                                                                                                                                                                                                                                                   VARIANT EHK SER-160.
MEDLINE=99215719; PubMed=10201536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
                                                                                 MEDLINE=95059228; PubMed=7526210;
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Aarhus/Ghent-2DPAGE; 7405; IEF
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EMBL; M19156; AAA59468.1; --
EMBL; M77663; AAA59199.1; --
EMBL; L20218; AAB59438.1; --
EMBL; L20219; AAB59439.1; --
                                                                    VARIANT EHK THR-150
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-!- SIMILARITY: BELONGS TO THE STRIATIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS CALMODULIN IN A CALCIUM DEPENDENT MANNER. MAY FUNCTION AS SCAFFOLDING OR SIGNALING PROTEIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-BOUND (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain."; J. Biol. Chem. 275:19970-19977(2000).
PRINTS; PR01248; TYPE1KERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                                                                                                 /FTId=vAR_003830.
Y -> D (IN EHK; SEVERE PHENOTYPE).
/FTId=vAR_003831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castets F., Rakitina T., Gaillard S., Mogrich A., Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                              GLY/PHE/SER-RICH
                                                                                                                                                               /FTId=VAR_010505.
                                                                                                                                                                                                                                                                        /FTId=VAR_003828.
                                                                                                                                                                                    /FTId=VAR_010506.
M -> T (IN EHK).
                                                                                                                                                                                                                                003826
                                                                                                                                                                                                                                                   FTIG=VAR_003827.
                                                                                                                                                                                                                                                                                   R -> P (IN EHK).
/FTId=VAR_003829.
                                                                                                                                                                                                        /FTIG=VAR_010507
N -> H (IN EHK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                       -> H (IN EHK).
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                                                                                                                                                                                                                                                             C (IN EHK)
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                                                                                                                                           GLY/SER-RICH.
                                                                                                          LINKER 12.
                                                                                                                                                                                                                                                                                                                                                            Score 59;
Pred. No.
                                                                                       LINKER 1.
                                                                                                                                                                                                                              /FTIG=VAR
                                                                            COIL 1A.
                                                                                                 COIL 1B.
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                                                                                                                                                                                                                                                                                                                                                           31.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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hes 10; Conserv
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                                 Polymorphism.
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Q9NRL3;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ocstroidea: Calliphoridae; Lucilia.
NCBI_TaxID=7375;
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CAUTION: The name "Zinedin" probably originates from the name of
the famous soccer player from Marseille (Zinedine Zidane)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor from the sheep blowfly Lucilia cuprina.";
Insect Blochem. Mol. Biol. 27:479-488(1997).
-!- FUNCTION: RECEPTOR FOR ECDYSONE. BINDS TO ECDYSONE RESPONSE ELEMENTS (ECRES) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR1 SUBSPANILY.
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0
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PRINTS; PR00320; GEN.-.

SMART; SM00320; WD40; 6.

PROSITE; PS00082; WD_REPEATS_1; 1.

PROSITE; PS00294; WD_REPEATS_2; 4.

PROSITE; PS02094; WD_REPEATS_REGION; 1.

Calmodulin-binding; Repeat; WD repeat; Colled coil.

Colled Coil.

(Colled Coil.

(FOTENTIAL).

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15-JUL-1999 (Rel. 38, Last annotation update)
Eddysone receptor (Eddysteroid receptor) (20-hydroxy-ecdysone ECR OR NR1H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97449774; PubMed=9304790;
Hannan G.N., Hill R.J.;
"Cloning and characterization of LCECR: a functional ecdysone
                                                                                                                                                                                                                                                                                                                                                          WD 2.
WD 3.
WD 5.
WD 5.
WD 6.
WD 6.
WD 7.
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LAD -> GTR (IN REF. 2).
: 4DA016A8FF7EDB5E CRC64;
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0; Mismatches
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                                                                                                                                                                                           EMBL, BC004910; AAH04910.1; -. InterPro: IRPR001680; WD40. Pfam; PF004400; WD40; 7. PRINTS; PR00320; GPROTEINBRPT.
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Matches 11; Conserv
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489
542
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Wed Oct

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Ferser A., Hamin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherfor S., Seeger K., Simon S., Slmmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fsihi H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takiff H.E., Eiglmeier K., Bergh S., Cole S.T.; "Gene arrangement and organization in a approximately 76 kb fragment encompassing the oric region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P46390; O53126;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein).
SSB OR ML2684 OR MLCB1913.20C.
                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0031; NUCLEAR_RECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 1; Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HORMONE-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C1511452ED37D359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           MODULATING (POTENTIAL).
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                     Interpro; IPR001556; Hormone_rec_lig.
Interpro; IPR001723; Strdhormone_receptor.
Interpro; IPR001628; Zf-C4.
Interpro; IPR001648; Zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; Zf-C4; 1.
PRINTS; PR00198; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00430; LNF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                           C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21128732; PubMed-11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-97124199; PubMed-8969512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiology 142:3147-3161(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              83075 MW;
                                                                                                                                         EMBL; U75355; AAB81130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             300
366
321
361
674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                           301
301
337
454
757 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSB_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-1- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR REPLICATION OF THE CHROMOSOME. IT IS ALSO INVOLVED IN DNA RECOMBINATION AND REPAIR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thalamus;
MEDLINE-21181559; PubMed-11284713;
Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
"Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Thalamus; MEDILNE=99278519; PubMed=10347254; Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Lovenberg T.W., Roland B.L., Wilson K.J., Jackson M.R., Erlander M.G.; "Cloning and functional expression of the human histamine H3
                                                                                                                                                                                                                                                                                                                                                                              EMBL; ALSOSSE,
Leproma; ML2684; -.
Leproma; ML2684; -.
HSSP; P02339; 1EVG.
InterPro; IPR000424; SSB.
Pfam; PF0436; SSB.
PROSITE; PS00735; SSB.2; FALSE_NEG.
PROSITE; PS00736; SSB.2; FALSE_NEG.
DNA-binding; DNA repair; DNA replication; Complete proteome.
POLY-GLY.
124 133
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HH3R_HUMAN STANDARD; PRT; 445 AA.
09Y5N1; 09H4R8; 09GZXZ;
01-MAR-2002 (Rel. 41, Greated)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
HRH3 OR GPCR97.
                                                                                                    -i-SIMILARITY: BELONGS TO THE SSB FAMILY.
-i-CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
30.8%; Score 58.5; DB 1; Length 168;
Best Local Similarity 52.0%; Pred. No. 6.7;
Matches 13; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION. MEDLINE-20568725; PubMed-11118334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor, HH4R.";
Biochem. Biophys. Res. Commun. 279:615-620(2000).
                                                                                                                                                                                                                                                                                                                                        EMBL; L39923; AAB53120.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmacol. 55:1101-1107(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 GPSLRYATAKVNKASRSGGGGGFG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQCL----AARAGGGGGGG 22
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                                                                                                                                                                                                                                                                                                                                                          EMBL; AL583926; CAC32216.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeda J.P., Babbage A.K., Bagguley C.L.,
RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Beare D.M.,
Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y.,
Clapg S., Cobley V.B., Coller R.E., Connor R., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dunn M.,
RA Elington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA HURKLE E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.M., Johnson D.M.,
RA Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Minte S., Mattry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milme S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Swann M., Sycamore N., Frael C., Shownkeen R., Sims S.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whithehead S.L., Witteker P., Willey D.L., Walliams S.A.,
RA Wilming L., Waray P.W., Hubbard T., Purbin R.,
RA Wilming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
RA Wilming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
RA Wilming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
RA Wilming L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
RA Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "" SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

"" ALTERNATIVE PRODUCTS: AT LEGST 7 ISOFORMS; 1 (SHOWN HERE), 2;
3/H35; 4; 5; 6 AND 7; ARE PRODUCED BY ALTERNATIVE SPLICING.

" TISSUE SPECIFICITY: EXPRESSED PREDOMINANTY IN THE CNS, WITH THE GREATEST EXPRESSION IN THE THALAMOS AND CAUDATE NUCLEGS. THE FELATIVE EXPRESSION IN THE TRALAMOS AND CAUDATE NUCLEGS. THE RELATIVE EXPRESSION IN THE TRALAMOS AND SPECIFIC MANNER.

" RELATIVE EXPRESSION IN THE SYPRESSED IN THE THALAMOS, CAUDATE NUCLEGS AND CEREBELLUM WHILE ISOFORMS 5 AND 6 SHOW A POOR EXPRESSION. ISOFORMS 5 AND 6 SHOW A POOR ANTICED ANTICED ANTICED SHOW A POOR ANTICED ANTICE
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The DNA sequence and comparative analysis of human chromosome 20.";
-! FUNCTION: THE H3 SUBCLASS OF HISTAMINE RECEPTORS COULD MEDIATE THE HISTAMINE SIGNALS. IN CNS AND PERIPHERAL NERVOUS SYSTEM. SIGNALS CONSTITUTIVE ACTIVITY (SPONYANEOUS ACTIVITY IN THE ABSENCE OF AGONIST). AGONIST STIMULATION OF ISOFORM 3 NIETHER MODIFIED ADENYLATE CYCLASE ACTIVITY NOR INDUCED INTRACELLULAR CALCIOM
Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P., "Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iodoproxyfan while isoforms 1 and 3 bind it with high affinity.
                                                                                                                                                                                                                    Wiedemann P., Bonisch H., Bruss M.;
"An amino acid variation in the human histamine h3 receptor from patient suffering from orthostatic dysregulation.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                Ullmer C., Zirwes E., Lubbert H.; "Cloning and functional expression of the human histamine H3S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-280.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                          Biochem. J. 355:279-288(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
                                                               human histamine H3 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                    Ullmer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K -> KKMKKKTCL (IN ISOFORM 2)
A -> V (IN ORTHOSTATIC DYSREGULATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · · · ) (POTENTIAL).
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Pred. No. 17;
                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Alternative splicing; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2ACF7440FBE95B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
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E -> D (IN REF. 1 AND 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 5).
MISSING (IN ISOFORM 6).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC, )
MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Homeobox even-skipped homolog protein 2 (EVX-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY
                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                           EMBL; AF140538; AAD38151.1; EMBL; AB045369; BAB20090.1; EMBL; AJ296652, CAC51025.1; EMBL; AJ278550; CAC3434.1; EMBL; AL078633; CAC04014.1; EMBL; AF365791; AAK50040.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 E
48671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%;
62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ARAGGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3est_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                       MIM; 604525;
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003828:
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TRANSMEM
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TRANSMEM
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
one cut domain family member 2 (ONECUT-2 transcription factor) (OC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              SEQUENCE OF 144-300 FROM N.A.
MEDLINE-91257849; PubMed-1675198;
D'Esposito M., Morelli F., Acampora D., Migliaccio E., Simeone A.,
                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00027; HOMEOBOX_1: 1.
PROSITE: PS50071; HOMEOBOX_2: 1.
DNA-binding; Developmental protein; Homeobox; Nuclear protein.
                                                                                                                                                            "EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is localized at the 5' end of HOX4 locus on chromosome 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6AA99041BA151C3F CRC64;
                                             Birren B., Linton L., Nusbaum C., Lander E.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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POLY-ALA.
POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC009336; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000047; HTH_repressr.
Interpro; IPR001356; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M59983; AAA52414 1; --
EMBL, M59982; AAA52414 1; JOINED.
HSSP; P14653; 1872.
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16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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PRINTS; PRO0031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00046; homeobox; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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476 AA;
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                                   SEQUENCE FROM N.A.
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095948;
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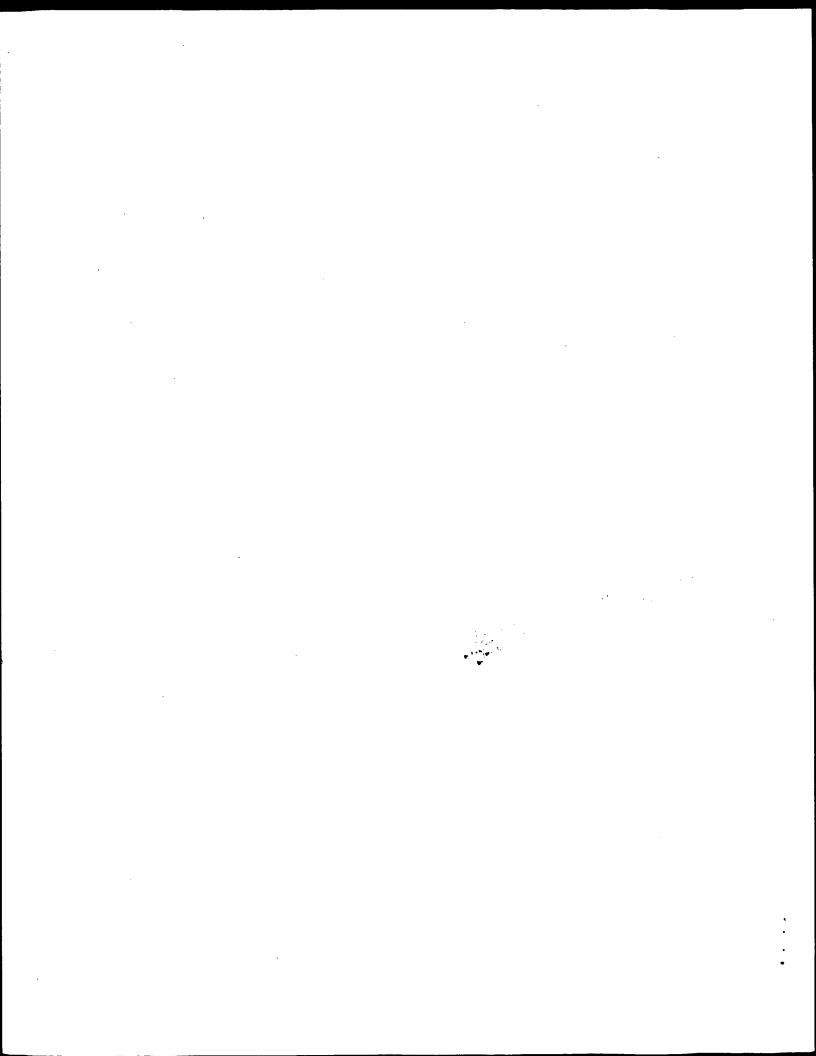
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MEDLINE-99115605; PubMed-9915796;
MEDLINE-99115605; PubMed-9915796;
MEDLINE-99115605; PubMed-9915796;
Macquemin P., Lannoy V., Rousseau G.G., Lemaigre F.P.;
Macquemin P., Lannoy V., Rousseau G.G., Lemaigre F.P.;
Maccord C. Lannow Maccord Maccor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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15-JUL-1998 (Rel. 36, Last annotation update)
Brain-specific homeobox/POU domain protein 1 (BRN-1 protein).
POUJF3 OR OTF8 OR BRN1 OR BRN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%; Score 58; DB 1; Length 485; 65.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
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); Mismatches
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POLY-HIS.
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InterPro; IPR003356; Homeobox.
Pfam; PF02376; CUT; 1.
Pfam; PF00046; homeobox; 1.
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TRANSFAC; T03259; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX;
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P31361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%; Score 58; DB 1; Length 495; 91.7%; Pred. No. 19; 1; Indels rative 0; Mismatches 1; Indels
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                                                                                                                                                                 EMBL; M88299; AAA39960.1; -
PIR; S31223; S31223.
HSSP; P14899; LOCT.
HGD; MGI:102564; Pou3f3.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
InterPro; IPR00135; Pou0. 1.
PFIAM: PF00157; Pouv. 1.
PRINTS; PR00268; POUDOMAIN.
PRODOM; PD000583; Pouv. 1.
SMART; SM00389; HOX; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00015; POU1. 1.
Nuclear protein; DNA binding; Homeobox.
DOMAIN 28
                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY.
POLY-ALA.
POLY-ALA.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POU.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              186 2
267 2
313 3
401 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Search completed: October 9, 2002, 09:00:15 Job time: 5.3831 secs

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October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                  US-09-422-838C-28
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                        Perfect score:
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| SPTREMBL_19:*
| Sp_archea:*
| Sp_archea:*
| Sp_bacteria:*
| Sp_fung:*
| Sp_fung:*
| Sp_fung:*
| Sp_human:*
| Sp_nivertebrate:*
| Sp_mivertebrate:*
| Sp_mhc:*
| Sp_mhc:*
| Sp_nammal:*
| Sp_nammal:**
| Sp_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	0919C9 Oryza sativ 0943k0 oryza sativ 091yb2 arabidopsis 091yb2 arabidopsis 091270 homo sapien 09125 spodoptera 09669 catharanthu 09xe89 sorghum bic 09xe89 sorghum bic 09xe8 homo sapien 09byd8 homo sapien 09byd8 homo sapien 09byd8 mus magien 09byd8 homo sapien 09byd8 homo sapien 09byd8 homo sapien
SUMMARIES	ID	0916209 0943K0 091782 099770 0991863 0986841 098699 099126 01126 01126 011476 011476 011476 096502 096703
	DB	
	Query Match Length DB	360 253 199 612 612 137 137 1474 496 500 689 689 707
эÞ	Query Match	38.4 35.8 35.8 35.8 34.7 34.7 34.7 34.7 34.7 34.7 34.7 34.7
	Score	73 68 66 66 66 66 66 66 66 66
	Result No.	10 6 7 7 8 8 8 8 8 10 11 11 11 11 11 11 11 11 11 11 11 11

	Cayote nomo sapien	Cagnot Clona savig	U91d54 oryza sativ	Q9vjk4 drosophila				Caveur grosophila	. Q9u2il caenorhabdi	Q9u2i0 caenorhabdi	096755 branchiosto	09ase5 orvza satiit	OD67+0 -4	College Streptomyce	Q9s0r8 streptomyce	Q942u6 orvza sativ	VEND STATE OF LOO	Contro arabidopsis	Uscle/ schizophyll	0942r8 oryza sativ	Q9ccc0 mycobacteri	Q49843 mycobacteri	027258 drosonbila	Obstance decembers	Section diosophila	U96828 drosophila	Q9sxi9 oryza sativ	O61080 acanthamoeh	09sz70 arabidonsis	090011 5000	Saplen Saplen	U9W149 drosophila	VYIWC8 oryza sativ	Q9ftk4 oryza sativ
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ALIGNMENTS

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                                                                                                                      Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. NIPPONDARE;
Saski T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                       38.4%; Score 73; DB 10; Length 360; 56.0%; Pred. No. 0.72; tive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                   Submitted (UNI-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AP002525: BAB07996.1; -
InterPro: IPR00571; Zf-CCCH.
Ffam: PF00642; zf-CCCH; 4.
SMART: SM00356; ZnF_C3H1; 4.
SEQUENCE 360 AA; 37368 MW; 5105598D7E1C77B2 CRC64;
                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 AA.
                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LEGPMWRMGLGGGGGGGGGGGG 50
                           PRELIMINARY;
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nes 14; Conservative
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ID Q943K0
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RESULT 1
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Query Match
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Gaps
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Arabidopsis thaliantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; Eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obermaier B., Ottenwaelder B., Duchemin D., Zeitler K., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
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Pred. No. 1.5;
                                                                                                                                                                       STRAIN=CV. NIPPONBARE;
STRAIN=CV. NIPPONBARE;
SSASH T., MASSUMOTO T., Yamamoto K.;
SSASH T., MASSUMOTO T., Yamamoto M.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0039A07.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003235; BAB64100.1; "-
EMBL; AP003235; BAB64100.1; "-
                                                                                                                                                                                                                                                                              37.4%; Score 71; DB 10; Length 253; 55.6%; Pred. No. 0.86; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submittad Alpr.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; All6316; CAB87755.1;
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR002395; Kininogen.
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PRINTS: PRO01301; CYTOCHROME_C; UNKNOWN_1.
PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
HYPOCTHELICAL PROTECTION.
SEDUBRICE 199 AA: 21539 MW; E5D28AC167B3FBFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 21.5 KDA PROTEIN.
                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     3 GPTLRQCLAARAGGGGGGGGGGEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 35.8%;
Local Similarity 34.8%;
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                  P0039A07.6 PROTEIN.
P0039A07.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                              NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE-2027482; PubMed=10819331; Mirosawa M., Ohara O.; MEDILINE-2027482; PubMed=10819331; Mignatine-2027482; PubMed=1081848 K., Hirosawa M., Ohara O.; Nagaser L., Kikuno R., Ishikawa K., Hirosawa M., Chara Lage promptete sequences of unidentified human "prediction of the coding sequences of 100 new cDNA clones from brain "prediction of the large proteins in vitro."; DNA Res. 7:143-150(2000).
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0
                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 4; Length 612;
Pred. No. 4.4;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu J. Wang L., Hu X., Pang Y.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF325155; AAL01786.1; ... Hypothetical protein protein protein protein call protein SEQUENCE 66 AA; 6998 MW; C5626A8FFA9C9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence Analysis of the Spodoptera litura Multicapsid
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 7.0 KDA PROTEIN.
Spodoptera litura nucleopolyhedrovirus.
Viruses; dsp
01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus Genome.";
Virology 287:391-404(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLRQCLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB040891; BAA95982.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.8%;
                                                                         KIAA1458 PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 63.6'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Matches 12; Conserv
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5 TLRQCLAARAGGGGGGGGGIEGP 26
                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 RQCLAARAGGGGGGGI 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. NIPPONBARE;
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                      Q9XE89;
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                                                                                 RESULT 8
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                                                                   Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Wataryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                            Veau B., Oudin A., Clastre M., Chenieux J.C., Rideau M., Hamdi S.; "Genes encoding glycine-rich Catharanthus roseus proteins with RNA binding motifs.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Veau B., Oudin A., Courtois M., Chenieux J.-C., Hamdi S., Rideau M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
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0
                                                                                                                                                                                                                                                                                                           34.7%; Score 66; DB 10; Length 137; 50.0%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
34.7%; Score 66; DB 10; Length 160;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 11; Conservative 4; Mismatches 7: Indele
                                                                                                                                                                                       Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
RMBL, AP200321; AAF31402.1; -.
HSSP; P09651; HHA1.
INTERPCO; IPR000504; RRM.
Fram; PP00076; rrm; 1.
SWART; SW00360; RRM; 1.
PROSITE; PS00102; RRM; 1.
PROSITE; PS00102; RRM; 1.
SROUENCE 137 AA; 14162 MW; 4FABADB9C7A989FC CRC64;
                                                                                                                                                                                                                                                                                                                                      7; Indels
         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA BINDING PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 160 AA; 16264 MW; DCDC9F63C983F5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE GLYCINE-RICH RNA-BINDING PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AA.
                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                   80 TVNEAQSRGSGGGGGGGFRGP 101
                                                                                                                                                                                                                                                                                                                                                    5 TLRQCLAARAGGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                  Local Similarity 50.09
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vinceae; Catharanthus.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00360; RRM;
                                                                                                                          NCBI_TaxID=4058;
                                                                                                                                                                               binding motifs.
                                                                                                                                                           Veau B.,
                                                                                                                                                                                                                                                                                                          Query Match
  Q9M6A1;
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                                                                                                                                                                                                                                                                                                                            Matches
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Q9M699
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Gaps

0

Indels

4; Mismatches

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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 39.1 KDA PROTEIN.
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                  Lidea V., Lou A., Messing J.W.;
"Microsynteny analysis of 22-KDa zein cluster in maize and sorghum.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR061282; AAD22156.1;
Hypothetical protein.
SEQUENCE 369 AA; 39080 MW; DAA3C65088F106CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Yamamoto K., "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%; Score 66; DB 10; Length 369; Best Local Similarity 40.0%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.7%; Score 66; DB 10; Length 413; 64.7%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP001539; BAA92912.1; -.
Hypothetical protein.
SEQUENCE 413 AA: 45035 MW; 4FEC2A4C5D1271CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                          369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 PAKKASISASVGGGGGGGGGGGTVWRRRGPCSGSRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PTLRQCLAARAGGGGGGGGIEGPTLRQ--CLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 AA.
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2; Mismatches
                                                                                                                                                                     -NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                     PRT;
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PRELIMINARY;
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"A set of ordered cosmids and a detailed genetic and physical map for the B wb Streptomyces coelicolor A3(2) chromosome.";
wol. Microbiol. 21:77-96(1996).
EMBL; AL515667; CAC21636.2;
Incerpro; IPR003838; DUF214.
SEQUENCE 496 AA: 49548 MW; 54E110C4F86231A4 CRC64;
                                                                                                                                                                                                                                                                                                                         Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Isogal T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H., Wagatsuma T., Nagal K., Sugawara M., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
01-DEC-2001 (TREMBLREL)
01-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 34.7%; Score 66; DB 4; Length 474; Local Similarity 45.0%; Pred. No. 5.8; Pred. No. 5.8 at 18; Conservative 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ninomiya K., Iwayanagi T.;
"NEOD human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027619; BAB55238.1;
SEQUENCE 474 AA; 51313 MW; OBCA301518F20DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update) PUTATIVE INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLR-----QCLAARAGGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
Seeger K.J., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Gaps

2, Mismatches

Conservative

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Kato T., Satch S., Okabe H., Kitahara O., Ono K., Kihara C.,
Kato T., Satch S., Okabe H., Kitahara O., Ono K., Furukawa Y.;
Tanaka T., Tsunoda T., Yanada Y., Nakamura Y., Furukawa Y.;
Isolation of a novel human gene, MARKII, homologous to MARK3 and its involvement in hepaticellular carcinogenesis.";
Neoplasia 3:4-9(2001).
INGOINGENETY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBI. ABM9127; BAB33380.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%; Score 66; DB 5; Length 500; 56.5%; Pred. No. 6.1; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                    Percy C.M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53946 MW; 1416327086FE7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
MAP/MICROTUBULE AFFINITY-REGULATING KINASE LIKE 1.
                                                                                                                                               Last sequence update)
Last annotation update)
               4 PTLRQCLAARAGGGG------GGGGIEGPTLRQCLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 688 AA.
                                                                                                      500 AA
                                                                                                                                                                                                                                 Rhabditidae, Peloderinae, Caenorhabditis.
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Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                        Science 282:2012-2018(1988).
EMBL, 278013, CAB01420.1; -.
Interpro; PPR001254; Trypsin.
PR001TE; PS50240; TRYPSIN.DOM; 1.
Hydrolase; Serine protease.
SEQUENCE 500 AA; 53946 WW; 14163
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                                                                                                        PRT;
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Local 13; Conservative
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                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                 F15B9.5 PROTEIN.
                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                              019476
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                                                                                RESULT 12
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7 CRSRRGGGGGGGGFRG 23
                                                                                                                                                                                                Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                   9 CLAARAGGGGGGGIEG 25
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Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BRAIN;
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                                                                                                                                                                                        Query Match
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Q9Y648
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                                                                                                                                                                       Gaps
InterPro; IPR000449; UBA.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TYRC; 1.
SMART; SM00165; UBA; 1.
PROSITE; PS00010; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
APP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 688 AA; 75261 MW; A03B5A7943ACD086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21245130; PubMed-11347906;
Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XX.
The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
                                                                                                                                          34.7%; Score 66; DB 4; Length 688; 45.0%; Pred. No. 8.2;
                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.7%; Score 66; DB 4; Length 689; 45.0%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689 AA; 75449 MW; 439B11FD33D78B34 CRC64;
                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                  3 GPTLR-----QCLAARAGGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLR-----QCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                        689 AA
                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           707 AA
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for large Proteins in vitro.";
DNA Res. 8:85-95(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:85-95(2001).
EMBL; AB058763; BAB47489.1; -.
                                                                                                                                                                                                                                                                                                                          KIAA1860 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 45.0%;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KERATIN 2 EPIDERMIS.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                              18;
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                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                  096JG7
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Q96JG7
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Q61869
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Herzog F., Winter H., Schweizer J.;
"The large type II 70-kDa keratin of mouse epidermis is the ortholog of human keratin K2e.";
J. Invest. Dermatol. 102:165-170(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                    -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            34.7%; Score 66; DB 11; Length 707; 64.7%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.7%; Score 66; DB 4; Length 752; 45.0%; Pred. No. 8.9; tive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drewes G., Mandelkow E.M.;
"MARK1, homologue of MARK1, MARK2 and MARK3.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057448; AAL25683.1;
Kinase; Serine/threonine-protein kinase.
SEQUENCE 752 AA; 82519 WW; 4B430FFD2B150E7A CRC64;
                                                                                                                                                                                                                           Pfam; PF00038; filament; 1.
PRINTS; PR01276; TYPE2KERATIN.
PROSTTE; PS00226; IF; 1.
Coiled coil; Intermediate filament.
SEQUENCE 707 AA; 70977 MW; DS8FASEGE30BBB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MARK4 SERINE/THREONINE PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                          EMBL; X74784; CAA52788.1; - ...
MGD; MGI:96699; Krt2-17.
InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
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2;

Gaps

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Indels

Length 770;

DB 5;

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SQ SEQUENCE 770 AA; 82032 MW; 5C6D2A2D8C9CDD58 CRC64;
                                                                  Best Local Similarity
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                                                   Query Match
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                                                                                                                                                                                                                                                                                    Q9LD54;
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                                                                                        Matches
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                                                                        SEQUENCE FROM N.A.
MEDIINE-99263496; PubMed-10329000; '
Heus H.C., Hing A., Baren M.Jvan, Joosse M., Breedveld G., Wang J.C.,
Burgess A., Donnis-Keller H., Berglund C., Scherer S.W., Rommens J.M.,
                                                                                                                                                          Oosira B.A., Heutink P.; "A physical and transcriptional map of the preaxial polydactyly locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fulluna M., Takamura K.;
Fulluna M., Takamura M.;
Fulluna M., Fulluna M., Fulluna M.;
Fulluna M., Fulluna 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.5%; Score 65.5; DB 4; Length 355; 57.1%; Pred. No. 5;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD41D18CC811F0E9 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                        on chromosome 7q36.";
Genomics 57:342-331(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-L- SIMILARITY: WITH OFFIER HOMEOBOX PROTEINS.
EMBL: AF107453: AAA4467.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1228; EGGSHELL.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00318; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 3.
NOA_TER 355 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 LAAAASGTGGGGGGGGGASGGTSGSCSPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Helicase; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20130953; PubMed-10664149;
                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001952; Eggshell.
Interpro; IPR001356; Homeobox.
Interpro; IPR000047; HTH_repressr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFam; PF00098; zf-CCHC; 6. SMART; SM00487; DEXDc; 1. SMART; SM00490; HELICC; 1. SMART; SM00343; ZnF_CZHC; É
                                                                                                                                                                                                                                                                                                                                                                                                  PF00046; homeobox; 1.
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nes 16; Conservative
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto R.;
Subnittea (advisor) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
-: SUBCELLULAR ELOCATION: 1.
-: SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; APO01080: BAA90348.1;
-: InterPro; IPR001993: Mitoch_carrier.
InterPro: IPR001993: Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridipĺantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0453A06.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 381;
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48.1%; Pred. No. 6.1;
tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCERT PRO0926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER; 2.
PROSTIE; PS00215; MITOCACHCERRIER; 2.
INDET MEMBLANDE; MITOCHONGTION; TRANSMEMBLANDE; TRANSPORT.
SEQUENCE 381 AA; 40761 MW; F3A0E3CEBD950778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                  2 EGPTLRQCLAARAGGGGGGG-----GIEGPTLRQC 31
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                                                                                                                                                                                                                                                                                                              381 AA
                                                                   3; Mismatches
ch 34.5%; Score 65.5; 1 Similarity 43.2%; Pred. No. 10; 16; Conservative 3; Mismatches
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Best Local Similarity 48.19
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
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                                                                   Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Abardon J.B., Sutton G.G., Wolfer B.D., R.A. Baul M.A., Baul M.A., Bauch M.A., Bardell M.D., Zhang O., Chen L.X., R.A. Ball M.A., Bauch M.A., Bardell J., Bayrak taroglu L., Beasley E.M., Ballew R.M., Baud M.A., Baxendale J., Bayrak taroglu L., Beasley E.M., R. Ballew R.M., Bauch M., Bauch J., Borkstein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chadra I., R.A. Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chadra I., R.A. Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chadra I., R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plunkov S., M., Poster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., R.A. Burtis K.C., Busngelista C.C., Ferraz C., Ferrac C., Ferrac C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A. Hostin D., Hauvey D., Heiman T.J., Hernandez J.R., Houck J., M. Harvey D., Heiman T.J., Hernandez J.R., Ibedyam C., R.A. Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z., Mark D., Mount S.M., Moy M., Murphy L., Murzhy D.M., Nebson D.L., Merklub G. Milshina N.V., Mobarry C., Morris J., Mosher D.L., Mark D., Mount S.M., Moy M., Murphy L., Murzhy D.M., Nelson D.L., R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., R. Spier E., Spradling R.N., Nolyon W., Wubby S., Wubo S., Zhan M., Zhong F.N., Zhong W., Zhon X., Zhan M., Zhong S., Yao Q., A., R. Sheng X.H., Zhong F.N., Rollong W., Wubo X., Zhan M., Zhong S., Wubo S., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%; Score 65; DB 5; Length 452; 73.3%; Pred. No. 7.1; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47875 MW; 0F7ABD53014E3E5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 AA.
                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Drosoph
Science 287:2185-2195(2000)
EMBL; AE003651; AAF535411:
Flyaase; FBgn0032587; CG5953.
SEQUENCE 452 AA, 47875, MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AAGGGGGGGGGVVGP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 ARAGGGGGGGGIEGP 26
                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
    NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG13257 PROTEIN.
CG13257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09VP99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
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RA MEDLINE-20196006; Pubbked-10731132;
RA Admans ND., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan I.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazeż R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Barker E.G., Helt G., Champe M., Pfelffer B.D.,
RA Ballew R.W., Basu A., Barker E.G., Helt G., Champe M., Pfelffer B.D.,
RA Ballew R.W., Basu A., Buck J., Brokstein P., Bolshakov S.,
RA Besson K.Y., Benock J., Brokstein P., Bolshakov S.,
RA Berlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahke C., Perrier B., Durbin P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Perrier B., Duno P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Perrier B., Duno P.,
RA Hostin D., Houtov D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houtov D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houtov D., Helman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li J., Ling Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li, J., Ling Y., Lin X.,
RA Hostin D., Houtov D., Mulphy B., Murphy D., Murphy D., Nathetei B., Mointcoh T.C., Morris J., Mosherefi A.,
RA Holson D.W., Pittman G.S., Pen N., Stupsk M. P., Shen H.,
RA Reinert K., Remighton K., Saunders R.D.C., Scheler F., Shen H.,
RA She B.C., Siden Kiamos I. Simpson M., Stupsk M., Wary D.M., Nathates B., Mount S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA She B.C., Siden Kiamos I. Simpson M., Stupsk M., Wary S., Pachon S., Randongs E.W., Schen K., Sanders R.D.C., Scheler F., Shen H.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinsenbach J., Wang G.D., Sheng X.H., Whong S., Lang G. L., Shen K.H., Remischer C., Turner R., Weinsenbach J.S., Zaveri I., Rangelin R., Shong X.H., Wang S., Lang R., Weinsen D., Sheng X.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AA; 15131 MW; 7A065C21C1376079 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00261; GLYCO HORMONE_BETA_1; UNKNOWN_1. PROSITE; PS01209; LDLRA_1; 1. PROSITE; PS50068; LDLRA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001545; Glyco_hormone_beta.
InterPro; IPR002172; LDL_recept_A.
Pfam; PF00057; Idl_recept_a; I.
SMART; SM00192; LDLa; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 TLLCLGISLGMAATAAAAGGGGGGGAAP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TLRQCL-----AARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequent-DEC-2001 (TrEMBLrel. 19, Last annosINGLE-STRANDED DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0037034; CG13257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 51.69
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9AFI5
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Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelfifer B.D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.W., Benns P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Borkova D., Botchan M.R., Boutok J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Boutok J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cadalys S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cadalys S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,
RA Borkova D., Boones M., Dugan Rochis S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Men M., Glasser K.,
RA Lasko P., Lei Y. Levitsky A.A., Li J., Li Bey M., Miller M., Malush F., Karpen G.H., Rezen Mount S.M., Now M., Murphy B., Murphy E., Murphy E., Murphy E., Murphy E., Murphy E., Murphy E., Smith T.,
RA Meine B.C., Siden-Klamos I., Slupsen M., Skupski M.P., Smith T.,
RA Reinert K., Reanington R., Nurskern D.R., Paller F., Shen H.,
RA Shieska R., Teetor C., Turner R., Venter E., Shen H.,
RA Shieska R., Teetor C., Turner R., Venter E., Wang X.,
RA Shieska R., Teetor C., Turner R., Venter E., Spraching S., Yully B., Murphy S., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worler E., Wen S., Schoeler F., Weisser
                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                          Gaps
         Reddy M.S., Muniyappa K.; "Biochemical properties of single-stranded DNA-binding proteins from Mycobacteria.";
                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                                                                                                                                            Score 64.5; DB 2; Length 165;
Pred: No. 3.1;
3; Mismatches 9; Indels 5
                                                                                    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF349434; AAK30583.1; -
                                                                                                                                                                                                                    165 AA; 17401 MW; 8786415C16F26F39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O. MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                107 GPSLRYATAKVNKASRSGGGGGGGGGGGRR0 139
                                                                                                                                                                                                                                                                                                                                                       3 GPTLRQCL----AARAGGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                       33.9%;
                                                                                                                                                                                                                                                                              33.9%
Query Match
Best Local Similarity 48.5%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                 InterPro; IPR000424; SSB.
pfam; PF00436; SSB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                              HSSP; P02339; 1EYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG13055 PROTEIN.
                                                                                                                                                                                                               DNA-binding.
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09VV01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09VV01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
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RR RT RT DR DR DR DR SQ
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Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong Y. H., Zhong F. N., Zhou X., Zhu S., Zhu X., Smith H.O., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:135-2156(2000).
EMBL; AEO03528; ARF49521.1; -FlyBase; FBgn003583; CG13055. SEQUENCE 309 AA; 33224 MW; 9DAEB67784852A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                            33.7%; Score 64; DB 5; Length 309; 57.9%; Pred. No. 6.5; tive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0036; BZIP_BASIC; 1.
DNA-binding; Nuclear protein.
SEQUENCE 331 AA; 34985 MW; A414C19D4ADCC91E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL032627; CAB54381.1; -.
                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                         12 ARAGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001871; bZIP.
InterPro; IPR003102; pKID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.99
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 GGGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00170; bZIP; 1.
Pfam; PF02173; pKID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y41C4A.4B PROTEIN.
Y41C4A.4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                    Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                           Y41C4A.4A PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steward C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                            090211
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                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                  RESULT 24
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RESULT 27

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ij
   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karabinos A., Riemer D., Erber A., Weber K.;
"Homologues of vertebrate type I, II and III intermediate filament
(IF) proteins in an invertebrate: the IF multigene family of the
Cephalochordate Branchiostoma.";
FEBS Lett. 47:15-18(198).
Interpro; IPR002952; Eggshell.
Interpro; IPR002952; Eggshell.
Interpro; IPR002957; Keratin_I.
Interpro; IPR003858; Ribosomal_S30.
Pfam: PF00038; filament; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (Tremscreet) 19, Last annotation update)
INTENDEDIATE FILAMENT PROTEIN E1.
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Buaryota; Metazoa; Chordata; Cephalochordata; Branchiostoma.
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                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 5; Length 333;
Pred. No. 6.9;
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                                                                                                                                                                  Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
DNA-binding; Nuclear protein.
SEQUENCE 333 AA; 35261 MW; BF02CE6398F6D058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 AA; 44892 MW; 85FE742F07751B24 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 28:2012-2018(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
EMBL; AL032627; CAB54382.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
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MEDLINE=99019308; PubMed=9804163;
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PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GGGGGGGISGMWTEEKPTMR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.78;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GGGGGGGIEG-----PTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001871; bZIP.
InterPro; IPR003102; pKID.
Pfam; PF00170; bZIP; 1.
Pfam; PF02173; pKID; 1.
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 GGGGGGGVPGPS 181
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                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=6239;
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Targeted Gene Disruption of the avermectin O-methyltransferase gene and polytketide synthase gene from Streptomyces avermitilis.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

BEBL; AF275943; AAG09812.1;
RICEPPO; IPR001327; Acyltransf domain.
RICEPPO: IPR001327; Acyltransf domain.
RICEPPO: IPR003880; Phosphopant_attach.
REMI: PF00109; ketoacyl-synt; 2.
REMI: PF00109; ACP DOMAIN; 2.
REMI: PF00109; ACP DOMAIN; 2.
REMI: PF00112; PF005PH0PANTETHEINE; UNKNOWN_1.
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                                                                                                                                                                                                                                                Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
SASAMI T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0456F08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002901; BAB39414.1; InterPro; IPR002937; Amino_oxidase. InterPro; IPR00205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 529 Aa; 55981 MW; 0A5DA55CDD076D24 CRC64;
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                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AVERNECTIN POLYKETIDE SYNTHASE (FRAGMENT).
Streptomyces avermitilis.
          529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 3626 AA.
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          PRT;
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Best Local Similarity 51.78
Watches 15; Conservative
PRELIMINARY;
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                                                                                                                                                     P0456F08.14 PROTEIN. P0456F08.14.
                                                                                                                                                                                                                  Oryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
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SEQUENCE
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                           ACCOORDING TO BE ACCOURTED TO
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A Ikeda H., Monomanya T., Usami M., Ohta T., Omura S.;
A Ikeda H., Monomanya T., Usami M., Ohta T., Omura S.;
A Ikeda H., Monomanya T., Usami M., Ohta T., Omura S.;
A Ikeda H., Monomanya T., Usami M., Ohta T., Omura S.;
A Ikeda H., Monomanya T., Us.A., 96:9509-9514(1999).
B Proc. Natl. Acad. Scil. U.S.A., 96:9509-9514(1999).
B FROGIZ ARONO794; Ketoacyl-synt.
InterPro; IPR000794; Ketoacyl-synt.
InterPro; IPR000384; Zn_carbOpept.
InterPro; IPR000834; Zn_carbOpept.
InterPro; IPR000834; Zn_carbOpept.
IR Ffam; PF00698; Acyl_transf; 3.
IR Ffam; PF00650; Pp-binding; 3.
IR PROSITE; PS000606; B_KETOACYL_SYNTHASE; 2.
IR PROSITE; PS000606; B_KETOACYL_SYNTHASE; 2.
IR PROSITE; PS000012; PHOSPHORANFETHEINE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                      Streptomyces avermitilis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. NIPPONBARE;
Sasaki T., Watsumoto T., Yamamoto K.;
Sasaki T., Watsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
"Oryza sativa nipponbare(GA3) genomic CNA;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003272; BAB67948.1; -26D9B2C86935BCOB CRC64;
SEQUENCE 113 AA; 11708 MW; 26D9B2C86935BCOB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.7%; Score 64; DB 2; Length 3972; 54.5%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphopantetheine; Transferase.
SEQUENCE 3972 AA; 416852 MW; 2A293695B032B1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P0506E04.26 PROTEIN.
                                                                                                                                                          (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                        PRT; 3972 AA.
                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                              TYPE I POLYKETIDE SYNTHASE AVES 1.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99380548; PubMed=10449723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQCLAARAGGGGGGG 22
Best Local Similarity 54.59
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                   09S0R8;
                                                                                                                Q9S0R8
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                                                                              RESULT 29
Q9SOR8
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(without alignments)
247.023 Million cell updates/sec
                                                                                                      October 9, 2002, 08:50:51; Search time 16.1874 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                  1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_032802:*
                                                                                                                                                                               US-09-422-838C-29
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                        BLOSUM62
                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                        Searched:
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.PAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.PAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:* /SIDSI/gcgdata/hold-geneseq/genesegp-embl/AA1989.DAT:*/SIDSI/gcgdata/hold-geneseq/genesegp-embl/AA1990.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1996.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	TPO-mimetic peptid Linear thrombopoie TPO-mimetic peptid TPO-mimetic peptid CYCLIC or linear t TPO-mimetic peptid TPO-mimetic peptid Thrombopoietin mim Thrombopoietin mim Thrombopoietin mim TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid
SUMMARIES	ID	AAB17300 AAY96522 AAB17299 AAB17299 AAB16963 AAB17293 AAB17293 AAY96528 AAB17281 AAB17281
	h DB	221222222222222222222222222222222222222
	Lengt]	
æ	Query Match Length DB	100.0 95.6 95.6 95.6 92.2 92.2 92.2 92.2
	Score	180 180 172 172 172 166 166 166 166 166
	Result No.	1 2 3 4 4 6 6 7 7 10 110

WPI; 2000-350702/30.

12 166 92.2 42 21 AAB1730B 166 92.2 66 21 AAB17311 166 92.2 269 21 AAB16553 17 162 90.0 268 21 AAB16559 18 158 87.8 36 21 AAB16559 19 158 87.8 36 21 AAB17303 22 157 87.2 36 21 AAB17303 23 155.5 86.4 37 21 AAB17303 24 155.5 86.4 37 21 AAB17294 25 154.5 85.8 39 21 AAB17294 26 154.5 85.8 39 21 AAB17294 27 154.5 85.8 39 21 AAB17295 28 154.5 85.6 36 21 AAB17295 29 154.5 85.6 36 21 AAB17295 20 149.5 83.1 35 21 AAB17295 31 146 81.1 40 21 AAB17291 32 143 72.2 AAB17291 33 136.5 75.8 33 21 AAB17297 34 130 72.2 32 AAB17289 35 123.5 68.6 33 21 AAB17297 36 14, 32 21 AAB17287 37 116 64.4 32 21 AAB17287 38 116 64.4 32 21 AAB17287 39 116 64.4 32 21 AAB17287 40 110.5 61.4 29 21 AAB16975 41 100.5 59.2 29 21 AAB16976 42 11 AAB17287 43 110.5 61.4 29 21 AAB16976 44 100.5 59.2 29 21 AAB16976 45 100.5 59.2 29 21 AAB16976	ynthetic TMP-TMP hrombopoietin mi ynthetic TMP-TMP MP-TMP-FC protei	FC-TMP-TMP protein TPO-mimetic peptid Thrombopoletin mim TPO-mimetic peptid TPO-mimetic peptid	nrombopolet PO-mimetic PO-mimetic PO-mimetic PO-mimetic	Thrombopoietin mim TPO-mimetic peptid	
166 92.2 166 92.2 166 92.2 166 92.2 167 92.2 168 92.2 168 92.2 168 92.2 168 92.2 168 92.2 168 92.2 158 87.8 157 87.2 157.5 86.4 154.5 85.8 154.5 85.8 154.5 85.8 154.5 85.6 154.5 85.6 154.8 85.6 154.8 85.6 154.8 85.6 154.8 85.6 154.1 85.6 154.1 85.6 154.1 85.6 155.5 86.4 166.5 10.6 110.5 61.4 110.5 61.4 110.5 61.4 110.5 61.8 110.5 61.8 110.5 61.8 110.5 61.8 110.5 61.8 110.5 61.8 110.5 61.8 110.5 61.8	21 AAB17 21 AAY96 21 AAB17 21 AAB16 21 AAY96 21 AAB16	21 AAY96 21 AAY96 21 AAB17 21 AAB17 21 AAB17	21 AAB17 21 AAB17 21 AAB17 21 AAB17 21 AAB17 21 AAB17	21 AAB17 21 AAB17 21 AAB17 21 AAB17 21 AAB17 21 AAB17	21 AAB17 21 AAY96 21 AAY96 21 AAB17 21 AAB16 21 AAB16 21 AAB16 21 AAB16 21 AAB16 21 AAB16
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	annano	888777	418800	9 H H # 80 0 10 C	
	284002		155 1 154 154 154	149 149 136 136 123 113	11 110 110. 100. 106. 106.

ALIGNMENTS

Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic: VBGF; immunosuppressive; EPO; TPO; CTLAf; minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropicitin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. TPO-mimetic peptide sequence SEQ ID NO:356. Feige U, Liu C, Cheetham J, Boone TC; AAB17300 standard; Peptide; 36 AA. 99WO-US25044. 99US-0428082. 98US-0105371 31-OCT-2000 (first entry) (AMGE-) AMGEN INC. WO200024782-A2. 25-OCT-1999; 22-OCT-1999; 23-OCT-1998; 04 - MAY - 2000 Synthetic. AAB17300; RESULT 1 AAB17300

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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: C (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (A1)a-F1-(X2)b, where (I) c-P1. (L2)d-P2. (L3)d-P2. (L3)d-P2. (L3)d-P2. (L3)d-P2. (L3)d-P3. (L3)d-P3. (L3)d-P2. (L3)d-P3. (L3)d-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin; mimetic; TMP: TPO: platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 180; DB 21; Length 36; 100.0%; Pred. No. 2.2e-14; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linear thrombopoietin mimetic peptide compound 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                   Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96522 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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DXX
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A compound which binds to an mpl receptor comprising a thrombopoietin commette peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], commette peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], commette peptide (TMP_2 are amino acid sequences varying from at least comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, x_1-x_1_2, x_1-x
                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; manunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoletin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 180; DB 21; Length 36; 100.0%; Pred. No. 2.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQALAARAGGGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17298 standard; Peptide; 36 AA.
                                                                                                                                                                                         Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
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Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
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Best Local Similarity
                                                 WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
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The present invention describes composition of matter (I) comprising an (XI)a-F1-(XI)b, where: FI = an Fc domain, XI and X2 = are each (XI)a-F1-(X2)b, where: FI = an Fc domain, XI and X2 = are each independently selected from -(LI)c-P1-(LI)c-P1-(LI)d-P2.

(LI)c-P1-(LZ)d-P2-(L3)e-P-3, or -(L1)c-P1-(LZ)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently sequences of harmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently independently linkers; and a, b, c, d, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently law eytostatic, antiasthmatic, thrombolytic and immunosuppressive cc have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are consenting cancer, asthma, thrombosis, or autoimmune diseases. The compositions are consenting cancer, asthma, thrombosis, or autoimmune diseases. The area of a longer composition of the complement fixation, and possibly placental transfer. AAA69443 cc banding, complement fixation, and possibly placental transfer. AAA69443 cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.6%; Score 172; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQALAARAGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                               Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17299 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.4
Matches 34; Conservative
                                                           autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present invention describes composition of matter (I) comprising an Fred domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(LI)c-PI-(L2)d-P2.

(LI)c-PI-(L2)d-P2-(L3)d-P2.

(LI)c-PI-(L2)d-P2-(L3)d-P2.

(LI)c-PI-(L2)d-P2-(L3)d-P2.

(Mere PI, P2, P3, and P4 = are each independently sequences of harmacologically active peptides, LI, L2, L3, and L4 = are each independently linkers; and at b. c, d, e, and f = are each independently controlly active peptides, LI, L2, L3, and L4 = are each independently linkers; and at b. c, d, e, and f = are each independently controlly active peptides, LI, L2, L3, and L4 = are each independently linkers; and at b. c, d, e, and f = are each independently controlly controlly active and b. c, d, e, and f = are each independently controlly controlly controlly controlly controlly controlly controlly controlly composition can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are before or a FC domain (tather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein Abiding, complement fixation, and possibly placental transfer. Aba69443 cto Aba69526 and Aba16955 to Aba18003 represent uncleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 172; DB 21; Length 36;
Pred. No. 1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclic or linear thrombopoietin mimetic peptide compound 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                               The present invention describes composition of matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQALAARAGGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQCLAARAGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                      Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96521 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.6%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 94.49 hes 34; Conservative
                    autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                  Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4 mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytocoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinses;
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                Score 172: DB 21; Length 36;
Pred. No. 1.9e-13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                   1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                            1 IEGPTLRQCLAARAGGGGGGGGGEGPTLRQCLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                             AAB16963 standard; Protein; 36 AA.
                                                                      Claim 16; Page 61; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371
99US-0428082
      Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                      95.68;
                                                                                                                                                                                                                                                             Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                     WPI; 2000-365108/31.
                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                               AAB16963;
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                               RESULT 6
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The present invention describes composition of matter (I) comprising an Fr domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from - (L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L3)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F3-(L3)e-F
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Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQALAARAGGGGGGGGGTEGPTLRQALAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                         Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044.
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                                                                                                                          autoimmune diseases -
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Matches 34; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
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22-OCT-1999;
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The present invention describes composition of matter (I) comprising an (X1)<sup>2</sup> Fe domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)<sup>2</sup> FF1-(X2)<sup>2</sup>, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)<sup>2</sup> C-P1-(L2)<sup>4</sup> C-P2.

**C (L1)<sup>2</sup> P1-(L2)<sup>4</sup> P2-(L3)<sup>4</sup> P2-(L3)<sup>4</sup> P2-(L3)<sup>4</sup> P2-(L3)<sup>4</sup> P2-(L3)<sup>4</sup> P3-(L4)<sup>4</sup> P2-(L3)<sup>4</sup> P3-(L3)<sup>4</sup> P3-(L4)<sup>4</sup> P3-(L4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin; mimetic; TWP: TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HTV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
       \begin{array}{ll} & pharmacologically \ active \ peptides, \ useful \ for \ treating \ cancer \ autoimmune \ diseases \end{array}.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.2%; Score 166; DB 21; Length 36; 94.4%; Pred. No. 9.2e-13; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin mimetic peptide compound 6.
                                                                                                   Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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A compound which binds to an mpl receptor comprising a thrombopoietin is new. TWP 1 and TWP 2 are amino acid sequences varying from at least control to 14 residues in length comprising x 2-x 10, x 2-x 11, x 2-x 12, x 1-x 1-3, x 1-x 1-4, x 1-x 1-0, x 1-x 1-1, x 1-x 1-2, x 1-x 1-2, x 1-x 1-2, x 1-x 1-2, x 1-x 1-3, and 2 x 1-x 1-4, x 1-x 1-1, x 1-2, x 1-x 1-2, x 1-x 1-3, and 2 x 1-x 1-4, x 1-4, x 1-1, x 1-1, x 1-2, x 1-x 1-2, x 1-x 1-3, and 2 x 1-x 1-4, x 
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                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%; Score 166; DB 21; Length 36; 94.4%; Pred. No. 9.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                           Claim 16; Page 62; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96528 standard; peptide; 41 AA
       Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20..27
/label= linker
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/label= TMP_2
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                                          WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
       Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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AAB17282;
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                                                                                                                                                                                                                                                     RESULT 11
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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; amunosuppressive; EDO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothalial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                            ch 92.2%; Score 166; DB 21; Length 41; il Similarity 94.4%; Pred. No. 1e-12; 1ndels 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                        1 IEGPTLRQALAARAGGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                      AAB17281 standard; Peptide; 42 AA.
                                                                      Claim 16; Page 65; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371.
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                    Cheetham J;
                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
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                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                 WPI; 2000-365108/31.
                                                                                                                                                                                                      Sequence 41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
        (AMGE-) AMGEN INC
                      Liu C, Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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The present invention describes composition of matter (I) comprising an Fe domain, harmwacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a-F1-(X2)b, where (II) c-P1, (II)2-P1-(II2)d-P2, (II)3-P2 (II)3-P3, and P4 = are each independently sequences of where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are ach independently inkers; and a, b, c, d, e, and f = are ach independently linkers; and a, b, c, d, e, and f = are ach independently linkers; and a, b, c, d, e, and f = are ach independently linkers; and a, b, c, d, e, and f = are ach independently linkers; and a, b, c, d, e, and f = are ach independently linkers; and and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention are activities. DNAs, vectors and host cells from the present inventions are consequenced and an expected and antional cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer of the use of an frodromain (rather than a Fab domain) can provide a longer consequence used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1;
                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%; Score 166; DB 21; Length 42; 94.4%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQALAARAGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                  Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17282 standard; Peptide; 42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 94.45
Best Local Similarity 94.45
Matches 34; Conservative
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                                                                                                                                autoimmune diseases -
WPI; 2000-350702/30.
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22-OCT-1999;
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The present invention describes composition of matter (I) comprising an (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and 1inkers. Where (I) is: independently selected from -(L1)c-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2, (L3)e-P3-(L4)f-P4 pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                  be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fe domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fe receptor binding, protein to AAA69526 and AAB16955 to AAB18003 represent nucleotide and anino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; MMF; inhibitor; erythropoietin; thrombopoietin; intendentic; IL-1; TMF; antagonist; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; avascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                92.2%; Score 166; DB 21; Length 42; 94.4%; Pred. No. 1.1e-12; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQALAARAGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17308 standard; Peptide; 42 AA.
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Best Local Similarity 94.4%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                42 AA;
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: independently selected from -(L1)c-P1.-(L3)c-P2. (L3)c-P2. (L3)c-P2. (L3)c-P2. (L3)c-P2. (L3)c-P3. or -(L1)c-P1.-(L3)c-P2. (L3)c-P3. or -(L1)c-P1.-(L3)c-P3. or -(L3)c-P3. or -(L3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein to Androise, complement fixation, and possibly placental transfer. AA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.2%; Score 166; DB 21; Length 42; 94.4%; Pred. No. 1.1e-12; ative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96530 standard; Protein; 42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin mimetic peptide.
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                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                 AAB17311 standard; Peptide; 60 AA.
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99US-0428082.
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The present invention describes composition of matter (1) comprising an CC domain, plantmacologically active peptides, and linkers. Where (1) is: Fc domain, plantmacologically active peptides, and linkers. Where (1) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2-(X1)a-F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease: cytostatic; antiasthmatic; thrombolytic; VBGF; immnosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 92.2%; Score 166; DB 21; Length 60; Local Similarity 94.4%; Pred. No. 1.5e-12; nes 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16960 standard; Protein; 269 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA69446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
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The present invention describes composition of matter (1) comprising an (X1)<sup>24</sup>-F1-(X2)<sup>5</sup>, where: F1 = an Fc domain; X1 and X2 = are each (X1)<sup>24</sup>-F1-(X2)<sup>5</sup>, where (I) is: condependently selected from - (L1)<sup>22</sup>-F1-(L2)<sup>4</sup>-F2-(L3)<sup>4</sup>-F2-(L3)<sup>4</sup>-F2-(L3)<sup>4</sup>-F2-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L3)<sup>4</sup>-F3-(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_TMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least X_2-X_1_3, X_2-X_1_1, X_2-X_1_1, X_1-X_1_1, X_1-X_1_2, X_1-X_1_2, X_1-X_1_3, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQALAARAGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96531 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgG1 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24834
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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X_-1-X_-1-4 , X_-1=1, X_-1, X_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA minetic; IL-1; TNE; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vychtoxic; T cell lymphocyte antigen 4; tumour necrosis factor; vscular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                       DB 21; Length 269;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                             92.2%; Score 166; DB 21; 94.4%; Pred. No. 6.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                             1111111 | 11111111111111111 | 11111 | 11111 | 11111 | 234 IEGPTLROWLAARA 269
                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQALAARAGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB16959 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0428082
                                                                                                                                                                                                                                                                                                                                                 34; Conservative
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16959;
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                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB16959
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)=-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(Li)C-F1-(Li)C-F1-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-(Li)d-F2-
pharmacologically active peptides; L1, L2, L3, and L4 = are each independently independently linkers; and a, b, c, d, e, and f = are each independently independently linkers; and a, b, c, d, e, and f = are each independently no or 1, provided that at least 1 of and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention are be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer That life or incorporate functions such as Fc receptor binding, protein Abiding, complement fixation, and possibly placental transfer. AAA69443 A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide: therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; vyttotxoir 7 cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 162; DB 21; Length 268; 94.3%; Pred: No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111 | 1111111111111111111 | 1111 | 258 | 234 IEGPTLROWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQALAARAGGGGGGGGGTEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17301 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 94.3
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Thrombopoietin; mimetic; TWP: TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer than 18-11fe or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 Ab binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_l-(L_{-1})_nTMP_2], is new. TMP_l and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "optionally modified by bromoacetyl or PEG"
                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                               87.8%; Score 158; DB 21; 91.7%; Pred. No. 7.8e-12;
                                                                                                                                                                                                                                                                          1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                           Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       AAY96523 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Llu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105348.
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                                                                                                                                                                                                                                      91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                  Best_Local Similarity 91.74
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                            36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96523;
                                                                                                                                                                                                Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                  AAY96523
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                          8×38888888888
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Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiaschmatic; thrombolytic; VEGF; amunosouppressive; PEO; TFO; CTLA4; mimetic; IL-1; TNF; antagonist; Cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                 21; Length 36;
                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and
                                                                                                                                                                   87.8%; Score 158; DB 21;
                                                                                                                                                                                                                1 IEGPTLRQALAARAGGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                    AAB17303 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0428082.
                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                 Best Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-0CT-1999;
                                                                                                                                                       Sequence
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                         AAB17303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                         AAB17303
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can useful for treating cancer, astima, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer. A binding, complement fixation, and possibly placental transfer. AAA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (1) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)a-T1-(X2)b. where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P2-(L3)e-P3-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoinmune disease; cytostatic; antiasthmatic; thrombolytic; VGGF; munosoppressive; BPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; MMP: inhibitor; erythropoietin; trombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; avscular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%; Score 157; DB 21; Length 36; 91.7%; Pred. No. 1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17307 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
              8×333333333335×8
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Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note "optionally linked to an Fc molecule"
                                                                                                                                                                                                                             87.2%; Score 157; DB 21; Length 36; 91.7%; Pred. No. 1e-11; 1ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                      1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2000 (first entry)
                                                                                                                                                                                                                                               87.2%
Query Match
Best Local Similarity 91.7%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96524;
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 22
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10 to 14 residues in length comprising X_-2-X_{-1}, X_-2-X_{-1}, X_-2-X_{-1}, and X_-2-X_{-1}, X_-1-X_-1, X_-1-X_-1, X_-1-X_-1, X_-1-X_-1, X_-1-X_-1, X_-1-X_-1, X_-1-X_-1, X_-1, X_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) is (XI)a-FI-(XZ)b, where: Fl = an Fc domain, XI and X2 = are each independently selected from -(LI)c-FI -(LI)c-PI-(LZ)d-P2, -(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2-(LZ)d-P2
                                                                                                                                                                                                                                                                                                                                                                                                                               aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.2%; Score 157; DB 21; Length 36; 91.7%; Pred. No. 1e-11; 3; Indels iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQALAARAGGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17294 standard; Peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17294
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently loor 1, provided that at least 1 of a and b 1s 1. The composition can activities. DNAs, vectors and host cells from the present invention can useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer. A binding, complement fixation, and possibly placental transfer. AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; Immunosuppressive; EPO; TPO; CTLA4; mimetic; LI-1; TNF; antagonist; cytotoxic rell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                             DB 21; Length 37;
                                                                                                                                                                                                     Indels
                                                                                                                                                            1 IEGPTLRQALAARA-GGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                        AAB17295 standard; Peptide; 38 AA.
                                                                                                                                                                                         34; Conservative
                                                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                                                                                                                              dest Local Similarity
                                                                                                                                               37 AA;
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                               AAB17295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                     RESULT 24
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  à
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The present invention describes composition of matter (I) comprising an RC domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-TE-(XZ)b, where: FI = an FC domain; XI and XZ = are each independently selected from -(Li)c-PI-(Li)c-PI-(LZ)d-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-(L3)a-P2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371.
99US-0428082.
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WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                       25-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                   04-MAY-2000.
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O or 1, provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an For domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as For receptor binding, protein A binding, complement fixation, and possibly placental transfer. AA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an (XI)a-FI-(X2)b. where: FI = an Fc domain; XI and X2 = are each independently selected from -(LI)c-FI-(LI)d-F2.

-(LI)c-FI-(LZ)d-F2-(L3)e-F2, or -(LI)c-FI-(LZ)d-F2-(L3)e-F3-(H3)e-F2-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H3)e-F3-(H
                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                           Score 155; DB 21; Length 38;
Pred. No. 1.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQALAARA--GGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17304 standard; Peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                     86.1%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                             38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
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                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
  8.8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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The present invention describes composition of matter (I) comprising an (XI)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each (XI)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(LI)c-PI, -(LI)c-PI-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(LZ)d-PZ-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-FP-(L3)-
                          be used for producing pharmaceutical compositions. The compositions are be used for producing pharmaceutical thrombosis, or autoimmune diseases. Useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 Ab inding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, mimetic; IL-1; TNF; antagonist; ammy: inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                  85.8%; Score 154.5; DB 21; Length 39; 87.2%; Pred. No. 2.2e-11; Live 0; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQALAARAGGG---GGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17305 standard; Peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                        39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17305;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The present invention describes composition of matter (I) comprising an CC Fc domain, planamacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from - (L1)c-P1, -(L1)c-P1-(L2)d-P2, (L3)d-P2, (
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TTO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endthelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                            DB 21; Length 39;
                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQALAARAGGG---GGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                       85.8%; Score 154.5; DB 2:
87.2%; Pred. No. 2.2e-11;
ative 0; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17306 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                              Best Local Similarity 87.29
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                      39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17306;
                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8×333335×3
                                                                                                                                                                                                                                                                                                                                                                                       Qγ
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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                      Gaps
                                                                                                     0;
                                                                         85.6%; Score 154; DB 21; Length 36; 88.9%; Pred. No. 2.3e-11;
                                                                                                                                                                                                                                                                                                                                              'note= "optionally linked to an Fc molecule"
                                                                                                   4; Indels
                                                                                                             1 IEGPTLRQALAARAGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                         Pred. No. 2.3e
0; Mismatches
                                                                                                                                                                                                                                           Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                               AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                             15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                   label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                       /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24834.
                                                                                                                                                                                                                    04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0105348
                                                                                           32; Conservative
                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-365108/31.
                                                      36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                    Sequence
                                                                                                                                                                                                   AAY96526;
                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                          Matches
                                                                                                                                                             RESULT 28
                                                                                                                                                                      AAY96526
ID AAY9
                                                                                                                                                                                         δ
                                                                                                                              g
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The present invention describes composition of matter (I) comprising an (X1)<sup>2</sup> and 1.2.2 F. domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)<sup>2</sup> are (X2)<sup>2</sup> where: Fl = an FC domain; X1 and X2 = are each independently selected from (L1)<sup>2</sup>-Fl. (L2)<sup>4</sup>-Fl. (L2)<sup>4</sup>-Fl. (L2)<sup>4</sup>-Fl. (L2)<sup>4</sup>-Fl. (L3)<sup>4</sup>-Fl. 
activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. applastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; avscular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                        Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                             85.6%; Score 154; DB 21;
88.9%; Pred. No. 2.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17296 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                    36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17296;
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 29
           8×36666666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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The present invention describes composition of matter (I) comprising an CF c domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)F-P4 (L2)d-P2-(L3)e-P3-(L4)F-P4 (L2)d-P2-(L3)e-P3-(L4)F-P4 (L3)e-P3-(L3)e-P3-(L4)F-P4 (L3)e-P3-(L3)e-P3-(L4)e-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)F-P4 (L3)e-P3-(L3)e-P3-(L4)F-P4 (L3)e-P3-(L3)e-P3-(L4)F-P4 (L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide: therapeutic agent; fusion: Fc domain; cancer;
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VESF;
immunosuppressive: EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist;
MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                   85.0%; Score 153; DB 21; Length 42; 81.0%; Pred. No. 3.5e-11; Ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQALAARA-----GGGGGGGGGEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felge U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17292 standard; Peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                        Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                           42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17292;
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17292
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to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                        Gaps
                                                                                                        7;
                                                                         83.1%; Score 149.5; DB 21; Length 35; 91.7%; Pred. No. 7.4e-11; Live 0; Mismatches 2; Indels 1:
                                                                                                                                       1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                       Search completed: October 9, 2002, 08:58:57
Job time: 16.1874 secs
                                                                                                                 Conservative
                                                                                           Query Match
Best Local Similarity
                                                            Sequence 35 AA;
                                                                                                                       33;
                                                                                                                          Matches
                                                                                                                                                                                 qq
                          S X X S
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Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 76, Appli
Sequence 76, Appli
                                                                   October 9, 2002, 08:55:27; Search time 5.98595 Seconds (without alignments) 146.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl
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Appli
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Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, A
Sequence 6, A
Sequence 2, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, 1
Sequence 7, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
Sequence 2,
Sequence 2,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                             1Ssued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/AA_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                                                                                                            1 IEGPTLRQALAARAGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-100-664A-2
US-09-100-664A-4
US-09-100-664A-4
US-08-987-466-4
US-09-240-359-4
US-08-319-866-2
US-08-319-866-2
US-08-985-090-2
US-08-985-090-2
US-09-165-543-2
US-07-776-272-16
US-08-471-115B-6
US-08-471-028A-2
US-08-471-028A-2
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                                                                                                                                                                                                        231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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                                                                                                                       US-09-422-838C-29
                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                        BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                  55: ...
                                                                                                                              Perfect score:
                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                           Database, :
                                                                                                                                            Sequence:
                                                                   Run on:
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Sequence 2, Sequence 2, Sequence 2,

Sequence 2 Sequence 2 Sequence 2

PCT-US93-02147A-2

US-08-284-941-2 US-08-447-642-2 US-09-236-503-2

Sequence 13, Appl Sequence 193, Appl Sequence 13, Appl Sequence 13, Appl Sequence 193, Appl Sequence 193, Appl Sequence 193, Appl Sequence 17, Appl Sequence 17, Appl Sequence 185, Appl	ddw '#6T Dompho	CTOR STRANSFORMED WITH SAID SEREBY, METHOD OF PRODUCING SAID POLYPEPTIDE AND ANTIBOD
14 2 US-08-764-640-13 14 3 US-08-764-640-193 14 3 US-08-973-225-13 14 3 US-08-973-225-13 14 3 US-09-244-298A-193 14 4 US-09-516-704-193 15 2 US-08-764-640-17 15 2 US-08-764-640-17 15 3 US-08-764-640-18 15 3 US-08-973-225-18 15 3 US-08-973-225-185 15 3 US-08-973-225-185 15 3 US-08-973-225-185 15 3 US-09-244-298A-185 15 4 US-09-516-704-18 16 2 US-08-754-640-18	ALIGNMENTS	17.1 19.666-038A-3 10.666-038A-3
28 59 32.8 31.8 32.8 32.8 33.4 59.9 32.8 33.4 59.9 32.8 34.8 59.9 32.8 34.9 59.9 32.8 44.1 559.32.8 44.4 559.32.8 45.4 559.32.8		US-08-64-038A-3 US-08-64-038A-3 Sequence 3, Application US/0864038A Sequence 3, Application US/0864038A Patent No. 6001592 GENERAL INFORMATION: TITLE OF INVENTION: CONTAINING SAID TITLE OF INVENTION: CONTAINING SAID TITLE OF INVENTION: SAID POLYPEPTIDE TITLE OF INVENTION: SAID POLYPEPTIDE TITLE OF INVENTION: TO SAID POLYPEPTIDE TITLE OF INVENTION: SAID POLYPEPTIDE TITLE OF INVENTION: TO SAID POLYPEPTIDE TITLE OF INVENTION: TO SAID POLYPEPTIDE TITLE OF INVENTION: SAID POLYPEPTIDE TITLE OF INVENTION: TO SAID POLYPEPTIDE CORRESPONDENCE ADDRESS: ADDRESSEE: 812-5 Hirano CITY: Tsu-city STREE: Mie-prefecture COUNTY: JAAAN ZIP: 514-01 COMBUTER: EADAble FORM: MEDIUM TYPE: DISKette, 3.50 inch, 1 COMBUTER: EADABLE FORM: MEDIUM TYPE: DISKette, 3.50 inch, 1 COMBUTER: Mie-prefect 6.1 COMBUTER: Mie-prefect 6.1 COMBUTER: May 28, 1997 APPLICATION NUMBER: US/08/08/44.038A PRIOR APPLICATION NUMBER: 15-July.1996 ATORNEY/AGENT INPORMATION: REGISTRATION NUMBER: 22,389 REFERENCE/POCKEY UNBERS: F-56.10 TELEPONE: (212)966-2340 INFORMATION FOR SEO ID NO: 3: LENGTH 738 TYPE: Amino acid TOPELCOMMUTICATION INFORMATION: TELEFAX: (212)966-2340 INFORMATION FOR SEO ID NO: 3: LENGTH 738 MOLECULE TYPE: Manile epithelial cell FEATURE: PROMITE FORMITE COMBUTER: MATHOR: FORMITE LENGTH 738 LENGTH 738 LENGTH 738 REGISTRATION MIRBER TYPE: MATHOR: MAT

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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                          STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                 COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : | ||||||||:
403 PERRPSIRMRQGGGGGGG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PTLRQALAARAGGGGGGGI 23
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 amino acids
                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS.0
Query Match
Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackensack
New Jersey
                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                      New Jersey
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                                                                                                        Hackensack
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US-09-100-664A-4
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                                                                                                                                                                                                                                      GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JUSTIN
APPLICANT: PRICE, JUSTIN
APPLICANT: PRICE, JUSTIN
APPLICANT: PRICE, JUSTIN
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
                Query Match
Best Local Similarity 58.6%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/110/PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
NAME: Jackson Esq., David A.
REGISTRATION UNDHER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-487-580
TELEKX: 201-487-580
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                 459 LAAALAAAGAGGGGGGGGGALAAALAA 487
                                                                                         6 LRQALAARAGGGGGGGGIEGPTLRQALAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/09100664A
; Patent No. 6057129
; GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 2, Application US/09100664A Patent No. 6057129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YOUNG, MICHAEL W. APPLICANT: KLOSS, BRIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 PERRPSIRMROGGGGGGG 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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CITY: Hackensack
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Best Local Similarity
Matches 11; Conserva
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US-09-100-664A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                       US-09-100-664A-2
US-08-864-038A-3
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Sequence 4, Application US/09100664A
Sequence 4, Application US/09100664A
Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: BLAU, JUSTIN
APPLICANT: PICE, JEFFREY
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%; Score 64; DB 3; Length 440; 55.0%; Pred. No. 2.7;
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SISIEM: RC-LUS/MS-LUSS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
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PF-0442 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,466
                                                                                                                                                                                                                                                            // Sequence 4, Application US/09240359
// Patent No. 6255456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                    553 ASALRAGGGGGGGGGMAP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  9 ALAARAGGGGGGGGIEGP 26
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                                                                                   Ouery Match 35 09
Best Local Similarity 72.29
Matches 13, Conservative
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                      LIBRARY: GenBank
CLONE: 829179
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STREET: 31,,
TTV: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                       ; CLONE: 8
US-08-987-466-4
                                                                                                                                                                                                                                          US-09-240-359-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08987466
Patent No. 5922595
GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A.
APPLICANT: Gooding, Douglas A.
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
CORRESPONDENCE ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Liba Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,466
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                         NAME: Jackson Esq., David A
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELERAN: 201-487-5800
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0442 US
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                       403 PERRPSIRMRQGGGGGGGV 422
                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 4 PTLRQALAARAGGGGGGGG 23
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                  TOPOLGGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                        ; HYPOTHETICAL
US-09-100-664A-4
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US-08-987-466-4
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Gaps
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35.0%; Score 63; DB 2; Length 584; 72.2%; Pred. No. 4.7; tive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Fisher, Douglas A.
APPLICANT: Gooding, Doug
APPLICANT: Streeter, Dave
TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPPRATING SYSTEM: DOS
SOFTWARE: PRAKERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,359
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Sequence 2, Application US/08319866
; Patent No. 5929223
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Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 445 aminc
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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34.4%; Score 62; DB 2; Length 360;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 12; Conservative 1; Mismatches 3; Indels
GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
APPLICANT: Yin, Jerry C.
APPLICANT: Yin, Jerry C.
APPLICANT: Regulski, Michael
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi, Stewart & Olstein STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bohinski, Robert J.,
APPLICANT: Whitsett, Jeffrey A.
TITLE OF INVENTION: Nucleic Acid Sequences
TITLE OF INVENTION: Controlling Lung Cell-
TITLE OF INVENTION: Specific Gene Expression
MIMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORIET OF THE TOTAL OF THE TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALO
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 360 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 QQAAAAVGGGGGGGG 42
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MEDIUM TYPE: 3.5 inc.
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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STATE: New Jersey
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STREET: Two
Trav: Lexington
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FESCUL 108-985-090-2

Sequence 2, Application US/08985090

Sequence 1, No. 58858130

Patent No. 58858130

PALECANT: Andrew D.J. Goodearl

APPLICANT: Andrew D.J. Goodearl

TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR INDHABER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%; Score 62; DB 2; Length 371; 52.0%; Pred. No. 3.9; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TEM PC compatible
COMPUTER: TEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: human thyroid transcription factor-1 US-08-442-809A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                 ATJOANDLANDS OLSTEIN TO THE THIOT M. NAME: OLSTEIN NUMBER: 24,025 REFERENCE/DOCKET NUMBER: 271010-360 TELEPHONE: 201-994-1700 TELEPHONE: 201-994-1744
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           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,809A
FILING DATE: 17-MAY-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,030
REGISTRATION NUMBER: 39,030
REFRENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,356
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
STRANDEDNESS:
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SOFTWARE: WordPerfect 5.1
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Best Local Similarity 52.03
Matches 13; Conservative
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APPLICATION NUMBER:
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Sequence 16, Application US/07776272
Patent No. 5612454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kaminuma, Toshihiko
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                                                                                                                                                                                   ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                       TITLE OF INVENTION: SUBTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Player, William E
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202-887-0400
202-887-0605
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FILING DATE: 19911129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1435
TTY: Washington
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es 13; Conserv
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                                                                                                                                                      LENGTH: 445
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                                                                                                                                                                        TYPE: PRT
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APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE 413
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                                                                                                                                                                                                                                                                                                             APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39
                                                Ouery Match
33.9%; Score 61; DB 2; Length 445;
Best Local Similarity 42.9%; Pred. No. 6;
Matches 12; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
33.9%; Score 61; DB 3; Length 445;
Best Local Similarity 42.9%; Pred. No. 6;
Matches 12; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                :| | ||||||| : ||
285 EAGEATLGGGGGGSVASPTSSSGSSSR 312
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                         8 QALAARAGGGGGGGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
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285 EAGEATLGGGGGGSVASPTSSSGSSSR 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        Sequence 2, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09167354A Patent No. 6136559 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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; MOLECULE TYPE: protein US-08-985-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                  US-09-165-543-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-165-543-2
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APPLICANT: Tajima, Masahiro
TITLE OF INVENTION: Process for Purification of Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
33.9%; Score 61; DB 4; Length 445;
Best Local Similarity 42.9%; Pred. No. 6;
Matches 12; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.6%; Score 60.5; DB 1; Length 26; 50.0%; Pred. No. 0.39;
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player
STREET: 1233 20th St. N.W. P.O. Box 18218
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
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ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: IBM PC COMPATIBLE
TOWN PC COMPATIBLE
TOWN PC 
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United States of America
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Patentin Release #1.0, Version #1.30
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPAS DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 5939602artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELLING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-UN-1996
                                                                                                                                                                                                                     REFERENCE/DOCKER NUMBER: CGC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER: US/08/808,931
                                                                                                              APPLICATION NUMBER: US/08/472,028A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-06-808-931-2
. Sequence 2, Application US/08808931
; Patent No. 5939602
                                                                                                                                                                                                         36,129
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GENERAL INFORMATION:
APPLICANT: VOLTATH, Marie
APPLICANT: Potter, Sharon
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                             : 537 amino acids
amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Potter, Sha
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Pe
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                            800
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                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                          FILING DATE
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                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                   APPLICANT: Steck, Peter
APPLICANT: Steck, Mark A.
APPLICANT: Steck, Mark A.
APPLICANT: Jasser, Samar
APPLICANT: Yung, W.K. Alfred
APPLICANT: Yung, W.K. Alfred
APPLICANT: ATVISION. Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3
TITLE OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREFT: 555 Thirteenth Street, N.W., Suite 701-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 33.3%; Score 60; DB 4; Length 645; Best Local Similarity 41.5%; Pred. No. 11; Matches 17; Conservative 4; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/791,115B
30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08472028A
; Patent No. 5767373
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 2318
TELECOMMUNICATION INFORMATION: 202-683-7031
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                   ; Sequence 6, Application US/08791115B ; Patent No. 6262242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 645 amino acids amino acid
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FILING DATE: 30-JAN
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                               Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-08-791-115B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                    US-08-791-115B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
TITLE OF INVENTION: Thereof
                                                               Gaps
                                                               8; Indels 13;
Query Match 33.1%; Score 59.5; DB 1; Length 537; Best Local Similarity 37.2%; Pred. No. 11; Matches 16; Conservative 6; Mismatches 8; Indels 13
                                                                                                                   3 GPTLRQALAARAGGGGG------GGGIEGPTLRQALAAR 35
                                                                                                                                                                  39 GPTVG---SSKIEGGGGTTITTDCVIVGGGISGLCIAQALATK 78
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us-09-422-838c-29.rai

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Gaps
                                                            Gaps
                                                          13;
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                      DB 3; Length 537;
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                                                          Indels
                                                                                                                                   39 GPTVG---SSKIEGGGGTTITTDCVIVGGGISGLCIAQALATK 78
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                                                                                                 3 GPTLRQALAARAGGGGG------GGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GPTLRQALAARAGGGGG------GGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                         APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Potter, Sharon
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
TITLE OF INVENTION: Protoporphyrinogen Oxidase
                    Score 59.5; Di
Pred. No. 11;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 6023012artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/020,003 FILING DATE: 21-JUN-1996 ATTORNEY/ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JMBER: US 60/012,705
28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 60/013,612
                                                                                                                                                                                                                                  Sequence 2, Application US/09050603A Patent No. 6023012 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CG TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                  33.1%;
nilarity 37.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 537 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-050-603A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timo
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS ADDRESSE: No. 6023
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                        Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27709
                                                                                                                                                                                              RESULT 17
US-09-050-603A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                     QO
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                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                      33.1%; Score 59.5; DB 2; Length 537; 37.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Johnson, Marie
APPLICANT: Volrath, Sandra
APPLICANT: Ward, Eric
TITLE OF INVENTION: Promoters from Plant
TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              39 GPTVG---SSKIEGGGGTTITTDCVIVGGGISGLCIAQALATK 78
                                                                                                                                                                                                                                                                                                                                                     ----GGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/08/808,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6018105artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 860/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
FILING DATE: 21-FEB-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1846
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                        CGC 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08808323 Patent No. 6018105
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
                                                                                               TELEFAX: (919) 541-8689 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                         : 537 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 537 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.2v
Conservative
                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-808-323-2
                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-808-931-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10591-9005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
US-08-808-323-2
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                                                                                                                                                           LENGIH:
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RESULT 20
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                                                                                                                         APPLICANT: Voltath, Sandra
APPLICANT: Voltath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Waid, Eric
APPLICANT: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OURENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,420B
FLING DATE: 22-JUN-1998
CLASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/059,164
FLING DATE: 13-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,603
FLING DATE: 13-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/126,430
FLING DATE: 11-APR-1998
PRIOR APPLICATION NUMBER: US 60/126,430
FLING DATE: 28-EB-1996
PRIOR APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-EB-1996
PRIOR APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-EB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-EB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-EB-1996
PRIOR APPLICATION NUMBER: US 60/013,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1%; Score 59.5; DB 3; 37.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: GG 1847/CIP3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-UNN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,028
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             ; Sequence 2, Application US/09102420B
; Patent No. 6084155
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27709
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                          US-09-102-420B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-102-420B-2
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Gaps

13;

Indels

6; Mismatches

Conservative

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Sequence 2, Application US/09196268
Patent No. 6282837
GENERATION:
APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
CITY: Hawthorne
                                                                                                                                                                                                APPLICANT: Ward, Eric R
APPLICANT: Wolrath, Sandra
APPLICANT: Wolrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 537;
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3 GPTLRQALAARAGGGGG------GGGIEGPTLRQALAAR 35
                                          39 GPTVG---SSKIEGGGGTTITTDCVIVGGGISGLCIAQALATK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GPTVG---SSKIEGGGTTITTDCVIVGGGISGLCIAQALATK 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BLICATION NUMBER: US/09/071,296
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%; Score 59.5; I
37.2%; Pred. No. 11;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGC 1748/CIP
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                    US-09-071-296-2
; Sequence 2, Application US/09071296
; Patent No. 6177245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 537 amino acids
amino acid
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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STATE:
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COUNTRY:

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6; Mismatches
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37.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Ciba-Geigy Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/191,998
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09191998
; Patent No. 6307129
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,129
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TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
     537 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                    Query Match 33.19
Best Local Similarity 37.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-015-683-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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Best Local Similarity 37.29
Matches 16; Conservative
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; MOLECULE TYPE: protein
US-09-191-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 0 CLASSIFICATION:
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LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ward, Eric R
APPLICANT: Wolrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1%; Score 59.5; DB 4; Length 537; 37.2%; Pred. No. 11; tive 6; Mismatches 8; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GPTLRQALAARAGGGGG-----GGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Version #1.25
APPLICATION NUMBER: US/09/196.268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/015,683
                                                                                                                                                                                                                                                                              CGC 1748/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGC 1748/CIP
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
                                                                                                                  UMBER: US/09/196,268
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Ciba-Geigy Corporation
: 7 Skyline Drive
Hawthorne
                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFRENCE/DOCKET NUMBER: CGC 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09015683
Patent No. 6288306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CGC TELECOMUNICATION INFORMATION: TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 37.2%;
....nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                         : 537 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10532
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-196-268-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
US-09-015-683-2
                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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Gaps
                                                                                                                                                                                                                                                APPLICANT: Ward. Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
33.1%; Score 59.5; DB 4; Length 537; 37.2%; Pred. No. 11; tive 6; Mismatches 8; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                 3 GPTLRQALAARAGGGG------GGGIEGPTLRQALAAR 35
                                                                                          3 GPTLRQALAARAGGGGG------GGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 GPTVG---SKIEGGGGTTITTDCVIVGGGISGLCIAQALATK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09497698; Patent No. 6308458
GENERAL INFORMATION:
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1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 969;
                                                APPLICANT: BARR, PHILLP J
APPLICANT: BARR, MICHAEL C
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
ANDERCORD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                         3: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/284.941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REGISTRATION NUMBER: 30092
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 380316 COOLEY PA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%; Score 59.5; D 60.0%; Pred. No. 20; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AARAGGGGGGGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AAGAGGAGGAGGAGFR-PLAPR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2 Application US/08447642; Sequence 2 Application US/08447642; Patent No. 5989890; GENERAL INFORMATION:
      Sequence 2, Application US/08284941
patent No. 5863756
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      969 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
                                                                                                                                                                                                                            STREET: FIVE CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94306
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                                                                                                                                                                                                                                                                                                                  94306
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                                                                                                                                                                                                              ADDRESSEE:
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US-08-284-941-2
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                                                                                          Heifetz, Peter
HERBICIDE-TOLERANT PROTOPORPHYRINGEN
TITLE OF INVENTION: HERBICIDES ("PROTOX")
                                                                                                                                                                                                                                                                                                                                                     COMPUTER KEADABLE TOWN:

MANDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPACTIBLE
COMPUTER: TOWN PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/497,698
APPLICATION NUMBER: US/09/497,698
FILING DATE: 03-PED-2000
FILING DATE: 03-PED-2000
FILING DATE: 03-PED-2000
70-PETING DATE: 03-PED-2000
FILING DATE: 03-PED-2000
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: NO. 6308458artis Corporation
ADDRESSEE: NO. 6308458artis Gordenton
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 60/012,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
FILING DATE: 06-JUN-1996
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-497-698-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/102,420
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REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-1996
28-FEB-1996
21-JUN-1996
06-JUN-1995
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SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
                                APPLICANT: Volrath, Sandra
Johnson, Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  ZIP: 27709
COMPUTER READABLE FORM:
                                                                            Ward, Eric
                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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REFERENCE/DOCKET NUMBER: CHIR-009/00US TELECOMMUNICATION INFORMATION:
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirlar Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubrammalan, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/02147A FILING DATE: 19930309
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEO ID NO. 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             Floppy disk
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 969 amino acids TYPE: amino acid
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                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                         PALO ALTO
CALIFORNIA
                                                                    NUMBER OF SEQUENCES:
                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yin, Qun
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                                                                                                                                                                                                                                                                             94306
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                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                        STATE:
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APPLICANT: Riefer, Michael C
TITLE OF INVENTION: Compositions and Methods for PACE 4 and 4.1 Gene and
TITLE OF INVENTION: Polypeptides in Cells
TITLE OF INVENTION: Polypeptides in Cells
CURRENT APPLICATION NUMBER: US/09/236,503
CURRENT APPLICATION NUMBER: 08/447,642
EARLIER FILING DATE: 1995-05-23
EARLIER FILING DATE: 1995-06-23
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1994-08-02
EARLIER FILING DATE: 1992-03-09
SOFTWARE: PATENTING DATE: 1902-03-09
SOFTWARE: PATENTING DATE: 1902-03-09
SOFTWARE: PATENTING DATE: 1902-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1%; Score 59.5; DB 2; Length 969;
60.0%; Pred. No. 20;
tive 0; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2. Application PC/TUS9302147A
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 969;
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                                                                       PRIOR APPLICATION DATA:

**PLICATION DATA:

**PLICATION NUMBER: US 08/284,941

**PLICATION NUMBER: US 08/284,941

**ATTORNEY AGENT INFORMATION:

**NAME: NELEY PH.D. **RICHARD L.**

**REFERENCE/DOCKET NUMBER: 30092

**REFERENCE/DOCKET NUMBER: CHIR-009/01US

**PELEPHONE: (415) 843-5070

**TELEPHONE: CHARATERIZIUS:

**TELEPHONE: CHARATERIZIUS:

**PLOMEMATION FOR SEO ID NO: 2:

**SEQUENCE CHARATERIZIUS:

**PLOMEMATION FOR SEO ID NO: 2:

**PLOMEMATION FOR S
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33.1%; Score 59.5; D
Best Local Similarity 60.0%; Pred. No. 20;
Matches 15; Conservative 0; Mismatches
APPLICATION NUMBER: US/08/447,642
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Patent No. 6277590
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I: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 969 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.09
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-642-2
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US-09-236-503-2
                        FILING DATE: 23
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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LENGTH: 969
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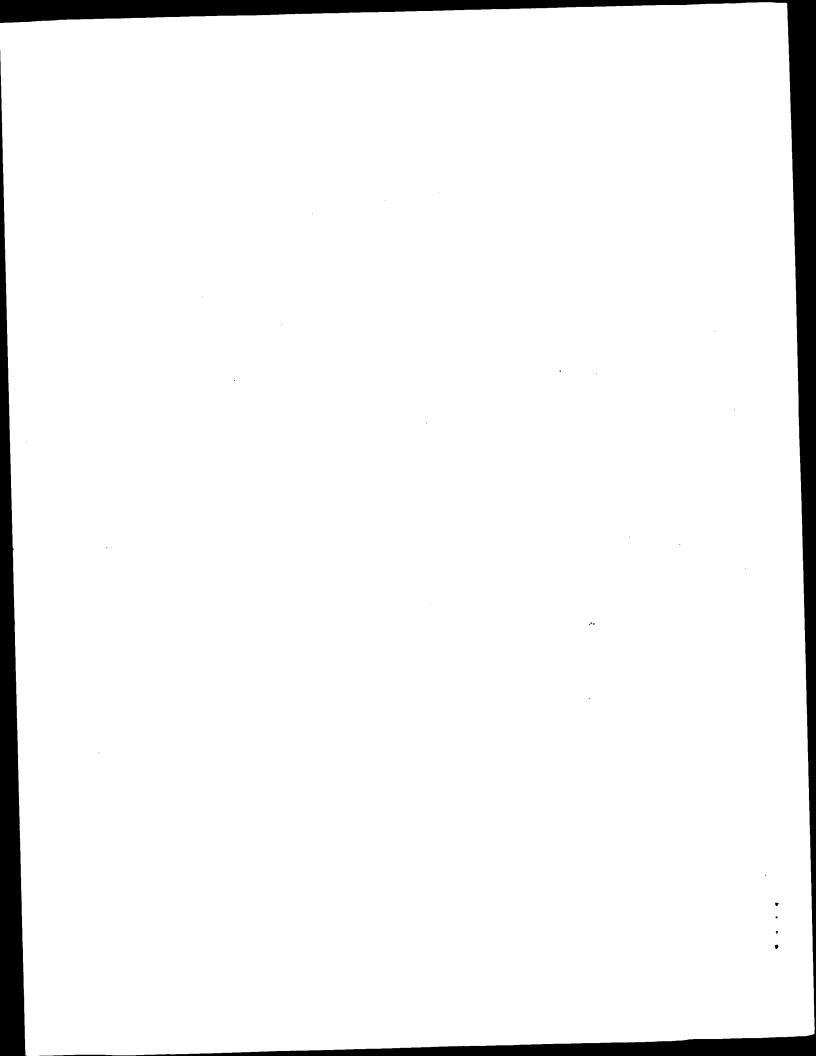
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Gaps
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PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.1%; Score 59.5; DB 5; Length 969; 60.0%; Pred. No. 20; tive 0; Mismatches 9; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                               ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                             STRANDEDNESS:
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                                                                               LENGIH:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.8%; Score 59; DB 2; Length 14; Best Local Similarity 92.9%; Pred. No. 0.3; Matches 13; Conservative 0; Mismatches 1; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Balasubramanian, Palaniappan
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                           APPLICATION NUMBER: US/08/764,640
FILING DAME: 11-DEC-1996
CLASSIFICATION: 514
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Patent No. 5869451
Patent No. 5869451 5837683
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: HTUDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: PK328
REPREBRUCE/DOOKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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: Five Moore Drive, P.C
Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
TYPE: amino acid
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                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
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US-08-764-640-193
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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MEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
                                                                                                                                                                                                                                                                                                                                                                                              y Match 32.8%; Score 59; DB 2; Length 14; Local Similarity 92.9%; Pred. No. 0.3; ly Indels hes 13; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
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Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08973225A; Patent No. 6083913 GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA ZIP: 27709 COMPUTER READABLE FORM:
                                                                                                                                        14 amino acids
                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-764-640-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLROALAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                        amino acid
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Qγ Op

Search completed: October 9, 2002, 09:06:33 Job time : 6.98595 secs



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

	Description		hypothetical prote	ical	e deox	myosin heavy chain		cal	ble ATP/	otein		$\overline{}$	glycine-rich RNA-b	probable membrane	hypothetical prote	Н	alanyl-tRNA synthe	glycine-rich RNA-b	RNA-binding glycin	transforming prote	probable Hflx - My		alanyl-tRNA synthe	insulin precursor	single strand bind			c prot		thyroid transcript	nomeotic protein H
SUMMARIES	1	Ē		113030			JQ1094		00100				5/1/3				3 6		62006							541771			1 0	A	
Length DB	- 1						5005																						401 2		
% Query Match Le		38.1	æ	38.1	^	. 10	36.7	10			9	S	2	5.	'n.	ъ.	'n.	'n.	35.0	'n	٠.	S	34.7	34.7	34.7	34.4	34.4	34.4	34.4	34.4	
Score		68.5	œ.	æ.	29	99	99	65	65	65	65	64	64	64	64	63.5	63	63	63	63	63		2	62.5	2	62	62	62	62	62	
Result No.		1	2	m	4	S	9	7	80	6	10	11	12	13	. 14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	

hypothetical prote hypothetical prote hypothetical prote unknown protein F2 FREAC-4 - human hypothetical prote insulin precursor DNA-binding protei glycine-rich RNA-b protein FGD2.4 { i hypothetical protein franscription fact transcription fact hypothetical protein keratin, 59K type	hypothetical glyci hdc protein - frui
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T29960 C86206 H85067 C96690 G02738 B71260 INSH S59853 T10479 F86514 F86341 A49642 F86624	S58064
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317 155 250 250 298 465 71 77 311 420 543 543 568	649
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61.5 61.6 61.6 61.6 60.5 60.5 60.6 60.6 60.6	09
330 330 330 330 344 440 440 440 440 440	45

064 hdc protein - frui ALIGNMENTS	- Arabidopsis thaljana (mouse-ear cress) vision 23-Apr-1999 #text_change 20-Jun-2000 M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro e Database, April 1999 3; GSPDB:GN00062; ATSP:F16J13.120	ana hypothetical protein T12H17.200 Score 68.5; DB 2; Length 339; Pred. No. 2.8; 8; Mismatches 13; Indels 3; Gaps 1; IECPTLRQALAARA 36 : : : MGSSPPMWGQQQAMAAMA 306	- fruit fly (Drosophila melanogaster) ster revision 13-Aug-1999 #text_change 17-Nov-2000 ell, B. rary, November 1998 distal X chromosome of Drosophila melanogaster. ted from GB/EMBL/DDBJ 363; NID:el331652; PID:el355938; PIDN:CAA21318.1 fn0025833 690/3	Score 68.5; DB 2; Length 806; Pred. No. 6.1; ; Mismatches 11; Indels 13; Gaps 1;
4.5 00 33.3 649 2 S58064	RESULT 1 T06612 hypotherical protein F16J13.120 - Arabidopsis thaljana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000 R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, i. Rseference number: 215789 A;Mcerence number: 215789 A;Mceresion: T06612 A;Molecule type: DNA A;Residues: 1-39 <-BEV> A;Residues: 1-39 <-BEV> A;Experimental source: cultivar Columbia; BAC clone F16J13.120 A;Map position: 4 A;Map position: 4	C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17 Query Match Best Local Similarity 38.5%; Pred. No. 2.8; Matches 15; Conservative 8; Mismatches 13; Indels Qy 1 IEGPTLRQALARAGGGGGGGGGGGGGTTRQALAARA 36 : : : :	RESULT 2 T13690 hypothetical protein EG0003.2 - fruit fly (Drosophila melanogaster) C.Species: Drosophila melanogaster C.Species: Drosophila melanogaster C.Bate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C.Accession: T13690 Submitted to the EMBL Data Library, November 1998 A.Reference number: 217699 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Molecule type: DNA A.Molecule Scales: 1-806 cAUR> A.Cross-references: EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA21318 A.Cross-references: F19Base:FB90025833 A.Introns: 37/3; 448/3; 611/2; 690/3	Query Match 38.1%; Score Best Local Similarity 34.0%; Pred. Matches 16; Conservative 7; Mis

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A; Residues: 1-201 <ROT>
A; Residues: 1-201 <ROT>
A; Residues: 1-201 <ROT>
A; Residues: 1-201 <ROT>
A; Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z78013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A;Experimental source: clone F15B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: tomato ringspot virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C;Accession: JQ1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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F;923-978/Region: alanine/glycine/proline-rich
F;983-1030/Domain: SH3 homology <SH3>
F;1034-1168/Region: alanine/glycine/proline-rich
F;107/Binding site: ATP (Lys) #status predicted
F;311/Binding site: phosphate (Ser) (covalent) #status experimental
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0
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Pred, No. 7.3;
                                                                                                                                                                                        Score 67; DB 1; Length 1168;
Pred. No. 12;
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Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                    4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Rott, M.E.; Tremaine, J.H.; Rochon, D.M.
J. Gen. Virol. 72, 1505-1514, 1991
A;Title: Nucleotide sequence of tomato ringspot virus RNA-2.
A;Reference number: JQ1093; MUID:91311402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F15B9.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 20.2K protein - tomato ringspot virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1996
A.Reference number: 219351
A.Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            920 OILGAKGGGGGGGRGRGGPSPSGAVSPR 947
                                                                                                                                                                                                                                                                                                                                             8 QALAARAGGGGGGGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 RAGGGGGGGTE----GPTLRQALAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain raspberry
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61.5%;
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Best Local Similarity 50.0%;
Matches 14; Conservative
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP:F15B9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JQ1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Aintrons: 1/3; 37/3; 60/2; 100/2; 153/3; 179/3; 208/2; 242/3; 287/3; 371/3; 428/
C; Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; 5H3 homology
C; Reywords: actin binding: ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein; F; 10-653/Domain: myosin motor domain homology <a href="https://domain.myosin.myop.nebinding">https://domain.myosin.myop.nebinding</a> motor domain motology <a href="https://domain.myop.nebinding.html">https://domain.myop.nebinding.html</a> (AP)</a>
F; 543-564 Region: actin binding #status predicted
F; 571-1168/Domain: carboxyl-terminal <CTD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myosin heavy chain IC - Acanthamoeba castellanii
N;Contains: myosin Arpase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Accession: A33891. C34448; A24146
C;Accession: A33891. C34448; A24146
A;Title: The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like and non-my A;Reference number: A33891; MUID:88016163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: this gene and protein are called MIB in this paper
R; Brzeska, H; Lynch, T.J.; Martin, B.; Korn, E.D.
B; Biol. Chem. 264, 19340-19348, 1989
A; Tille: The localization and sequence of the phosphorylation sites of Acanthamoeba myos
A; Reference number: A34448; MUID:90037074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: C34448
A.Molecule type: protein
A.Residues: 308-314, 1x, 16-329 CBRZ>
C.Comment: In this protein, the coiled-coil rod-like region found in many myosin heavy he protein is globular and does not self-associate into filaments.
C.Genetics:
                                                                                                                                                                                                                                                                 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Chlamydomonas reinhardtii probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Chlamydomonas reinhardtii C:Species: Chlamydomonas reinhardtii C:Species: Chlamydomonas reinhardtii C:Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000 C;Accession: S57795; S66368 F:Smell G:Dr. Min. B:: Lefebbre, P.A. R:Smell G:Dr. Min. B:: Lefebbre, P.A. Plant Mol. Biol: 28, 443-444, 1995 A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the A;Title: Characterization of the Characteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L07561; NID:g945420; PIDN:AAC37438.1; PID:g945421 A;Accession: S66368 A;Accession: S66368 A;Molecule type: mRNA A;Residues: 1-867 <SMW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross references: EMBL:L07561; NID:9945420; PIDN:AAC37438.1; PID:9945421
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A;Residues: 1-1168 <JUN>
A;Cross-references: GB:J02974; NID:9155624; PIDN:AAA27707.1; PID:9155625
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Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                 3 GPTLRQAL-----AARAGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 34/3; 159/2; 210/3; 265/3; 329/3; 406/1; 837/3
C;Keywords: carbon-carbon lyase; photoreceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PTLRQALAARAGGGGGGGGIEG-PTLRQAL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 38.1%;
Local Similarity 50.0%;
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;675-883/Region: basic
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A; Residues: 1-867 <SMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S57795
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S57795
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A/Introns: 86/3
C:Superfamily: laccase
C:Superfamily: laccase
C:Superfamily: laccase
C:Superfamily: laccase
C:Superfamily: laccase
C:Superfamily: laccase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-49/Domain: propeptide #status predicted <PRO>
F:50-619/Product: laccase #status predicted <MANT>
F:516-372/Domain: amino-terminal beta-barrel #status predicted <BB1>
F:131-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F:139, 282, 253, 430, 432, 444/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146, 189, 191, 482, 548, 550/Binding site: 200-0 cluster (His) (copper type 3) #status predicted
F:477, 549, 554/Binding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                   A.Molecule type: DNA
A.Residues: 379-619 <GE2>
A.Cross-references: GB:M14554; NID:9168823; PIDN:AAA33590.1; PID:9168824
C.Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquino
                                          Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A/Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospor
A/Reference number: A29762; MUID:87067412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Neurospora crassa
C; Date: 30-28p-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C; Accession: B28523
R; Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Cham. 263, 885-896, 1988
A:Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino-A; Reference number: A28523; MUID:88087214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 1; Length 619;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · Neurospora crassa (strain TS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.1%; Score 65; DB 1; Length 619;
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live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RQALAARAGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 RQALAARAGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 RQDSQAERYGGGGGGGCNSPINRQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laccase (EC 1.10.3.2) precursor
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C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G87033
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Cole, S.T.; Eiglmeier, K.M.
K.M. Butherford, K.M.
K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Schatce number: A86909; MUID:21128732; PMID:11234002
A;Accession: G87033
A;Scature 5 preliminary
A;Molecule type: DNA
A;Residues: 14488 <570>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.Alternate names: urishiol oxidase
C;Species: Neurospora crassa
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: A28523; A29762
B;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A;Titler: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and
                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ML0997
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Start codon: GTG
C.Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:AL450380; NID:g13093026; PIDN:CAG31378.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: B2235_C2_202 protein
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C; Accession: S7293
R; Smith, D.R.; Robison, K.
Submitted to the RMEL Data Library, November 1993
A; Reference number: S72587
A; Accession: S72938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.1%; Score 65; DB 2; Length 488; 45.8%; Pred. No. 9.1; tive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%; Score 65; DB 2; Length 518; 45.8%; Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 GESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQALAARAGGGGGGGGIEGP 26
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A; Residues: 1-518 <SMI>
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A; Residues: 1-619 <GER>
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Gaps . 0

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A;Experimental Source: Strain 945C
A;Experimental Source: Strain 945C
A;Experimental Source: Strain 945C
A;Experimental Source: Strain 945C
Briones, M.B. J. G.; Relnach, F.C.; Arruda, P.; Abreu, F.B.; Carraro, D.M.; Carrer
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.B.; Ferreira, A.J.S.
as.Neto, E.; Doccena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
Submitted to GenBank, June 2000
Submitted to GenBank, June 2000
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La A; Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Miyaki, C.
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
J.D.; Junqueira, M.C.; Maclina, M.C.; Ge Oliveira, M.C.; Ge Oliveira, R.C.; Palmieri,
R.G.; Nunes, L.R.; Oliveira, M.C.; Ge Sa, R.G.; Santelli, R.V.; Sawa
Rodrigues, V.; Rosa, A.J. de M.; de Rosa 21r, V.E.; de Sa, R.G.; Santelli, R.V.; Saya
A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; de Silva, A.J.
M.; Tsuhako, M.H.; Vallada, H.; Van Silvys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
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A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A83515; MUID: 20365717
A; Note: for a complete list of authors see reference number A59328 below
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C;Date: 18-Ang-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: C82844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alanyi-tRNA synthetase XF0124 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y41C4A.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T26808
R;Steward, C. Species: C, Accession: C, Accession (C, Accession) (C, Acc
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
35.6%; Score 64; DB 2; Length 333;
Best Local Similarity 76.9%; Pred No. 8.2;
Matches 10; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                             Score 64; DB 2; Length 331;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                 1; Indels
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C; Superfamily: fos/jun DNA-binding domain homology
                                                                                            A; Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C; Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: clone Y41C4A
A; Experimental source: clone Y41C4A
                                                                                                                                                                                                                                           35.6%;
76.9%;
                                                                                                                                                                                                                                                       35.6%
Query Match
Best Local Similarity 76.9%
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 GGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z20269
A; Accession: T26808
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A;Molecule type: DNA
A;Residues: 1-916 <SIM>
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A; Residues: 1-333 <WIL>
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                                                                                    A; Gene: CESP:Y41C4A.4a
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                                                               C;Genetics
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                                                                                                                                                                                        C; Accession: $71779
R; Guillinan, M.J.; Niu, X.
A; Reference number: $71779; MuID: 96311016
A; Reference number: $71779; MuID: 96311016
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-167 GUID: 07074604. DIENNIARATAINA 1. DIENIAGATAENS
A; Residues: 1-167 GUID: 07074604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acene: GRP1
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
E;7-14/Domain: ribonucleoprotein repeat homology <RRM4>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YLR338w - yeast (Saccharomyces cerevisiae)
Alternate names: hypothetical protein L8300.13-a
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 20-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 05-Nov-1999
                                                                               glycine-rich RNA-binding protein GRP1 - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: U32310; NID: 9974604; PIDN: AAA75104.1; PID: 9974605
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 35.6%; Score 64; DB 2; Length 167; Local Similarity 61.1%; Pred. No. 4.4; as 11; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y41C4A.4a - Caenorhabditis elegans
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submitted to the EMBL Data Library, January 1994
submitted to the Sequence of S. cerevisiae cosmid 8300.
A;Description: The Sequence of S. cerevisiae A;Reference number: S69312
A;Reference number: S69312
A;Accession: S69312
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C;Keywords: transmembrane protein
F;142-158/Domain: transmembrane #status predicted <TM1>
F;201-217/Domain: transmembrane #status predicted <TM2>
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A;Molecule type: DNA
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A; Residues: 1-285 <DUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S69312
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C. Species: Mycobacterium tuberculosis (strain H37RV)
C. Species: Mycobacterium tuberculosis
C. Date: 17-7ul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
R. C. Date: 17-7ul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
R. Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Rajandream, M.A.; Rogers, R.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1998
A. Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.; Tile: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; A. Reference number: A70500; MuID: 98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:298209; GB:AL123456; NID:93261838; PIDN:CAB10901.1; PID:e33228
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'.5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific, splice form I N'Contains: 3'.5'-cyclic-nucleotide phosphodiesterase, cAMP-specific, splice form II C'Species: Drosophila melanogaster.
C'Date: 28-oct.1995 #sequence_revision 19-uul-1996 #text_change 17-Nov-2000
C'Accession: 85543; 819662; 855842; 85584; A26651
J. Mol. Biol. 222, 533-565, 1991
J. Mol. Biol. 222, 553-565, 1991
J. Melerence number: S19662; MUID:92085274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: hilx
C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                A.Cross-references: EMBL:X60063; NID:962927; PIDN:CAA42665.1; PID:962928 C;Superfamily: jun transforming protein; fos/jun DNA-binding domain homology C;Keywords: DNA binding; nucleus; transcription regulation F;237-277/Domain: fos/jun DNA-binding domain homology <FyD>
                                                        Cibate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999 C.Accession: $20099 | R.Barti, M.; Butchins, J.T.; Vogt, P.K. Oncogene 6, 1623-1631, 1991 | A.7tile: The chicken junb gene and its product. A.Reference number: $20099; MUID:920198832 | A.Accession: $20099; MUID:920198832 | A.Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-495 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Pred. No. 10;
tive 0; Mismatches 10; Indels
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45.8%; Pred. No. 15;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63;
Pred. No. 1
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                                  C; Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%;
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Best Local Similarity 58.38
Matches 14; Conservative
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A; Residues: 1-777 <QIU>
A;Cross-references: EMBL:X55174
A;Accession: S19662
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A; Residues: 1-323 <HAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine-rich RNA-binding protein RGP-1c - wood tobacco
C.Species: Nicotiana sylvestris (wood tobacco)
C.Species: Decelog4 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C.Accession: S41773
B.Hirose, T.: Sugita, M.: Sugiura, M.
Nucleic Acids Res. 21, 3981-3987, 1993
A.Title: cDNA structure, expression and nucleic acid-binding properties of three RNA-bin
A.Reference number: S41771; MUID: 93382772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Nicotiana sylvastris (wood tobacco
C;Species: Nicotiana sylvastris (wood tobacco)
C;Accession: S59529
C;Accession: S59529
R;Hirose, T.: Sugita, M.; Sugiura, M.
Submitted to the EMBL Data Library, May 1993
A;Description: CDNA structure, expression and nucleic acid-binding properties of three A;Accession: S59529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D16206
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
E;7-74/Domain: ribonucleoprotein repeat homology <RRM1>
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C; Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F;7-74/Domain: ribonucleoprotein repeat homology <RRM1>
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1 Similarity 38.5%; Pred, No. 23; 10. 23; 15; Conservative 6; Mismatches 11: 12301
                                                                                                                                                                                                            6; Mismatches 11; Indels
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Pred. No. 5.5;
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                                           C'Genetics:
A'Gene: XF0124
C'Superfamily: alanine--tRNA ligase
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78 TVNEAQSRGSGGGGGGGFRG 98
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hes 11; Conservative
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A; Reference number: A59328
A; Contents: annotation
                                                                                                                                                                            Best Local Similarity
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A; Residues: 1-165 <HIR>
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A; Residues: 1-165 <HIR>
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                                                                                                                                                      Query Match
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S41773
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R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
FEBS Lett. 349, 205-209, 1994
A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degra
A;Reference number: S46258; MUID:94326921
A;Reference number: S46258
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A; Molecule type: protein
A; Residues: 85-105 (-58N>
R; Sanger, F.: Tuppy, H.
Biochem. J. 49, 481.490, 1951
A; Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investi
A; Reference number: A90341
A; Accession: A90341
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 25-54 (-58A)
B; R; Cheng, R.; Kawakishi, S.
B; Cheng, R.; Rawakishi, S.
Bur. J. Blochem. 223, 759-764, 1994
A; Title: Site-specific oxidation of histidine residues in glycated insulin mediated b
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A; Molecule type: protein
A; Residucs: 57-82 <8787,
B; Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Bur. J. Biochem. 20, 183-189, 1971
Eur. J. Biochem. 20, 183-189, 1971
A; Heference number: A91185; MUID:71257721
A; Accession: A91185
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A;Residues: 57-82 <SAL>
R;Sanger, F.; Thompson, B.O.P.
Biochem. J. 53, 366-374, 1953
A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation
C; Accession: A40909; A92080; A92074; A91185; A90342; A90341; S48184; S48185; S46258; R; D'Agostino, J.; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L. Mocrinol. 1, 327-331, 1987. And A.Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic a A.Reference number: A40909; MUID: 88288209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: protein
A.Residues: 25-105 <NOL>
B.Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
J. Biol. Chem. 246, 1365-1374, 1917,
A.Filte: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A.Reference number: A22074; MUID:71116409
                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:M54979; NID:g163578; PIDN:AAA30722.1; PID:g163579
A,Experimental source: fetal pancreas
R;Nolan, C.; Margollash, E.; Peterson, J.D.; Steiner, D.F.
J. Biol. Chem. 246, 2780-2795, 1971
A;Title: The structure of boxine proinsulin.
A;Reference number: A92080; MUID:71166442
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F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-54/Domain: insulin chain B #status experimental <BCH>
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 25-30, 'x', 32-42, 'x', 44-54 <CH2>
A; Residues: 25-30, 'x', 32-42, 'x', 44-54 <CH2>
B; Ryle, A: Sanger, F:; Smith, L.F.; Kitai, R.
Biochem. J. 60, 541-556, 1955
A; Title: The disulphide bonds of insulin.
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A;Contents: annotation; amides; disulfides
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A, Residues: 25-54 <WEN>
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A; Residues: 1-105 <DAA>
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C;Accession: H83533
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradyn, Y.; Brady, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S. Larvy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. Reference number: A82950; MUID: 20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004524; GB:AE004091; NID:99946795; PIDN:AAG04292.1; GSPDB:GN001
A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 'MVCSFCCCCYNFRN', 4, 'P', 6, 'S', 94-777 <014>
A; Residues: 'MVCSFCCCYNFRN', 4, 'P', 6, 'S', 94-777 <014>
A; Residues: 'MVCSFCCCYNFRN', 4, 'P', 6, 'S', 94-777 <014>
A; Residues: 'MVCSFCCCYNFRN', 4, 'P', 6, 'S', 94-777 <014>
A; Residues: 'MVCSFCCCYNFRN', 4, 'P', 6, 'S', 94-777 <014>
A; Caros: references: EMBL: X5517
A; Denomer: A: Denomer, A: Basidues: A: Basidue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross_references: Pigase:FBgn0000479
A;Cross_references: P125/3: 165/2: 200/2; 262/3: 294/1; 407/3: 496/2; 534/2: 588/3: 7
A;Introns: 93/2: 125/3: 152/2: 165/2: 200/2; 262/3: 294/1: 407/3: 496/2: 534/2: 588/3: 7
C;Superfamily: 3',5'-cyclic-nucleotide phosphodisesterase lB, calmodulin-dependent; 3',5'-c;References: phosphoric diester hydrolase
C;Reywords: alternative splicing: phosphoric diester hydrolase
F;337-777/Product: cAMP-dependent 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F;439-667/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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; Species: Pseudomonas aeruginosa
; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 'MQAEQ',86-87,'IG',90-91,'QKYHSRYLKNRRHTLANVR',94-777 <Q13>
A;Cross-references: EMBL:X55174
A;Accession: S65544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.0%; Score 63; DB 2; Length 777; 72.2%; Pred. No. 22; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GPTLRQALAARAGGGGG-----GGGIEGPTLRQALA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: alaS; PA0903
C;Superfamily: alanine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%;
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ALAARAGGGGGGGGIEGP 26
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Matches 13; Conservative
                                                                                                                             A; Residues: 137-777 <Q12>
A; Residues: 137-777 <Q12>
A; Cross-references: EMBL:X55174
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A; Residues: 1-874 <STO>
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941Cine-rich RNA-binding protein. RGP-la - wood tobacco
C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 25-Dec:1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C;Accession: S41771
R;Hirose, T; Sugita, M; Sugiura, M.
Nucleic Acids Res. 21, 3981-3987, 1993
A;Title: CDNA structure, expression and nucleic acid-binding properties of three RNA-A;Reference number: S41771; MUID:93382772
A;Molecule type: mRNA
A;Residues: 1-156 CHIR>
A;Nolecule type: RMB-D16204; NID:9436789; PIDN:BAA03741.1; PID:9469070
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F;7-74/Domain: ribonucleoprotein repeat homology <RRNI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.D'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli,
Genomics 10, 43-50, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: EVX2, a human homeobox gene homologous to the even-skipped segmentation gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thyroid transcription factor-1 - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: 146089; S42104
R;Van Renterghem, P.H.G.; Dremier, S; Vassar, G.; Christophe, J.
Mol. Cell. Endocrinol. 112, 83-93, 1995
A;Title: Study of TTF1 gene expression in dog thyrocytes in primary culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X77910; NID:g457488; PIDN:CAA54868.1; PID:g457489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 2; Length 156;
Pred. No. 6.7;
4; Mismatches 6; Indels
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C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regu
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A; Residues: 1-371 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 13;
1; Mismatches
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52.48;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: B87245
R; Davies, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A; Aluthors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A; Reference number: A86909; MUID:21128732; PMID:11234002
A; Reference number: P87345
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
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A; Residues: 1-168 <STO>
A; Cross-references: GB:AL450380; NID:913093879; PIDN:CAC32216.1; GSPDB:GN00147
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                                                                                                                                                                                                                                                                                                                                                                        single strand binding protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Neirospora crassa
;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                          Gaps
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                                                                                                                         34.7%; Score 62.5; DB 1; Length 105; 40.6%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 62.5; DB 2; Length 168; 56.0%; Pred. No. 6.3; tive 3; Mismatches 3; Indels 5
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                      F;57-82/Domain: connecting peptide #status experimental <CPEP> F;85-105/Domain: insulin chain A #status experimental <AGH> F;31-91,43-104,90-95/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:AL356124; GSPDB:GN00116; NCSP:B9J10.290
Experimental source: BAC clone B9J10; strain OR74A
                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein B9J10.290 [imported] - Neurospora crassa
F;25-54,85-105/Product: insulin #status experimental <MAT>
                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                              1 IEGPTLRQALAARAGGGGGGGGGEGPTLRQAL 32
                                                                                                                                                                                                                                            2 EGPTLRQALA----ARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 EGRVGRIEMAWGGGGRRGGGGGGGGGVNG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GPSLRYATAKVNKASRSGGGGGFG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQAL----AARAGGGGGGG 22
                                                                                                                                                                      Conservative
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Matches 14; Conservative
                                                                                              Query Match
Best Local Similarity
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Residues: 1-201 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: C; Genetics: A; Gene: NCSP:B9J10.290
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A; Status: prelimina
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                                                                                                                                                                                                                                                                                                                                   RESULT 23
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Gaps

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Genetics:

Gaps

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Length 401; 9; Indels

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A; Map position: 14613-14413
A; Map position: 14613-14413
A; Introns: 26/2; 155/1
A; Introns: 26/2; 155/1
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 192-248/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                   34.4%; Score 62; DB 2; 52.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
A;Cross-references: GDB:132588; OMIM:600635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| | :||||||||| | :||
256 QQQLQQDSGGGGGGGGGTGCPQQQQA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                    7 RQALAARAGGGGGGGGGIEGPTLRQA 31
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                                                                                                                                                                                                                                                                                                34.4%
Query Match
Best Local Similarity 52.0%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homeotic protein HB9 - human
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A; Introns: 9/3; 43/3; 70/3
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A; Residues: 1-317 <MIL>
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A; Residues: 31-401 <SAI>
A; Cross-references: EMBL:X82850; NID:g695582; PIDN:CAA58053.1; PID:g695583
A; Cross-references: EMBL:X82850; NID:g695582; PIDN:CAA58053.1; PID:g695583
A; Cross-references: EMBL:X82850; NID:g695582; PIDN:CAA58053.1; PID:g695583
B; Cross-references: EMBL:X82850; NID:g695582; PIDN:CAA58053.1; PID:g695583
A; Title: The complete nucleotide sequence of the mouse thyroid-specific, enhancer-binding A; Reference number: S53724; MUID:g9526463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: EMBL:U33627; NID:g1113816; PID:g1000129
R;Ikeda, K.; Clark, J.C.; Shaw-White, J.R.; Stahlman, M.T.; Boutell, C.J.; Whitsett, J.R. J. Biol. Chem. 270, 8108-8114, 1995
A;Title: Gene structure and expression of human thyroid transcription factor-1 in respir A;Reference number: A56451; MUID:95229626
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A; Residues: 31-401 <IKE>
A; Cross-references: GB:U19816; NID:9767832; PIDN:AAC50125.1; PID:9767833
A; Cross-references: GB:U19816; NID:9767832; PIDN:AAC50125.1; PID:9767833
B; Salardi, A; Tassi, V.; de Filippis, V.; Civitareale, D.
B; Salardi, A; Tassi, V.; de Filippis, V.; de Filippi
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R;Hamdan, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thyroid transcription factor 1 - human

N.Alternate names: Drosophila NK-2 homolog A; thyroid nuclear factor

N.Alternate names: Drosophila NK-2 homolog A; thyroid nuclear factor

C; Species: Homo sapiens (man)

C; Species: 1966 #sequence_revision 06_Jun-1997 #text_change 17-Nov-2000

C; Accession: G02321; G02039; A56451; S53723; S53725; G02041

R; Hamdan, H

R; Hamdan, H

A; Reference number: H01047

A; Accession: G02321
                                                                                                                                                                                                                                                                                                                             Gaps
                                                 A;Gene: TTF-1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Seywords: DNA binding; homeobox; nucleus; transcription regulation
F;162-218/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 31-255, 'HE', 258-401 <HA3>
A; Cross-references: EMBL: U33749; NID: g1072047; PID: g1072048
C; Genetics:
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A:Status: preliminary; translated from GB/EMBL/DDBJ
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A)Status: preliminary; translated from GB/EMBL/DDBJ
A)Molecule type: DNA
A)Residues: 1-71 <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-401 <HAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, August 1995
                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 QQQLQQDSGGGGGGGGGAGCPQQQQA 250
                                                                                                                                                                                                                                                                                                                                                                                                                   7 RQALAARAGGGGGGGGIEGPTLRQA 31
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A;Molecule type: mRNA
A;Residues: 31-271,'G',272-401 <OGU>
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R; Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A; Itile: A novel human homeobox gene distantly related to proboscipedia is expressed
A; Reference number: A53662; MUID:94327547
A; Reference number: A53662; MUID:94327547
A; Reference number: A53662
A; Rocession: 
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A;Experimental source: strain Bristol N2; clone F36A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F36A4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29960
c;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: A53662
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A;Cross-references: GDB:136411; OMIM:142994
A;Gross-references: GDB:136411; OMIM:142994
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Superfamily: unassigned homeobox; nucleus; transcription regulation
E;244-300/Domain: homeobox homology <HOX>
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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51.5%; Pred. No. 14;
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Matches 17; Conservative 1; Mismatches 8; Indels 7; Gaps 2;

Search completed: October 9, 2002, 09:05:08 Job time : 9.09368 secs

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OM protein - protein search, using sw model

Run on: October 9, 2002, 08:51:41; Search time 4.29977 Seconds

Title: Without alignments)

Title: US-09-422-838C-29

Sequence: 180

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database: SwissProt_40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		P79772 gallus gall			P25245 tomato ring	_			_		P27921 gallus gall	drosop	P01317 bos taurus	-			canis			рошо	рошо		homo	рошо	trepo	homo sapie	-		_	O55165 rattus norv	33	7656	P53783 mus musculu	Foods arabidopsis
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7 RQALAA------RAGGGGGGGGGIEGPTLRQALAARA 36

043525 homo sapien P29122 homo sapien 09ug16 homo sapien 009029 mesocritectur P23091 avian muscu P04265 xenopus lae 003152 homo sapien P21952 mus musculu P20267 rattus norv P55480 brassica na P13645 homo sapien P54865 cellulomona	A. .e.) .ion factor genesis) (Winged	ertebrata; Euteleostomi; S; Phasianidae; Phasianinae; Iacovoni J.S., Vogt P.K.;	coduced through a collaboration cs and the RME outstation e are no restrictions on its its content is in no way Usage by and for commercial ittp://www.isb-sib.ch/announce/	egulation.	1; Length 394; 9; Indels 11; Gaps 1;
59.5 33.1 872 1 CIQ3_HUMAN 59.5 33.1 969 1 PAC4_HUMAN 59.32.8 36.9 1 BET3_MESAU 59.32.8 36.9 1 TMAF_AVL54 59.32.8 419 1 CCC_XENLA 59.32.8 449 1 OCTC_HUMAN 59.32.8 449 1 OCTC_HUMAN 59.32.8 551 1 CH60_BRANA 59.32.8 593 1 CH60_BRANA 59.32.8 593 1 KLCJ_HUMAN 59.32.8 644 1 XYND_CELFI	LT 1 CHICK CHICK STANDARD; PRT; 394 AA. 15-DEC-1998 (Rel. 37, Created) 16-DEC-1998 (Rel. 37, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Forkhead box protein D3 (HNF3/FH transcription f. Foxba.) Foxba. Gallus qallus (Chicken)	Vallus (Chicken). Jailus (Chicken). Juria; Aves; Chordata; Craniata; V Luria; Aves; Neognathae; Galliforme IXID=9031; E FROM N.A. FENDYO, -97141794; PubMed=8988052; enhoven B.S., Freyaldenhoven M.P., nt cell growth induced by avian wiin Res. 57:123-129(1997).	-: FUNCTION: PROBABLE TRANSCRIPTION FACTOR: SUMILARITY: CONTAINS I FORK-HEAD DOMAIN. This SWISS-PROT entry is copyright. It is produced through between the Sviss Institute of Bioinformatics and the European Bioinformatics Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrained by non-profit institutions as long as its content entities requires a license agreement is not removed. Usage by and or send an email to license@isb-sib.ch).	R EMBL; U37274; AAC60066.1;	/ Match 38.1%; Score 68.5; DB Local Similarity 46.3%; Pred. No. 2.3; les 19; Conservative 2; Mismatches 7 RQALAA
	33.0	OC BUSINESS OC BUS	CC Third CC		Query Match Best Local Matches 1

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                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION SITE.

RX BEZESKA H., Lynch T.J., Martin B., Korn E.D.;

RT Acanthamceba myosins I. An improved method for locating the canthamceba myosins I. An improved method for locating the canthamceba myosins I. An improved method for locating the canthamceba myosins I. A PROTEIN THAT BINDS TO F-ACTIN E HAS ATPASE C. I. FUNCTION: MYOSIN IS A PROTEIN THAT BINDS IN SINGLE-HEADED. DIMER OF A HEAVY C. SUBUNIT: MYOSIN I HEAVY CHAIN: IS SINGLE-HEADED. DIMER OF A HEAVY C. I. SUBUNIT: MYOSIN I HEAVY C. AND ALIGHT CHAIN. TO PROFILE MYOSIN I CAN THEREFORE MOVE ACTIN RELACHS CONFIDED MEMBRANES.

C. I. DOMAIN: TH. BINDS DIRECTLY TO ANIONIC PHOSPHOLIPID MEMBRANES.

C. I. DOMAIN: THO SINGLE MOVE ACTIN RELACH SINGLE MOLECULES.

THE NUCLEOTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE MOLECULES.

THE NUCLEOTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE MYOSIN I TO CROSS-LINK ACTIN ELAST THREE ISOFORMS OF MYOSIN I THORWAY.

C. I. SIMILARITY: COMPAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

C. I. SIMILARITY: COMPAINS 1 SH3 DOMAIN.

C. I. CAUTION: MAS ORIGINALLY THOUGHT TO BE MYOSIN IB.
                                                                                                                                                                                                                           MEDLINE-86259656; Pubmed-3014500; Hammer J.A. III, Jung G., Korn E.D.; Medline I. a true myosin."; "Genetic evidence that Acanthamoeba myosin I is a true myosin."; Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659(1986).
Proc. Nati. Acad. Sci. U.S.A. 84:6720-6724(1987).
                                                                                                        01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                               PRT; 1168 AA.
                                                                                                                                                                          Acanthamoeba castellanii (Amoeba).
Eukaryota: Acanthamoebidae: Acanthamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0193; MYOSINHEAVY.
PRINTS; PRO0452; SH3DOMAIN.
PRINTS: PRO0452; MYSDIn_Lhead; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P08799; 1LVK.
InterPro; IPR001452; SH3.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; PF00063; myosin_head; 1.
pfam; PF00018; SH3; 1.
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                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A.
                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A33891; MWAXIC.
                                                                                                                                                      Myosin IC heavy chain.
                                                                                                                                                                                                           NCBI_TaxID=5755;
                                                                                     MYSC_ACACA
P10569;
                                                                 RESULT 2
MYSC_ACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain genes.";
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOFIC CILIA AND
-!- FUNCTION: PORCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
FLAGELLA. PRODUCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitchell D.R., Brown K.S.; sequence analysis of the Chlamydomonas alpha and beta dynein heavy sequence analysis of the Chlamydomonas alpha and beta dynein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas reinhardtii flagellar alpha
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYNEIN HAS ATPASE ACTIVITY.

--- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS.

GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

--- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
phosphorylation; Multigene family; SH3 domain.
                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                        Score 67; DB 1; Length 1168;
Pred. No. 8.4;
4; Mismatches 10; Indels
                          MYOSIN HEAD-LIKE.
TAIL HOMOLOGY REGION 1 (TH.1).
                                                                                                                                                                                 127309 MW; D07084B373A37A32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dynein alpha chain, flagellar outer arm (DHC alpha).
ODA11 OR ODA-11.
                                                                                                                   GLY/PRO/ALA-RICH (TH.2).
                                                                        GLY/PRO/ALA-RICH (TH.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 4499 AA.
                                                                                                                                                ATP (POTENTIAL)
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell Motil. Cytoskeleton 37:120-126(1997).
                                                                                                                                                                                                                                                                                                                                                          920 QILGAKGGGGGGGRGRGGPSPSGAVSPR 947
                                                                                                                                                                                                                                                                                                                             8 QALAARAGGGGGGGGTEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=21GR;
MEDLINE=97329535; PubMed=9186009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1142-4499 FROM N.A.
                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002909; IPT_TIG.
InterPro; IPR001798; Kelch.
                                                                                                            SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, L26049; AAA57316.2; ...
InterPro; IPR003593; AAA.
InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001736; PLD.
Pfam; PF00630; Filamin; 1.
Pfam; PF01344; Kelch; 3.
SMART; SM00382; AAA; 3.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                                37.2%;
50.0%;
                                                                                                                                                                                                                                                                 Best Local Similarity 50.0° Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                   922
975
1035
1168
108
                   Myosin, ATP-binding; Pl
DOMAIN 671 922
DOMAIN 923 975
DOMAIN 976 1035
                                                                671 92
923 97
976 103
1036 116
101 10
311 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dynein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYHA_CHLRE
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                           DOMAIN
NP_BIND
MOD_RES
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
Hypothetical 20.2 kDa protein in RNA2.
Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses: ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                      MICROTUBULE-BINDING (POTENTIAL).
                                                                                                                                                                                             DB 1; Length 4499;
PROSITE; PS50194; FILAMIN_REPEAT; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                  10; Indels
                                                                                                                                                          (POTENTIAL)
319AC7FD30F1591A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.7%; Score 66; DB 1; Length 201;
                                                   COILED COIL (POTENTIAL).
                                                                                            COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91311402; Pubmed=1856689;
Rott M.E., Tremaine J.H., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
                                                               (POTENTIAL)
                                                                                COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY
9038506E18D7B450 CRC64;
                                                                                                                                      (POTENTIAL).
                                                                                                                                                  (POTENTIAL).
                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                              3 GPTLRQALAARAGGGGGGGGIEG---PTLRQAL 32
                                                                                                                                                                                           Score 66.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                       Pred. No.
                                        FILAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
                                                                                                                                                                  503606 MW;
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                                                                                                                                                                                                  51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D12477; BAA02044.1; -.
PIR; JQ1094; JQ1094.
                                                                                                                                                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.58;
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                          3023
3262
3515
1723
2026
2376
2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 61.5
hes 16; Conservative
                                                                                                                                                                4499 AA;
                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P04002; IWFA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                            Nepovirus.
NCBI_TaxID=12281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AA;
                                                                             2655
3003
3170
3486
1716
2019
2369
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P25245:
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                    Query Match
                                                                                                                     NP_BIND
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RESULT 5 LAC1_NEUCR

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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROW N.A., AND PARTIAL SEQUENCE.
MEDLINE-88087214; PubMed=2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
Antaracterization of two allelic forms of Neurospora crassa laccase.
J. Biol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
-!- FUNCTION: LIGMIN DEGRADATION AND DETOXIFICATION OF LIGMIN-DERIVED
PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALITIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                01-JAN-1988 (Rel. 06, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87067412; PubMe=2947240; Germann U.A., Lerch K., Terch K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted (Potential).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                      Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
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PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                         619 AA
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14554; AAA33590.1; -.
EMBL; M18333; AAA33591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 379-619 FROM N.
        STANDARD;
                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A28523; KSNCLO.
PIR; A29762; A29762.
        LAC1_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
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METAL
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FT FT FT FT FT FT FT FT

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Query Match
                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                    PHYB_SORBI
                 DOMAIN
                                                                                                                                                                                                                                                        Matches
                                                METAL
                                                                                                             METAL
                                                                                                                        METAL
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                                                           METAL
                                                                                                    METAL
                                                                     METAL
                                                                                METAL
                                                                                          METAL
                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                 qq
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF001394; Cu-oxidase; 3. PROSIE; 1. PROSIE; PS000079; MULTICOPPER_OXIDASE1; 1. PROSIE; PS00080; MULTICOPPER_OXIDASE2; 1. Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-FBB-1989 (Rel. 33, Last sequence update)
01-FBB-121001 (Rel. 40, Last annotation update)
1accase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
                                                                                                                                          0; Gaps
    COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted (Potential).

-i- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

-i- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Benkaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                       DB 1; Length 619;
                                                                                                                                          0; Mismatches 10; Indels
                                                                                                 68198 MW; FDED6D78B65048E3 CRC64;
                                                                                                                                                                                                                                      PRT; 619 AA
                                                                                                                         36.1%; Score 65; DB 1
58.3%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B28523; KSNCLT.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                    7 ROALAARAGGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                EMBL; M18334; AAA33592.1;
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat.
                550
554
559
1139
282
295
340
                                                                                                                                           Similarity
                                                                                                            619 AA;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                               NEUCR
                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                  Query Match
                                                                                                              SEQUENCE
                                                                                            CARBOHYD
                                                                                                       CARBOHYD
                                                                        CARBOHYD
                                                                                CARBOHYD
                                                 CARBOHYD
                                                            CARBOHYD
                                                                                                                                               Local
                                                                                                                                                                                                                                      LAC2_NEUCR
                                                                                                                                                Best Loca
Matches
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phytochrome B. ", 13:611-619(1947).
Plant Physiol. 113:611-619(1947).
Plant Physiol. 113:611-619(1947).
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS -- FUNCTION: REGULATORY EDESCONSERIES BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE FRED REGION. OF THE SPECTROM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS ANIMALLY TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PRY TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN.
BISPHOSPHATE CARBOXYLASE, RRNA, ETC. IT ALSO CONTROLS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Adropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.;
Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.;
"The phytochrome gene family in tomato and the rapid differential
evolution of this family in angiosperms.";
Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC ) (POTENTIAL)
OBBGCCDE18841145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H., Morgan P.W., Mullet J.E.;
                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 1; Length 619;
                                                                                                                                                                                       R (TYPE 2) (PROBABLE).
R (TYPE 3) (PROBABLE).
R (TYPE 3) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                   (TYPE 3) (PROBABLE).
(TYPE 3) (PROBABLE).
(TYPE 1) (PROBABLE).
                                                                    COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last Sequence update)
16-MAR-2002 (Rel. 41, Last annotation update)
Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV 58M;
MEDLINE=20188796; PubMed=10723737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. 58M;
MEDLINE=97198556; PubMed=9046599;
                                                                                                                                                          COPPER
COPPER
                                                                                                                                                                                                            COPPER
COPPER
                                                                                                                                                                                                                                                                                                           COPPER
                                                                                                                                                                                                                                                              COPPER
                                                                                                                                                                                                                                                                                      COPPER
                                                                                                                                   COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 RQALAARAGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 RODSOAERYGGGGGGGCUSPTNRO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 208-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68120 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHYB_SORBI
P93527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó:
 EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                         -!- SUBDATT: HOMODIMER (BY SIMILARITY).
-!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Discs overgrown protein Kinase (EC 2.7.1.-) (Double-time protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOPHORE (BY SIMILARITY).
IW: C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-HIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                         InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPASS C.
InterPro; IPR004359; HIS_KIN_Sig.
InterPro; IPR003661; His_KinA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                InterPro; IPR000014; PAS.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98337188; PubMed=9674431;
                                                                                                                                                                                                                          EMBL; AF182394; AAB41398.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129136 MW;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01133; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_c; 1.
SMART; SM00388; HISKA; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ARAGGGGGGGGIEGPTLRQALA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                               Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCO_DROME
076324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                       MEDLINE-98337187; PubMed-9674430;
Price J.L., Blau J., Rothenfluh A., Abodeely M., Kloss B., Young M.W.;
"Double-time is a novel Drosophila clock gene that regulates PERIOD
                                                                                                                                                                                  -1- FUNCTION: INVOLVED IN CIRCADIAN RHYTHMS, VIABILITY AND MOLECULAR OSCILLATIONS OF THE CLOCK GENES PERIOD (PER) AND TIMELESS (TIM). DBT REDUCES THE STABILITY AND THUS THE ACCHMILATION OF MONOMERIC PER PROTEINS, PROBABLY THROUGH PHOSPHORYLATION. NO EVIDENT CIRCADIAN OSCILLATION IS DETECTED IN HEAD.
                                                                                                                                                                                                                                                               -!- SUBUNIT: FORMS A COMPLEX WITH PER.
-!- TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS OF THE EYES
AS WELL AS IN THE REGION SITUATED BETWEEN THE OPTIC LOBE AND THE
CENTRAL BRAIN.
                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CASEIN KINASE I SUBFAMILY. COULD BE THE ORTHOLOG OF CKI-EPSILON.
 Kloss B., Price J.L., Saez L., Blau J., Rothenfluh A., Wesley C.S.,
Young M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN DBTL; LENGTHENS THE BEHAVIORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN DBIS; SHORTENS THE BEHAVIORAL
                            The Drosophila clock gene double time encodes a protein closely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biological rhythms, Transferase, Serine/threonine-protein kinase, ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 64; DB 1; Length 440; 55.0%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 AA; 48073 MW; B875891D5747391D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                             related to human casein kinase I epsilon.";
Cell 94:97-107(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF055583; AAC39134.1; -.
HSSP; P40233; 1CSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 PERRPSIRMRQGGGGGGV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLRQALAARAGGGGGGGG 23
                                                                                           MUTAGENESIS, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0002413; dco.
                                                                                                                                                         protein accumulation.";
Cell 94:83-95(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase;
PROSITE; PS00107; PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYA_THETH P74941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYA_THETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Ebkaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; PFC0272; DHHAL: 1.
Pfam; PFC0141; tRNA-synt_2c: 1.
PRINTS; PR00980; TRNASYNTHALA.
PROSITE; PSC00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
PROSITE; PSC00139; AA_TRNA_LIGASE_II_2; FALSE_NEG.
PROSITE; PSC0039; AA_TRNA_LIGASE_II_2; FALSE_NEG.
AMINDACY1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SEQUENCE 882 AA; 97454 MW; E60E3E34480CFC56 CRC64;
                                                                                                                                                                                                             medians—7,01144, Furned—2,00,047, Limmer S., Kreutzer R.; Lechler A., Martin A., Zulege T., Limmer S., Kreutzer R.; Lechler A., Martin A., Zulege T. Limmer S., Kreutzer R.; Lechler A., Martin A., Zulege T. Sa Kba fragment of overproduced alanyl-tRNA synthetase from Thermus thermophilus HB8 specifically interacts with tRNA ala acceptor helix."

1. CATALYTIC ACTIVITY: APP + L-alanine + tRNA(Ala) = AMP + CATALYTIC ACTIVITY: APP + L-alanine + tRNA(Ala) = AMP + CATALYTIC ACTIVITY: APP + L-alanine + tRNA(Ala) = AMP + CATALYTIC ACTIVITY: APP + L-alanyl-tRNA(Ala) = AMP + CATALYTIC ACTIVITY: APP + CATALYTY ACTALYTY ACTIVITY: APP + CATALYTY ACTALYTY ACTALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           16-OCT-2001 (Rel. 40, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1:7) (Alanine--tRNA ligase) (AlaRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63.5; DB 1; Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBGELUTAR LOCATION: Nuclear.
-1- SUBLITY: BILDS DIA AS A DIMER (BY SIMILARITY).
-1- SUBCELUTAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                          Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.NCBL_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 LEAGALFRALAEKAGGRGGRGGKGALAQGGGLDPRKAREAL 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQALAARAGGGGG-----GGGIEGPTLRQAL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92019832; Pubmed=1923529;
Hartl M., Hutchins J.T., Vogt P.K.;
The chicken junD gene and its product.";
oncogene 6:1622-1631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002106; AA_tRNA_ligase_II.
Interpro; IPR003156; DHHAl.
Interpro; IPR002318; tRNA-synt_2c.
                                                                                                                                                                                    STRAIN-HB8 / ATCC 27634;
MEDLINE-97351141; PubMed-9207019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription factor jun-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y08363; CAA69650.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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nes 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUND_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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-i- SUBUNT: MONOMER.
-i- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF
-i- ALTERNATIVE PRODUCTS: TARE STERIES AND SPLICE PATTERNS.
DIFFERENT TRANSCRIPTION START SITES AND SPLICE PATTERNS.
-i- DISEASE: MUTATION OF DUNCE PRODUCES FEMALE FLIES THAT ARE STERILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
cAMW-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Learning/DUNCE OR DNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen C.-N., Denome S., Davis R.L.; "Molecular analysis of cDNA clones and the corresponding genomic coding sequences of the Drosophila dunce+ gene, the structural gene for CAMP phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 83:9313-9317(1986).
-!- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)0 = ADENOSINE 5'-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00036; BIIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the memory gene dunce of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA; 33205 MW; A7F6D21A97DBB676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 223-584 FROM N.A. MEDLINE=87092243; PubMed=3025834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92085274; PubMed=1660926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 GPNGGAAAAGGGGGGGGGGGGELP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster.";
J. Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GPTLRQALAARAGGGGGGGGGEGP 26
                                                                                                                                                                                                                                                                                                                        InterPro; IPR002112; Leuzip_Jun.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0043; LEUZIPPRJUN.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%;
                                                                                                                                                                                                                        EMBL; X60063; CAA42665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00170; bZIP; 1
                                                                                                                                                                                                                                                       S20099; S20099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                 TRANSFAC; T02196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
242
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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AMIDES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; CAMP; Alternative splicing.

DOMAIN 305 310 PART OF CAMP BINDING SITE (BY SIMILARITY TO MAMMALIAN REGULATORY SUBUNIT OF TYPE 2

CAMP DEPENDENT PROTEIN KINASE).

THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88288209; PubMed-2456452;
D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.0%; Score 63; DB 1; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and nucleotide sequence analysis of complementary decyribonucleic acid for bovine preproinsulin."; Mol. Endocrinol. 1:327-331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99239BE33C620501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                   CAA38960.1; JOINED.
CAA38960.1; JOINED.
                                                                                                                                                        X55168; CAA38960.1; JOINED
                                                                                                                                                                                                          CAA38960.1; JOINED
                                                                                                                                                                                                                                               CAA38960.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1.
                                                                                                                                                                                                                                                                                                                                                                                                             PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 AA; 64875 MW;
                                                                                                                                     EMBL; X55167; CAA38960.1; -.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003607; HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0000479; dnc.
                                                                                                                                                                                           X55171; CAA38960.1;
                                                                                                                                                                                                                               CAA38960.1;
                                                                                                                                                                                                                                                                                M14979; AAC34201.1;
                                                                                                                                                                                                                                                                                                         M14981; AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ALAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                      M14982; AAC34201.1;
                                                                                                                                                                                                                                                                     M14978; AAC34201.1;
                                                                                                                                                                                                                                                                                            AAC34201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 SM00471; HDC; 1
                                                                                                                                                                                                                                                                                                                     PIR; A26651; A26651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                               M14980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                             EMBL;
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                                                                                                                  Sanger F., Tuppy H.;
"The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";
Blochem. J. 49:481-490(1951).
                                                                                                                                                                                                                                                                              "Isolation and characterization of proinsulin C-peptide from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97285914; PubMed=9141131; Bange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L., I.M. Bangel of insulin fibrils derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin)."; Proteins 27:507-516(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIGURE 47:30.7-310(1397.).
-1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INVESTORS CELL PERREABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 57-82.
MEDLINE=71257721; PubMed=5105368;
Salokangas A., Smyth D.G., Markussen J., Sundby F.;
"Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
Reynolds C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.expasy.org/spotlight/articles/sptlt009.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger F., Thompson B.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";
Blochem. J. 53:366-374(1953).
                                                                                                                                                                                                         SEQUENCE OF 57-82.
MEDLINE=71116409; PubMed=5545080;
Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D.,
Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-!- DATABASE: NAME-Protein Spotlight;
             MEDLINE=1116642; PubMed=4928892;
Nolan C., Margoliash E., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The structure of des-Phe bl bovine insulin.";
Acta Crystallogr. B 38:3028-3032(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ryle A.P., Sanger F., Smith L.F., Kitai R., "The disulphide bonds of insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                    Biol. Chem. 246:1365-1374(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                           from pancreas.";
Eur. J. Biochem. 20:183-189(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 60:541-556(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE=Issue 9 of April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M54979; AAA30722.1; -.
SEQUENCE OF 25-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 85-105.
                                                                                                     SEQUENCE OF 25-54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01585; IPBO.
PIR; A40909; A40909.
                                                                                                                                                                                                                                                                                                       pancreas."
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DISULFID
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                                                                                                                                                                                                                                                                   PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=72258016; PubMed=4626369; P.E., Steiner D.F.; Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; and "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
PRNRTS; SW00078; I.1GF; 1.
PROSTIE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                 34.7%; Score 62.5; DB 1; Length 105; 40.6%; Pred. No. 2.8; Live 5; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                11393 MW; 75307CF78E61C06A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Biochem. J. 60:556-565(1955).
                                                                                                                              INSULIN B CHAIN.
                                                                                                                                                 INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQALAARAGGGGGGGGGGTEGPTLRQAL 32
                                                                                                                                                                                                                                                                                                                                              58 VEGP---OVGALELAGGPGAGGLEGPPOKRGI 86
                                                     IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                     INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 247:4866-4871(1972).
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94280618; PubMed-8011164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Cell Biol. 13:377-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-54 AND 85-105.
                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                               Insulin; 1
                        ; 1CPH; 31-OCT-93.
; 1DPH; 31-OCT-93.
1PID; 07-DEC-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
               31-0CT-93
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor-II genes.
                                                               PF00049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procedure.
                                                                                                                                                                                                                                                                                                                                                                                                   INS_SHEEP
P01318;
                   1BPH;
                                                                                                                                                                                                                                                                         SEQUENCE
                                                        InterPro;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                 DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSB_MYCLE STANDARD; PRT; 168 AA.
P46390; 053126;
01-N0V-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein).
SSB OR ML2684 OR MLCB1913.20C.
--- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILTON-21128732; PubMed=11234002;
MEDILTON-21128732; PubMed=11234002;
Cole S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
                                                                                     HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 105;
                                                                                                                                     -i - SUBCELLULAR LOCATION: Secreted.-i - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 INSULIN B CHAIN.
54 C PEPTIDE.
105 INSULIN A CHAIN.
91 INTERCHAIN.
104 INTERCHAIN.
95
A; 11235 MW; 8B27C7FB9922BC7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.7%; Score 62.5; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQALAARAGGGGGGGGGIEGPTLRQAL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HESP, P01315, 91NS.
InterPro; IPR000739; Insulin_IGF_relaxin.
pfam; PF00049; Insulin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiology 142:3147-3161(1996).
                                                                                                                                                                                                                                                                                                                                                                                EMBL; U00659; AAB60625.1; -.
PIR; S16430; INSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.68;
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PRINTS; PR00277; INSULINB.
SMART; SM00078; I1GF: 1.
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                                                                                                                                   DISULFIDE BONDS
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Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Peltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Rutter S., Seeger K., Oliver K., Ouall M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.K.,
Barrell B.G.,
Massive gene decay in the leprosy bacillus.",
"Massive gene decay in the leprosy bacillus.",
"Massive Gene decay in the leprosy bacillus.",
"Taylor TON" THIS PROFEIN IS ESSEWIAL FOR REPLICATION OF THE
CHROMOSOME. IT IS ALSO INVOLVED IN DNA RECOMBINATION AND REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROPEROXIDASE, AND THYROTROPIN RECEPPOR. CRUCIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY A ROLE IN LUNG DEVELOPMENT AND SURFACTANT HOMEOSTASIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Thyroid transcription factor 1 (Thyroid nuclear factor 1) (TTF-1)
TTTF1 OR TTF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE SSB FAMILY.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: 19R00014; SSB.
Pfam: PF00436; SSB; 1.
PROSITE: PS00735; SSB_1; FALSE_NEG.
PROSITE: PS00736; SSB_2; FALSE_NEG.
DNA-binding; DNA repair; DNA replication; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 62.5; DB 1; Length 168; 56.0%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuan H.T., Bingle C.D.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                077C62E430623658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L39923; AAB53120.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DUNKIN-HARTLEY; TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GPTLRQAL----AARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 GPSLRYATAKVNKASRSGGGGGFG 131
                                                                                                                                                                                                                                       FRAMESHIFT IN POSITION 137.
                                                                                                                                                                                                                                                                                                                                                                                                                       AL022118; CAA17953.1; -. AL583926; CAC32216.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 168 AA; 17700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1EYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leproma; ML2684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAL Cell. Endocrinol. 112:83-93(1995).

--- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROPEROXIDASE, AND THYROTROPIN RECEPTOR. CRUCIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY A ROLE. IN LUNG DEVELORMENT AND SURFACTANT HOMEOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1hyroid transcription factor 1 (Thyroid nuclear factor 1) (TTF-1)
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: THYROID, LUNG AND CNS.
SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                              Transcription regulation; Activator; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Renterghem P.H.G., Dremier S., Vassar G., Christophe J., "Study of TTF-1 gene expression in dog thyrocytes in primary
                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                               112 AA; 12723 MW; AEEAEDF06905F9DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                      HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RQALAARAGGGGGGGGIEGPTLRQA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 QQQLQQDSGGGGGGGGAGCPQQQQA 90
                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96034516; PubMed=7589789;
                                                                                                                                                                            InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
                                                                                                                                              EMBL; U82718; AAB40921.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  34.4%;
52.0%;
                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Homeobox protein NKX-2.1).
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 52.0° nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  Nuclear protein.
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                                                                                                                                                                   P23441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTF1_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P23441;
                                                                                                                                                                                                                                                                                              NON_TER
DNA_BIND
                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TISSUE-Thyroid;
MEDLINE-95226464; PubMed-7711080;
Salardi A., Tassi V., de Filippis V., Civitareale D.;
Salardi A., Tassi V., de Filippis of human thyroid transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95229626; PubMed*7713914; Stahlman M.T., Boutell C.J., Ikeda K., Clark J.C., Shaw-White J.R., Stahlman M.T., Boutell C.J.,
                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                    TTF1.HUMAN STANDARD; PRT; 371 AA.

P43699; O14955; O14954;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17hyroid transcription factor 1 (Thyroid nuclear factor 1) (TTF-1)
17HYROID TTF1 OR NEX.2.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homosapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Gene structure and expression of human thyroid transcription factor-1 in respiratory epithelial cells."; J. Biol. Chem. 270:8108-8114(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE—Thyroid;
Endo T., Ohno M., Nakazato M.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Activator; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lung;
Hamdan H., Liu H., Jones C., Delemos R., Minoo P.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               Score 62; DB 1; Length 371;
Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oguchi H., Kimura S.;
Submitted (JaN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamdan H., Liu H., Delemos R., Minoo P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                               9; Indels
                                                                                                                                                POLY-ALA.
3F16CE8E562604D7 CRC64;
                                                                                                                                                                                  34.4%; bcc. No. 5.2.0%; Pred. No. 5.3.0%; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1261:307-310(1995)
                                                                                                                     POLY-GLY.
                                                                                                         HOMEOBOX
                                                                                                                                                                                                                                                                       226 QQQLQQDSGGGGGGGGGAGCPQQQQA 250
                                                                                                                                                                                                                                             7 RQALAARAGGGGGGGGTEGPTLRQA 31
                                                                                                               161 220 HU
234 243 PO
246 253 PO
294 303 PO
371 AA: 38539 MW;
InterPro; IPR001356; Homeobox.
          Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                  Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lung;
                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                              DNA_BIND
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                         TTF1_HUMAN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
-i- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROPENONIDASE, AND THYROTROPIN RECEPTOR. CRUCIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY ROLE IN LUNG DEVELOPMENT AND SURFACTANT HOMEOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWYGANPDPREPAI -> V (IN ISOFORM 2).
P -> H (IN REF. 6).
H -> P (IN REF. 6).
                                                                                                                                                      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLCING.
-1- TISSUE SPECIFICITY: THYROID AND LUNG.
-1- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; Homeobox; DNA-binding; Nuclear protein; Alternative splicing.
DNA_BIND 161 220 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%; Score 62; DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SF1E3B40A1BBD862 CRC64;
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11-0CT-2001 (Rel. 40, Last sequence update)
11-0CT-2001 (Rel. 40, Last annotation update)
11-0CT-2001 (Rel. 40, Last annotation update)
Homeobox even-skipped homolog protein 2 (EVX-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S -> T (IN REF. 6).
R -> G (IN REF. 6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pred. No. 9.6;
3; Mismatches
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POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 RQALAARAGGGGGGGGGIEGPTLRQA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X82850; CAA58053.1; -. EMBL; U19816; AAC50125.1; -. EMBL; U19756; AAA86099.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 600635;
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                                                                        D'Esposito M., Morelli F., Acampora D., Migliaccio E., Simeone A., Boncinelli E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D2 (Forkhead-related protein FKHLL7) (Forkhead-related transcription factor 9) (FREAC-9)
                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear
-!- SUBCELLULAR LOCATION: Nuclear
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS AND
NEUROGENESIS IN A BIPHASIC MANNER.
-!- SIMILARITY: BELONGS TO THE EVEN-SKIPPED FAMILY OF HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    "EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, is localized at the 5' end of HOX4 locus on chromosome 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Developmental protein; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.4%; Score 62; DB 1; Length 476; 78.6%; Pred. No. 12;
 Birren B., Linton L., Nusbaum C., Lander E.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6AA99041BA151C3F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC009336; -; NOT_ANNOTATED_CDS.
EMBL; M59983; AAA52414.1; -
EMBL; M59982; AAA52414.1; JOINED.
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POLY-ALA.
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                                            SEQUENCE OF 144-300 FROM N.A.
MEDLINE=91257849; PubMed=1675198;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 2.
                                                                                                                                             Genomics 10:43-50(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 ALGSRGGGGGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ALAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00389; HOX; ]
                                                                                                                                                                                                                                                                                                                                                                                                                P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 142991;
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SEQUENCE FROM N.A.
MEDLINE=98066765; PubMed=9403061;
Bristsson S., Berlz R., Lagercrantz S., Larsson C., Ericksson S., Cederberg A., Carlsson P., Enerbaeck S.;
"Cloning and characterization of freac-9 (FKHL17), a novel kidney-expressed human forkhead gene that maps to chromosome 1932-p34.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harrison K.A., Druey K.M., Deguchi Y., Tuscano J.M., Kehrl J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 1; Length 497;
Pred. No. 12;
0; Mismatches 5; Indels
                                                                                                                         Enerbaeck S.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAAF498D216BE019 CRC64;
                                                                                                                                                - FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
- SUBCELLULAR LOCATION: Nuclear.
- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY - ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00657; FORK_HEAD_1; 1
PROSITE; PS00658; FORK_HEAD_2; 1
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=94327547; PubMed=7914194;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                              EMBL; AF042832; AAC15421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 PTALLROGLKTDAGGGAGGG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PT -- LRQALAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T02485; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                SM00339; FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox protein HB9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                 063245;
                                                                                                                                                                                                                                                                                                                                                                          602211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                               REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HB9_HUMAN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                  -1. TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION. MEDLINE-20568725; PubMed-11118334; Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; Makamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; Molecular cloning and characterization of a new human histamine
  Homeobox; DNA-binding; Nuclear protein; Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HH3R_HUMAN STANDARD; PRT; 445 AA.
O9Y5N1; Q9H4K8; Q9G2X2;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61.5; DB 1; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0006AEAD71D594FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EGPTLRQAL-----AARAGGGGGGGGGEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 EPPLAERALAKVISPPVPASGTGGGGGGGGASGGT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Pharmacol. 55:1101-1107(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99278519; Pubmed-10347254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                 -1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                      EMBL; U07664; AAB60647.1; -. EMBL; U07663; AAB60647.1; JOINED.
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                      InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           40932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.2%;
Best Local Similarity 42.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                    PRINTS; PRO0046; homeobox; 1. PRINTS; PR00024; HOMEOBOX. SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                         135
177
301
325
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169
242
316
316
401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor, HH4R.";
                                                                                                                                                                                                                                                     P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Thalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRH3 OR GPCR97.
                                                                                                                                                                                                                                                                            MIM; 142994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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RA SEQUENCE FROM N.A. (ISOFORM 1). Burton J., Gilbert J.G.R., Ra Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Ballouks P., Matthews L.H., Ashurst J., Babade A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Basiley J., Barlow S.E., Enidgeman A.M., Brown A.J., Basiley O.P., Bird C.P., Blakey S.E., Enidgeman A.M., Brown A.J., Clark D.N., Clark S.Y., Clee C.M., RA Colley V.E., Collier R.E., Connor R., Corby N.R., Coley V.E., Collier R.E., Connor R., Dhami P., Dunn M., RA Coulson A., Collier R.E., Connor R., Dhami P., Dunn M., RA Elington A., Collfiths G.J., Peadman R., Dham M., Garner P., RA Elington A., G., Frankland J.A., Fraser A., French L., Garner P., Ra Farmmond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Harley D.M., Martin S.L., McConnachie L.J., McIay K., Mornach J.B., McLay K., Matter A., Parek A., Knights A., Laird G.K., Lawlor S., RA Milne S., Mistry D., Moconnachie L.J., McIay K., Nokurray A.A., Mollyer K., Parker A., Patel R., Peare T., Plumb R.W., Shownkeen R., Sims S., R. Rice C.D., Smith M.L., Socherlund C., Steward C.A., Sulston B.K., Swan M., Sycamore N., Taylor R., Tee, Sehra H.K., Shownkeen R., Sims S., Swan M., Sycamore N., Taylor R., Tee, J., Mollish J.M., Bentley D.R., Whitchead S.L., Whittehead T., Durbin R.M., Bentley D.R., Barker T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P., Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.; "Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                                                                                      Wiedemann P., Bonisch H., Bruss M.; wiedemann P., Bonisch H., Bruss M.; An amino acid variation in the human histamine h3 receptor from a patient suffering from orthostatic dysregulation."; patient suffering from orthostatic dysregulation."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ullmer C., Zirwes E., Lubbert H.; "Cloning and functional expression of the human histamine H3S "cloning and functional expression of the human histamine H3S "closetor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT VAL-280
                                                            SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
Biochem. Biophys. Res. Commun. 279:615-620(2000).
                                                                                                                  TISSUE=Thalamus;
MEDLINE=21181559; PubMed=11284713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                   human histamine H3 receptor.";
Biochem. J. 355:279-288(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
and R(-)-alpha-methylhistamine. Isoform 4 is unable to bind to
lodoproxyfan while isoforms 1 and 3 bind it with high affinity.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 4).
MISSING (IN ISOFORM 4).
MISSING (IN ISOFORM 5).
MISSING (IN ISOFORM 6).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
K -> KEMMKKRICL (IN ISOFORM 2).
K -> V (IN ORTHOSTATIC DYSREGULATION).
E -> D OTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                          Alternative splicing; Disease mutation.

DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> D (IN REF. 1 AND 5).
2ACF7440FBE95B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 14:
                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 EAGEATLGGGGGGSVASPTSSSGSSSR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 QALAARAGGGGGGGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                        EMBL; AF140538; AAD38151.1; -
EMBL; AB045369; BAB20090.1; -
                                                                                                                                                                               EMBL; AB019000; BAB17030.1; EMBL; AJ296652; CAC51025.1; EMBL; AJ278250; CAC39434.1;
                                                                                                                                                                                                                       EMBL; AL078633; CAC04014.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               108
129
156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FXD1_HUMAN S:
Q16676; Q12949;
01-NOV-1997 (Rel
01-NOV-1997 (Rel
30-MAY-2000 (Rel
                                                                                                                                                                                                                                                    MIM; 604525;
                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                      SEQUENCE OF 120-225 FROM N.A.
MEDLINE-9504592; PubMed-7957066;
Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
"Cloning and characterization of seven human forkhead proteins:
binding site specificity and DNA bending.";
EMBO J. 13:5002-5012(1994).
IF FOURTION: BINDING OF FREAC-3 AND FREAC-4 TO THEIR COGNATE SITES
RESULTS IN BENDING OF THE DNA AT AN ANGLE OF 80-90 DEGREES.

--- SUBCELLUIAR LOCATION: Nuclear.
--- SIMILARITY: CONTAINS I FORK-HEAD DOMAIN.
Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-related transcription factor 4) (FREAC-4).
                                                                                                                       MEDLINE=96355467; PubMed=8702877;
Ernstsson S., Pierrou S., Hulander M., Cederberg A., Hellqvist M.,
Carlsson P., Enerback S.;
"Characterization of the human forkhead gene FREAC-4. Evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                  regulation by Wilms' tumor suppressor gene (WT-1) and p53."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.9%; Score 61; DB 1; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D3E7854909CCBFAE CRC64;
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0; Mismatches
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POLY-ALA.
POLY-PRO.
POLY-ALA.
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POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00657; FORK HEAD_1; 1. PROSITE; PS00658; FORK_HEAD_2; 1. PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | | | | ||||||||| |
91 GPA--PAAGAGGGGGGGGGGG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U59832; AAC50661.1; -
EMBL; U59831; AAC50660.1; -
EMBL; U13222; AAA92039.1; -
HSSP; Q63245; ZHEH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.9
Matches 14; Conservative
                                               (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FH; I
                                                                                                           SEQUENCE FROM N.A.
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428
465 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00339
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DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Hypothetical protein TP0967.
TP0967.
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
One cut domain family member 2 (ONECUT-2 transcription factor) (OC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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                                                                                          485 AA
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POLY-GLY:
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                      MEDLINE-99115605; PubMed-9915796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52482 MW;
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TRANSFAC; T03259; -.
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Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
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                                                                                                  STANDARD;
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75
152 1
298 3
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM: 604894;
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083933;
                                                                                                ONC2_HUMAN
095948;
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                                                                                                                                                                   MEDLINE=98332770; PubMed=9665876; G.M., White O., Sutton G.G., Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Chidambaram M., Utterback T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- FUNCTION: BINDS CALMODULIN IN A CALCIUM DEPENDENT MANNER. MAY
-!- FUNCTION AS SCAFFOLDING OR SIGNALING PROTEIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-BOUND (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Zinedin, SG2NA, and striatin are calmodulin-binding, WD repeat proteins principally expressed in the brain."; J. Biol. Chem. 275:19970-19977(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20347911; PubMed-10748158; Castets F., Mattei M.-G., Castets F., Rakitina T., Gaillard S., Mogrich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.9%; Score 61; DB 1; Length 517; 60.0%; Pred. No. 16; 7; Indels .ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E224976333989DF6 CRC64;
bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NAR-2002 (Rel. 41, Created)
01-NAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 753 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001264; AAC65925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 161 P
517 AA; 56597 MW;
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es 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                               SEQUENCE FROM N.A.
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-!- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS

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                                                                                                                                                                                                                SIMILARITY).
--- SIMILARITY: BELONGS TO THE STRIATIN FAMILY OF WD-REPEAT PROTEINS.
--- SIMILARITY: COWTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
--- CAUTION: The name "Zinedin" probably originates from the name of the famous soccer player from Marseille (Zinedine Zidane)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ceratitis capitata (Mediterranean fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheatu; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C., "The Ceratitis capitata homologue of the Drosophila sex-determining gene Sex-lethal is structurally conserved, but not sex-specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                   SMART: SMUUJZU; MULY, STREEATS 1; 1.
PROSITE; PSSO0678; WD_REPEATS 2; 4.
PROSITE; PSSO082; WD_REPEATS 2; 4.
Calmodulin-binding; Repeat; MD_repeat; Coiled coil.
Collodain 69 136 COLLED COIL (POTEWTIAL).
CALMODULIN-BINDING (POTEWTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAVEOLIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9%; Score 61; DB 1; Length 753; 48.4%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAD -> GTR (IN REF. 2).
4DA016A8FF7EDB5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BENAKIO;
MEDLINE=98171464; PubMed=9502730;
                                                                                                                                                                                                                   EMBL; AF212940; AAF29527.1; -.
EMBL; BC004910; AAH04910.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 6.
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80581 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 753 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7213;
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061374:
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REPEAT
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            A1, A2, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN FIRE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN BABRYOS OF BATH SEXES. ALSO EXPRESSED IN THE PRODUCENTYOR CELLS OF THE GENMLINE.
-!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theil T., Zechner U., Klett C., Adolph S., Moeroey T.; "Chromosomal localization and sequences of the murine Brn-3 family of developmental control genes.".

Cytogenet. Cell Genet. 66:267-271(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUC-1990 (Rel. 15, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (BRN-3.0),
POUVFI OR BRN3A OR BRN3 OR BRN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                SMART; SM00300; RRW; 2.
PROSITE; PS50102; RRW; 2.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Repeat; Nuclear protein; Alternative splicing.
27 GLY/ASN-RICH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  CABA3DA5C2C8874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO.
MISSING (IN ISOFORM A1)
                                                                                                                                                                                                                                                                                                                                     RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60;
                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94215319; Pubmed=8162704;
                                                                                                                                                                                                EMBL; AF026145; AAC38968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                37188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.38;
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                                                                                                                                                                                                                                                    PRINTS; PR00961; HUDSXLRNA.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                            InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                      Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGGGGGGMGGP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 10; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                     110
196
68
95
                                                                                                                                                                                                                 HSSP; P19339;
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                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K1C1_MOUSE STANDARD; PRT; 569 AA.
K1C1_MOUSE STANDARD;
P02535, P08731;
P02535, P08731;
P01536, Rel. 01, Created)
01-AUG-1986 (Rel. 08, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Reratin, type I cytoskeletal 10 (Cytokeratin 10) (56 kDa cytokeratin)
KRT10 OR KRT1-10.
THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: BRAIN, PERIPHERAL SENSORY NERVOUS SYSTEM AND FRITHA. IN THE ADDITA MERVOUS SYSTEM BRN-3.0 PREDOMINATES IN THE MEDIAL HABENULA, SUPERFICIAL GRAY OF THE SUPERIOR COLLICULUS, RED NUCLEUS, MESENDEPRALIC NUCLEUS OF THE TRIGEMINAL GANGLION, NUCLEUS AMBIGUES, INFERIOR OLLIVARY NUCLEUS, AND PERIPHERAL SENSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                     SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS000465; POU_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-65207552; Pubmed-2581944;
Krieg T.M., Schafer M.P., Cheng C.K., Filpula D., Flaherty P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%; Score 60; DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34EC99D789EBE939 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   POU-IV BOX.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ISSPSL--ALMAGAGGAGAAGGGGGAHDGP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQALAARAGG----GGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                       GLY-RICH.
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                                                                                                                                                                                                                                    PIR; S09237.
HSSP, P14859; 10CT.
HSSP, P14869; 10CT.
InterPro; IPR001356; Homeobox.
InterPro; IPR001357; POU.
Pfam; PF001457; POU.
Pfam; PF00157; POU.
PRINTS; PR00128; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA; 42781 MW;
                                                                                                                                                                                                               EMBL; S69350; AAB30577.2; -. EMBL; X51959; CAA36218.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                          ProDom; PD000583; POU; 1
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                          TO CLASS-4 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               Developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 302:/94-800(1903).

-!- SUBUNIT: HETEROTETRABER OF TWO TYPE I AND TWO TYPE II KERATINS.

-!- SUBUNIT: HETEROTETRABER ASSOCIATED WITH KERATIN 1.

-!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND

MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)

MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)

-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                Steinert P.M., Rice R.H., Roop D.R., Trus B.L., Steven A.C.; "Complete amino acid sequence of a mouse epidermal keratin subunit and implications for the structure of intermediate filaments."; Nature 302:794-800(1983).
Steinert P.M., Roop D.R.; "Organization of a type I keratin gene. Evidence for evolution of intermediate filaments from a common ancestral gene."; J. Biol. Chem. 260:5867-5870(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H -> L (IN REF. 2).

E -> A (IN REF. 2).

GGRHGGS -> CGGRGGG (IN REF. 2).

S -> G (IN REF. 2).

K -> G (IN REF. 2).

S -> G (IN REF. 2).

K -> SGT (IN REF. 2).

KS -> SGT (IN REF. 2).
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LINKER 1.
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=83192464; PubMed=6188955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A02940; KRMSE1.
PIR; S07330; S07330.
HSSP; P10968; 1WGC.
MGD; MGI:96685; Krt1-10.
InterPro; IPR001664; IF.
InterPro; IPR001664; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556 K
57711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01248; TYPE1KERATIN. PROSITE; PS00226; IF; 1.
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569 AA;
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Gaps

4;

5; Indels

Mismatches

56.5%; Pred. No. tive 1; Mismatc

Best Local Similarity 56.59 Matches 13; Conservative

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                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.,
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBGINIT: HETERODIMER OF KIF3A AND KIF3C.
                                                                                                                                                                                                                                                                                                     Muresan V., Abramson T., Lyass A., Winter D., Porro E., Hong F., Chamberlin N.L., Schnapp B.J.; "KIF3C and KIF3A form a novel neuronal heteromeric kinesin that
                                 0;
                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
MEDLINE-9903372; Pubmed-9808286;
MATHER K., Gruber D., Bulinski J.C.;
Faire K., Gruber D., Bulinski J.C.;
"Identification of kinesin-like molecules in myogenic cells.";
"Call Biol. 77:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTE; PSO0411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
MOLOT protein: Microtubules; ATP-binding; Colled coil; Neurone.
DOMAIN 1 377 KINESIN-MOTOR (BY SIMILARITY).
     Score 60; DB 1; Length 569;
Pred. No. 22;
                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935A79A01F8BDC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (POTENTIAL).
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> DD (IN REF. 2).
                                                                                                                                         (IN REF.
                                                                                                                                      796 AA.
                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                        associates with membrane vesicles."; Mol. Biol. Cell 9:637-652(1998).
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY - PRO
                                              7 RQALAARAGGGGGGGGIEGPTLRQAL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ASN
                                                             SEQUENCE FROM N.A.
MEDLINE=98155212; PubMed=9487132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 2.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ223599; CAA11465.1; -. EMBL; AF083330; AAC33291.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89815 MW;
                         11; Conservative
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00129; KISc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
278
            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796 AA;
Query Match
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NP_BIND
                     Matches
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DB 1; Length 796;

33.3%; Score 60;

Query Match

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                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                               MEDLINE=9111256; PubMed=1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T.; "The Drosophila suppressor of sable gene encodes a polypeptide with regions similar to those of RNA-binding proteins."; Mol. Cell. Biol. 11:894-905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Voelker R.A., Graves J.P., Gibson W., Eisenberg M.T.; "Mobile element insertions causing mutations in the Drosophila suppressor of sable locus occur in DNase I hypersensitive subregions of 5'-transcribed nontranslated sequences."; Genetics 126:1071-1082(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- DEVELOPMENTAL STAGE: AT ALL STAGES.
-i- SIMILARITY: HAS REGIONS SIMILAR TO THOSE OF RNA-BINDING PROTEINS.
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Pred. No. 46;
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1087 1162 RNA-BINDING (BY SIMILARITY).
1322 AA; 143555 MW; D5F534EB5702EA08 CRC64;
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                    263 GP----ATQSTAGGGGGGGGTSG 281
3 GPTLRQALAARAGGGGGGGGGIEG 25
                                                                                                                                                                                       Suppressor of sable protein.
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Search completed: October 9, 2002, 09:00:16 Job time : 5.3831 secs

us-09-422-838c-29.rsp

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October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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1 IEGPTLRQALAARAGGGGGGGGGGIEGPTLRQALAARA 36
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15: sp_rvirus:*
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17: sp_archeap:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

SP_plant:*
sp_rodent:*
sp_virus:*
SP_vertebrate:*

sp_mhc:* sp_organelle:* sp_phage:*

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7 1 9 09LGC9	Oglecs; 01-OCT-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel	01-OCT-2001	PUTATIVE ZINC FINGER PROTEIN P0462H08.19.	Oryza sativa (Rice).	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,	Ehrhartoideae: Orvzeae: Orvzeae:	NCBI_TaxID=4530;	SECTIFICE FROM N A	STRAI	Sasaki T., Matsumoto T., Yamamoto K.:	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC	Tone	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL: AP002525: Baba2006 1.	nter	Pfam; PF00642; zf-CCCH; 4.	SMART; SM00356; ZnF_C3H1;	SEQUENCE	Query Match 42.2%; Best Local Similarity 56.0%.	Matches	7	56
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"A set of ordered cosmids and a detailed genetic and physical map for the B wb Streptomyces coelicolor A3(2) chromosome.";
wol. Microbiol. 21:77-96(1996).
EMBL, AL512667; CAC21636.2:
Interpro: PR003838; DUF214.
Bram, PF02687; DUF214; I.
SEQUENCE 496 AA, 49548 MW; 54E110C4F86231A4 CRC64;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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Pred. No. 1;
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Sasaki T., Matsumoto T.,
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Seeger K.J., Harris D.;
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Pang Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,
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DR EMBL; AF200321; AAF31402.1; -..

DR HSSP; P09651; 1HA1.

InterPro; IPR00054; RRM.

DR Pfam; PP00076; rrm; 1.

RMART; SM00360; RRM; 1.

PROSITE; P550102; RRM; 1.

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OR SEQUENCE 137 AA; 14167 Ma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu J., Wang L., Hu X., Pang Y.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF322155; AAL01786.1; -. Hypothetical protein protein protein colored AR 5998 MW; C5626A8FFA9C9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence Analysis of the Spodoptera litura Multicapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA BINDING PROTEIN 1.
                                                                                                                                               Spodoptera litura nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 70; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                               01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                            MEDLINE=21425398; PubMed=11531416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 QQASSNRSGGGGGGGGGVVGAML 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 RQALAARAGGGGGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleopolyhedrôvirus Genome.";
Virology 287:391-404(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
59.1%;
                                                                                                                                 HYPOTHETICAL 7.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vinceae; Catharanthus.
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Veau B., Oudin A., Courtois M., Chenieux J.-C., Hamdi S., Rideau M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Clastre M.;
"Cloning of two cDNAs encoding crGRP2 and crGRP3 (Accession Nos. Ar200231 and Ar200322), the first members of the RRM-GRP family in Catharanthus roseus (GRG00-049).";
Plant Physiol. 122:1459-1459(2000).
BMBL; AR200323; AAF31404.1;
HSSP; P09651; IHA.
                                                                                                                                                                                                                                                              Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20277482; Pubmed-10819331;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human
genes.XVII.The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
EMBL: AB040891; BAA95982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.9%; Score 70; DB 10; Length 160; 54.5%; Pred. No. 1.4;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 160 AA; 16264 MW; DCDC9F63C983F5F2 CRC64;
                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GLYCINE-RICH RNA-BINDING PROTEIN 2.
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9
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MIAA1458 PROTEIN (FRAGMENT).
                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
 54.5%; Pred. No. 1.
                                                                                                                                                           . PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                              80 TVNEAQSRGSGGGGGGGFRGP 101
                                            5 TLRQALAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 TVNEAQSRGSGGGGGGGFRGP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TLRQALAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002952; Eggshell.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%;
                12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01228; EGGSHELL.
SMART; SM00360; RRM; 1.
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         Vinceae; Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00076; rrm; 1.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4058;
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                                                                                                                                                                     Q9M69;
                                                                                                                                                      669M60
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              Matches
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                                                                                                                        RESULT 6
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Q9P270
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reddy M.S., Muniyappa K.;
"Biochemical properties of single-stranded DNA-binding proteins from
Mycobacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                          38.9%; Score 70; DB 4; Length 612;
                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF349434; AAK30583.1; -. HSSP; P02339; 1EYG.
                           612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium smegmatis.
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AA; 17401 MW; 8786415C16F26F39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SINGLE-STRANDED DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  165 AA
                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GPSLRYATAKVNKASRSGGGGGGGGGGGGSRQS 140
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                                                                                                                     Pred No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sem
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                                                                                                                                                                                                   4 PTLRQALAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                      10 PSLSLSLRERAGGGGGGGGGG 31
                                                                                                                        63.68;
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                                                                                                            Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000424; SSB. Pfam; PF00436; SSB; 1. DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 17; Conservative
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NON_TER
SEQUENCE
                                                                                          Query Match
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Q9LD54;
                                                                                                                                       Matches
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Q9AFIS
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PSI PROTEIN.
                                     PSI PROTEIN.
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Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Banaroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTATIVE DNA BINDING PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                             Gaps
       -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Mawes H.W., Lemcke K., Mayer K.F.X.; submitted (MAR-2000) to the EMBL/GenBank/DDDJ databases.
                                   INNER MEMBRANE (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AP001383; BA492280.1; --
EMBL; AP001389; BA493248.1; --
EMBL; AP001080; BA493348.1; --
Interpro; IPR001993; Mitoch_carrier.
Interpro; IPR0012067; Mit_carrier.
                                                                                                                                                                                                                                                                                            38.3%; Score 69; DB 10; Length 381; 51.9%; Pred. No. 4.1; 1.1; Indels 1; Mismatches 10; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049638; CAB40946.1; -.
EMBL; AL161533; CAB78248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         INCEPTION TRANSMITTOCARRIER.
PRINTS; PR00926; MITOCARRIER; 2.
PROSITE; PS00215, MITOCHOLICARRIER; 2.
Inner membrane; MITOCHONDATION; Transmembrane; Transport.
SEOURNCE 381 AA, 40761 MW; F3A0E3CEBD950778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding.
GROUENCE 339 AA; 35785 MW; A7E3A9C73B6BBE21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 LEEDEMQTPVQGGGGGGGGGGGGGMGSPPMMGQQQAMAAMA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQALAARAGGGGGGGGGGEGPTL---RQALAARA 36
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 38.1%; Score 68.5; 1. Similarity 38.5%; Pred. No. 4.115; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q27258;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                            4 PTLRQALAARAGGGGGGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                        1:11 | 111111 | 1:1:
23 PHARRALALRVGGGGGGPAFASLTVRE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 38.3%
Query Match
Best Local Similarity 51.9%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 027258
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Q27258
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RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addms M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt W., Hoskins R.A., Galle R.F.,
RA Sutton G.C., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.W. Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Benos P.V., Berman B.P., Bhaddari D., Bolshevo S.,
RA Ballew R.M., Benos P.V., Berman B.P., Bhaddari D., Bolshevo S.,
RA Burtis K.C., Busam D.A., Buther H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buther H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Diagan-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriaz S., Felischmann W.,
RA Fosler C., Gabrielian A.E., Garg M., Diagan-Rocha S., Planck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Medazoa, Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILNE-95172378; PubMed-7867926;
Siebel C.W., Admon A., Rio D.C.;
"Soma-specific expression and cloning of PSI, a negative regulator of
                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GPESKRSLGSPEYANNSSNMSSGSGGGGGGGGGGASITQAIAQAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GPTLRQAL-----AARAGGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50583; PFKB_KINASES_1; UNKNOWN_1.
SEQUENCE 796 AA; 81588 MW; 4B9423E033677EF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68.5; DB 5;
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   797 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TXPE_1.
InterPro; IPR002173; PfkB.
InterPro; IPR002173; PfkB.
SMART; SM00322; KH; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P element pre-mRNA splicing.";
Genes Dev. 9:269-283(1995).
                                                                                                      PSI OR EG:EG0003.2 OR CG8912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0014870; Psi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S75665; AAB50636.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
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Kimmel B.C., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lako P., Lei Y., Levitsky A.A., Li J., Liz., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Nurphy B., Murphy L., Muzny D.M., Nelson D.L., A. Malson K., Nixon K., Nixon D.R., Pacleb J.M., Palazcolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinston K., Sauders R.D.C., Scheeler F., Shen H., A. Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., San E.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., R. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Strong R., Sun S., N., Wocdage T., Worley K.C., Wu D., Yang S., Yao Q.A., M. Milliams S.M., Wocdage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. Wolliams S.M., Wocdage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng L., A., Myers E.W., Rubin G.M., Venter J.C.; R. Sinith H.O., R. Schence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Murphy L., Harris D., Barrell B.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.1%; Score 68.5; DB 5; Length 797; 34.0%; Pred. No. 9.4; ive 7; Mismatches 11; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GPESKRSLGSPEYANNSSNMSSGSGGGGGGGGGGGGGGASITQAIAQAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO31863; CAA21318.1; -
FlyBase; FBgn0014870; Psi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQAL------AARAGGGGGGGGGTEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00322; KH; 4.
PROSITE; PS5084; KH_TYPE_1; 4.
SROSITE; PS0583; PFKB_KINASES_1; UNKNOWN_1.
SEQUENCE 806 AA; 84180 WW; CC9A6367110CA8FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
SEQUENCE 797 AA; 81716 MW; 4A56DE9109AFCF1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EG:EG0003.2 PROTEIN.
PSI OR EG:EG0003.2 OR CG8912.
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                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TYPE_1.
InterPro; IPR002173; PfkB.
Pfam; PF00013; KH-domain; 4.
SMART; SM00322; KH; 4.
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InterPro; IPR004088; KH_TYPE_1.
InterPro; IPR002173; PfkB.
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SMART; SM00322; KH; 4.
                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0014870; Psi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Small G.D., Min B., Lefebvre P.A.;
"Characterization of a Chlamydomonas reinhardtii gene encoding a protein of the DNA photolyase/blue light photoreceptor family.";
Plant Mol. Biol. 28:443-454(1995).
-i - Smitharity: BELONGS TO THE DNA PHOTOLYASE CLASS-1 FAMILY.
EMBL: LO7561: AAC37438.1;
-HSSP; P00914; IDNP
                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 867;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLRel. 19, CLONE NTRELIA SETTION UPDATED)
01-DEC-2001 (TREMBLREL SETTION UP
38.1%; Score 68.5; DB 5; Length 806; 34.0%; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                 11; Indels
                                                                                                                                                                3 GPTLRQAL------AARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000474; DNA_photolyase.
InterPro; IPR002081; DNA_photolyase_1.
Pfam; PF00875; DNA_photolyase_1.
ProDom; PD004390; DNA_photolyase; 1.
PROSITE; PS00394; DNA_photolyase; 1.
PROSITE; PS00691; DNA_PHOTOLYASES_1_1; 1.
Chromophore; FAD; Flavoprotein.
SEQUENCE 867 AA; 91337 MW; 613FDED4DBC7E536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA.
                                                              7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.1%; Score 68.5; 150.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 PGMLDAAGAAGGGGGGGGGAGLAGLPGVLQGL 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PTLRQALAARAGGGGGGGGGTEG-PTLRQAL 32
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95359403; PubMed=7632915;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
Query Match
Best Local Similarity 34.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPH1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-21 GR
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Tanaka T., Tsunoda T., Yamaoka Y., Nakamura Y., Furukawa Y.;
"Isolation of a novel human gene, MARKII, homologous to MARK3 and its
involvement in hepatocellular carcinogenesis.";
Meoplasia 3:4-9(2001).
-i-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                      Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0456F08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 68; DB 10; Length 529; 55.2%; Pred. No. 7.2;
                                                                                                                                                Score 68; DB 4; Length 474;
Pred. No. 6.4;
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EMBL; AP002901; BAB39414.1; ...
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 529 AA; 55981 MW; 0A5DA55CDD076D24 CRC64;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027619; BAB55238.1;
SEQUENCE 474 AA, 51313 WW; OBCA301518F20DED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MAP/MICROTUBULE AFFINITY-REGULATING KINASE LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   284 GSTIRSTFHGGQVRDRRAGGGGGGGGVQNGPPASPTLAHEA 323
                                                                                                                                                                                                                                                                                    3 GPTLR-----QALAARAGGGGGGGGGIEGPTLRQALAARA 36
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
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MEDLINE-21226021; PubMed-11326310;
                                                                                                                                                       Query Match 37.8%;
Best Local Similarity 45.0%;
Matches 18; Conservative
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nes 16; Conservative
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P0456F08.14.
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01-DEC-2001
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Q9BYD8
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Gaps
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                                                                                                                            SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyTKC; 1.
SNART; SM00165; UBA; 1.
SNART; SM00165; UBA; 1.
PROSITE; PS00101; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SROIIENCE 688 AA; 75261 MW; A0385A7943ACD086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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45.0%; Pred. No. 9.2;
tive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                   37.8%; Score 68; DB 4; Length 688, 45.0%; Pred. No. 9.2; tive 1; Mismatches 15; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MARK4 SERINE/THERDNINE PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIAA1860 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                       3 GPTLR-----QALAARAGGGGGGGGGIEGPTLRQALAARA 36
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EMBL, AB049127; BAB39380.1; -. HSSP; Q63450; 1A06.
Interpro: IPR000719; EUK_pkinase.
Interpro: IPR001290; Ser_thr_pkinase.
Interpro: IPR001245; Tyr_pkinase.
Interpro: IPR000449; UBA.
Pfan; PP00069; pkinase; 1.
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Best Local Similarity 45.0%
Matches 18; Conservative
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Matches 18; Conservative
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Q96JG7
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NCBI_TaxID=9606;

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                                           Drewes G., Ebneth A., Preuss U., Mandelkow E.M., Mandelkow E., "MAK, a novel family of protein kinases that phosphorylate microtubule-associated proteins and trigger microtubule disruption.";
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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Sasaki T., Matsumoto T., Yamamoto K.;
Oryta sativa nippombare(GA3) genomic DNA, chromosome 1, PAC
Clone:P0506E04.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003272; BAB67948.1; -- SEQUENCE 113 AA; 11708 MW; 26D9B2C86935BC0B CRC64;
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Pred. No. 2.1;
3; Mismatches 6; Indels
                                                                                                                                                                                                          Score 68; DB 4; Length 752;
                                                                                                                      Drewes G., Mandelkow E.M.;
"MARK1, homologue of MARK1, MARK2 and MARK3.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057448; AAL153683 1.
Kinase; Serine/threonine-protein kinase.
SEQUENCE 752 AA; 82519 MW; 48430FFD2B150E7A CRC64;
                                                                                                                                                                                                                     Pred. No. 10;
1; Mismatches 15; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                              3 GPTLR-----QALAARAGGGGGGGGGIEGPTLRQALAARA 36
                                                                                                                                                                                                                                                                                                                                    113 AA.
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Eukaryota; Acanthamoebidae; Acanthamoeba.
                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                    PRT;
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                     TISSUE=BRAIN;
MEDLINE=97262070; PubMed=9108484;
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                                                                                                                                                                                                                  45.0%;
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59.1%;
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les 18; Conservative
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          SEQUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                               TISSUE=BRAIN;
                                                                                                                                                                                                        Query Match
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokteer P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
RA Durbin K.J., Evangeliste C.C., Ferriac S., Fleischmann P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ibegwam C.,
SEQUENCE FROM N.A.
MEDLINE-88016163; PubMed-3477803;
Jung G., Korn E.D., Hammer J.A. III;
"The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                           Wang Z.Y., Wang F., Sellers J.R., Korn E.D., Hammer J.A. III;
"Analysis of the regulatory phosphorylation site in Acanthamoeba
myosin IC by using site-directed mutagenesis.";
Proc. Natl. Acad. Sci. U.S.A. 95:15200-15205(1998).
EMBL; AF051353; AAC98089.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.2%; Score 67; DB 5; Length 1186; 50.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1186 AA; 129459 MW; E37AD44A685803A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --2000 (TrEMBLrel. 13, Last sequence update)
-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                    and non-myosin-like sequences.";
Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               938 QILGAKGGGGGGRGRGGPSPSGAVSPR 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 QALAARAGGGGGGGIEGPTLRQALAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001609; myosin_head.
InterPro; IPR001452; SH3.
Pfam; Pr00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PROOL93; MYOSINHEAVY.
PRINTS: PRO0452; SH3DOMAIN.
FORDOM: PD000355; myosin_head; 1.
SMART; SM00242; MYSC: 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRK58E-2 PROTEIN.
QKR58E-2 OR QRK58E-2 OR CG5821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50002; SH3; SEQUENCE 1186 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00018; SH3; 1
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                MEDLINE-99079990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro:
NCBI_TaxID=7227;
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429 GSMLGRFLSNRGGGGGGGGGGGG 451

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SEQUENCE
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                                                                                                                  Q9FWD7
                                                                                         Q9FWD7
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                                                       RESULT 24
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                                                                           O9FWD7
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Slden Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylers R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J. G.,
RA Williams S.M., Wooddge T., Worley K.C., Wu D., Yang S., Yao Q., Zheng K.
RA Chong K.H., Zhong F.N., Zhon M., Zhong S., Zho Q., Zheng L.
RA Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
REMBL, AERO04457, ARR46845.1;
REMBL, RED00457, RH.
RA Chibs R.A., Myers R.M., RHENG, RHENG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating blology.":
Sclence 282:2012-2018((1998).
EMBL, 278013: CAB01420.1: -.
PROSTE: PS50240; TRYPSIN. DOM: 1.
Hydrolase; Serine protease; Serine protease; SEVINE 500 AA, 53946 MW; 1416327086FE7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00013; KH-domain: 1.
SMART: SMO0322: KH: LT
PROSITE: PS50084; KH_TYPE_1: 1.
PROSITE: PS50084; KH_TYPE_1: 1.
SEQUENCE 416 AA: 44144 MW; 095FF2F55DB7D2A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TLRQ-----ALAARAGGGGGGGGIEG 25
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.7%;
Best Local Similarity 59.3%;
Matches 16; Conservative 1
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F15B9.5 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     Buell C. R., Yudan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Bleal J. R., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalah H., Feldblyum T.V., Bowman C.L., Craven B., Utterback S.L., Fraser C.M.; Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (Aug. 2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ACC1634, AAG13445_11; -

EMBL, ACC1634, AAG13445_11; -

Enterpro; IPR003593; AAA.

Interpro; IPR003595; AAA.subfam.
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Huttunen S. and interspecific nucleotide variation at the nonA gene in Prosophila littoralis and D. virilis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ304359; CAC20082.1;
                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 10; Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 12;
2; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMRT; SW00382; AAA; 1.
ATP-binding; Hypothetical protein.
SEOUENCE 532 AA; 57290 MW; 7EAGCC4F4C6734C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 AA.
  532 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
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PRT;
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NON_TER 1 1
NON_TER 155 155
                                                                                                                        HYPOTHETICAL 57.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.7%;
51.9%;
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     PRELIMINARY;
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nes 12; Conserva
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE;
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                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                        OSJNBB0018B10.3
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huttunen S., Vieira J., Hoikkala A.;
"Levels and patterns of nucleotide variability and homopolymer length variation at the nonA gene in Drosophila virilis group species.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ304365; CAC20088.1;
                                                                                                                                                                                                                                                                                            Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Huttunen S., Campesan S., Hoikkala A.;
"Intra- and interspecific nucleotide variation at the nonA gene in brosophila littoralis and D. virilis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.1%; Score 65; DB 5; Length 155; 80.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 155
155 AA; 15336 MW; 5DCE33592CC84657 CRC64;
                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NONA PROTEIN (NO ON OR OFF TRANSIENT A) (FRAGMENT).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NONA PROTEIN (FRAGMENT).
                                                                                                                                        155 AA.
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0; Mismatches
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                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ304308; CACZ0031.1; AJ304301; CACZ0034.1; AJ304311; CACZ0040.1; AJ304320; CACZ0040.1; AJ304323; CACZ0049.1; AJ304329; CACZ0049.1; AJ304329; CACZ0059.1; AJ304332; CACZ0059.1; AJ304341; CACZ0067.1; AJ304341; CACZ0067.1; AJ304345; CACZ0067.1; AJ304355; CACZ0067.1; AJ304356; CACZ0079.1; AJ30436476; AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0043410; Dlit\nonA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ304305; CAC20028.1; -.
                                                                                                                                PRELIMINARY;
8 QALAARAGGGGGGG 22
                     11 || || || || || || || || || || 63 QAFRARGGGGGGGGG 77
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=VARIOUS STRAINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                         Drosophila littoralis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LI1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                              Q9GND8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                       RESULT 26
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                                                                                                           Q9GND8
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                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                         Huttunen S., Campesan S., Hoikkala A.; Intra and interspecific nucleotide variation at the nonA gene in Drosophila littoralis and D. Virills."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. BEMBL; AJ304362; CAC20085.1; FlyBase: FBgn0043410; Diit\nonA.
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80.0%; Pred. No. 4.7;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.1%; Score 65; DB 5; Length 156; 80.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                          156 AA; 15428 MW; 808202C5D5413BF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 156 AA; 15393 MW; 7B6202DB1A7DCD51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    8 QALAARAGGGGGGG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                       63 QAFRARGGGGGGGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                            156
Drosophila littoralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila littoralis.
                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 12; Conserv
                                                                                                        SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=47316;
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                                                                                                                             STRAIN-RU1;
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STRAIN=0981.0;
Huttunen S., Vieira J., Hoikkala A.;
Huttunen S., Vieira J., Hoikkala A.;
Huttunen S., Vieira J., Hoikkala A.;
"Levels and patterns of nucleotide variability and homopolymer length
"Levels and patterns of nucleotide variability and homopolymer length
"Levels and patterns of nucleotide variability and species:";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

NON_TER 158 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila flavomontana (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Fueryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Perygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                       Drosophila littoralis.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                  Huttunen S., Campesan S., Hoikkala A.;
Intra- and interspecific nucleotide variation at the nonA gene in
Drosophila littoralis and D. virilis.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ304350; CAC20073.1: -
EMBL; AJ304350; CAC20073.1: -
NON_TER 157
NON_TER 157
SEQUENCE 157 AA; 15450 MW; 7EE4AEEA984B78DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                      36.1%; Score 65; DB 5; Length 157; 80.0%; Pred. No. 4.7; tive 0; Mismatches 3; Indels
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158 Aa; 15791 MW; 9AC2614FC1A4C6A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NO ON OR OFF TRANSIENT A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 158 AA.
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Best Local Similarity 80.07
Matches 12; Conservative
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63 QAFRARGGGGGGGG 77
NONA PROTEIN (FRAGMENT).
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=47316;
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7. (SIDSI)/gcgdata/hold-geneseqy/geneseqy/emul/nallouning.
3. (SIDSI)/gcgdata/hold-geneseqy/geneseqy-embl/AAl981.DAT:*
4. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
5. (SIDSI)/gcgdata/hold-geneseqy-geneseqp-embl/AAl981.DAT:*
6. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
7. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
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9. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
110. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
111. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
112. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl981.DAT:*
113. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
114. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
115. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
116. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
117. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
118. (SIDSI)/gcgdata/hold-geneseqy/geneseqp-embl/AAl991.DAT:*
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Thrombopoietin mim
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TPO-mimetic peptid
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Thrombopoietin mim
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TPO-mimetic peptid
Synthetic TMP-TMP
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247.023 Million cell updates/sec
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                                                                                                                                                                                                          October 9, 2002, 08:50:51; Search time 16.1874 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747574 seqs, 111073796 residues
                                                                                                                            OM protein - protein search, using sw model
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Listing first 45 summaries
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AAB17282
AAB17308
AAY96530
AAY96530
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AAB16963
AAB17293,
AAY96525
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33 158 81.9 36 21 AAB17300 34 158 81.9 36 21 AAB17300 35 151.5 78.5 31 21 AAB17288 36 145 75.1 30 21 AAB17288 37 144 74.6 32 21 AAB17287 40 138.5 71.8 29 21 AAB17286 41 138.5 68.1 29 21 AAB17286 42 131.5 68.1 29 21 AAB17286 43 129.5 67.1 31 21 AAB16573 44 129.5 67.1 31 21 AAB16573 45 125.5 65.0 29 21 AAB16973 46 129.5 67.1 31 21 AAB16974 47 129.5 67.1 31 21 AAB16973 48 129.5 67.1 31 21 AAB16973 49 129.5 67.1 31 21 AAB16973 40 129.5 67.1 31 21 AAB16973 41 129.5 67.1 31 21 AAB16973 42 120.5 65.0 29 21 AAB16973 43 129.5 65.0 29 21 AAB16973 44 129.5 65.0 29 21 AAB16973 45 125.5 65.0 29 21 AAB16971 46 129.5 65.0 29 21 AAB16971 47 129.5 65.0 29 21 AAB16971 48 129.5 65.0 29 21 AAB16971 48 129.5 65.0 29 21 AAB16971 49 129.5 65.0 29 21 AAB16971 40 120.5 65.0 29 21 AAB16971 41 120.5 65.0 29 21 AAB16971 42 120.5 65.0 29 21 AAB16971 43 120.5 65.0 29 21 AAB16971 44 120.5 65.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 65.0 29 21 AAB16971 47 120.5 65.0 29 21 AAB16971 48 120.5 65.0 29 21 AAB16971 49 120.5 65.0 29 21 AAB16971 40 120.5 65.0 29 21 AAB16971 41 120.5 65.0 29 21 AAB16971 42 120.5 65.0 29 21 AAB16971 43 120.5 65.0 29 21 AAB16971 44 120.5 65.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 65.0 29 21 AAB16971 47 120.5 65.0 29 21 AAB16971 48 120.5 65.0 29 21 AAB16971 49 120.5 65.0 29 21 AAB16971 40 120.5 65.0 29 21 AAB16971 41 120.5 65.0 29 21 AAB16971 42 120.5 65.0 29 21 AAB16971 43 120.5 65.0 29 21 AAB16971 44 120.5 65.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 65.0 29 21 AAB16971 47 120.5 65.0 29 21 AAB16971 48 120.5 65.0 29 21 AAB16971 49 120.5 67.1 120.5 65.0 120.6	33 158 81.9 36 21 AAB17300 34 158 81.9 36 21 AAB17300 35 151.5 78.5 31 21 AAB17288 36 145 75.1 30 21 AAB17289 37 144 74.6 32 21 AAB17297 40 131.5 68.1 29 21 AAB17297 41 132 68.1 29 21 AAB17297 42 131.5 68.1 29 21 AAB17286 43 129.5 67.1 31 21 AAB16570 44 129.5 67.1 31 21 AAB16570 45 125.5 65.0 29 21 AAB16570 46 129.5 67.1 31 21 AAB16971 47 129.5 67.1 31 21 AAB16971 48 129.5 67.1 31 21 AAB16971 49 129.5 67.1 31 21 AAB16971 40 129.5 67.1 31 21 AAB16971 41 129.5 67.1 31 21 AAB16971 42 120.5 65.0 29 21 AAB16971 43 120.5 65.0 29 21 AAB16971 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 129.5 67.1 31 21 AAB16971 47 129.5 67.1 31 21 AAB16971 48 129.5 67.1 31 21 AAB16971 49 129.5 67.1 31 21 AAB16971 40 129.5 67.1 31 21 AAB16971 41 120.5 65.0 29 21 AAB16971 42 120.5 65.0 29 21 AAB16971 43 120.5 65.0 29 21 AAB16971 44 120.5 65.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 67.1 31 21 AAB16971 47 120.5 67.1 31 21 AAB16971 48 120.5 67.1 31 21 AAB16971 49 120.5 67.1 31 21 AAB16971 40 120.5 67.1 31 21 AAB16971 41 120.5 67.1 31 21 AAB16971 42 120.5 67.1 31 21 AAB16971 43 120.5 67.1 31 21 AAB16971 44 120.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 67.1 31 21 AAB16971 47 120.5 67.1 31 21 AAB16971 48 120.5 67.1 31 21 AAB16971 49 120.5 67.1 31 21 AAB16971 40 120.5 67.1 31 21 AAB16971 40 120.5 67.1 31 21 AAB16971 41 120.5 67.1 31 21 AAB16971 42 120.5 67.1 31 21 AAB16971 43 120.5 67.1 31 21 AAB16971 44 120.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 67.1 31 21 AAB16971 47 120.5 67.1 31 21 AAB16971 48 120.5 67.1 31 21 AAB16971 49 120.5 67.1 31 21 AAB16971 40 120.5 67.1 31 21 AAB16971 41 120.5 67.1 31 21 AAB16971 42 120.5 67.1 31 21 AAB16971 43 120.5 67.1 31 21 AAB16971 44 120.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 46 120.5 67.1 31 21 AAB16971 47 120.5 67.1 31 21 AAB16971 48 120.5 67.1 31 21 AAB16971 49 120.5 67.1 31 21 AAB16971 40 120.5 67.1 AAB16971 40 1	34 158 81.9 36 21 AAB17300 34 158 81.9 36 21 AAB17300 35 151.5 78.5 3 12 AAB17288 36 144 74.6 32 21 AAB17287 38 144 74.6 32 21 AAB17287 39 144 74.6 34 21 AAB17287 40 138.5 71.8 29 21 AAB17285 41 132.5 68.4 29 21 AAB16970 44 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16970 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301; A		158	81.9			AAB17289	Thought Inear
34 158 81.9 36 21 AAV96522 Linear thronomy 145 78.5 31 21 AAB17289 TPO-mimetic 167 74.6 32 21 AAB17287 TPO-mimetic 187 144 74.6 32 21 AAB17287 TPO-mimetic 187 144 74.6 32 21 AAP96520 Thrombopoiet 40 138.5 71.8 29 21 AAP96520 Thrombopoiet 40 138.5 71.8 29 21 AAB17285 TPO-mimetic 187 132 68.4 28 21 AAB17285 TPO-mimetic 187 132 68.1 29 21 AAB16970 TPO-mimetic 187 129.5 67.1 31 21 AAB16970 TPO-mimetic 187 129.5 67.1 31 21 AAB16971 TPO-mimetic 188.7 129.5 67.1 31 21 AAB16971 TPO-mimetic 188.7 125.5 65.0 29 21 AAB16971 TPO-mimetic 188.7 125.5 125	34 158 81.9 36 21 AAV96522 Linear throng 145 78.5 31 21 AAB17287 TPO-mimetic 156 145 74.6 32 21 AAB17287 TPO-mimetic 157 144 74.6 32 21 AAB17287 TPO-mimetic 158 144 74.6 32 21 AAB17287 TPO-mimetic 158 144 74.6 32 21 AAP96520 Thrombopoiet 159 144 74.6 32 21 AAV96520 Thrombopoiet 159 144 74.6 32 21 AAV96520 TPO-mimetic 159 144 74.6 32 21 AAB17286 TPO-mimetic 159 15 67.1 31 21 AAB16970 TPO-mimetic 159 15 67.1 31 21 AAB16970 TPO-mimetic 159 15 67.1 31 21 AAB16970 TPO-mimetic 159 15 67.1 31 21 AAB16971 TPO-mimetic 159 15 65.0 29 21 AAB16971 TPO-mimetic 159 15 65.0 29 21 AAB16971 TPO-mimetic 159 15 65.0 29 21 AAB16971 TPO-mimetic 159 150 15 65.0 29 21 AAB16971 TPO-mimetic 159 15 65.0 29 21 AAB17301; 36 AA. AAB17301;	34 158 81.9 36 21 AAV96522 35 151.5 78.5 31 21 AAB17288 36 145 75.1 30 21 AAB17288 37 144 74.6 32 21 AAB17297 39 144 74.6 32 21 AAB17297 40 138.5 71.8 29 21 AAB17286 41 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16970 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301, AAB17301; TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autonumune disease; cytostatic; antiasthmatic; thromboly immunosuppressive.		158	81.9			AAB17300	
35 151.5 78 5 31 21 AAB17288 36 145 75.1 30 21 AAB17288 37 144 74.6 32 21 AAP17297 38 144 74.6 32 21 AAV96520 40 138.5 71.8 29 21 AAV96527 40 138.5 67.1 31 21 AAB17286 42 131.5 68.1 2.9 21 AAB17286 43 129.5 67.1 31 21 AAB16970 44 129.5 67.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide: therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly mmp; inhibitor; erruthocoly TPO; CTLA4; mimetic; IL-1; TNP; MMP; inhibitor; erruthocoly TPO; CTLA4; mimetic; IL-1; TNP;	35 151.5 78 5 31 21 AAB17288 36 145 75.1 30 21 AAB17288 37 144 74.6 32 21 AAB17297 38 144 74.6 32 21 AAP16297 39 144 74.6 32 21 AAP16297 40 138.5 71.8 29 21 AAB16970 42 131.5 68.1 29 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 Standard; Peptide; 36 AA. AAB17301, TPO-mimetic peptide sequence SEQ ID NO.357. Modified peptide; therapeutic agent; fusion; Fc domain; immunosuppressive; ED; TPO; TPO; TPA; IPD; TPA	35 151.5 78 5 31 21 AAB17288 36 145 75.1 30 21 AAB17288 37 144 74.6 32 21 AAB17287 38 144 74.6 32 21 AAB17287 40 138.5 71.8 39 21 AAB17285 41 132 68.4 28 21 AAB17285 42 131.5 68.1 29.2 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB		158	81.9			AAY96522	IPO-mimetic pepti
36 145 75.1 30 21 AMB17287 TPO-numetic 37 144 74.6 32 21 AAB17297 TPO-numetic 38 144 74.6 32 21 AAB17297 TPO-numetic 39 144 74.6 32 21 AAB17297 TPO-numetic 39 144 74.6 32 21 AAB17297 TPO-numetic 39 144 74.6 32 21 AAB17297 TPO-numetic 41 13.2 68.1 29 21 AAB17285 TPO-numetic 74 120.5 67.1 31 21 AAB16979 TPO-numetic 74 120.5 65.0 29 21 AAB16979 TPO-numetic 74 120.5 65.0 39 21 AAB16979 TPO-numetic 75 120.5 65.0 39 21 AAB17301 TPO-numetic 800 ID NO:357.	36 145 75.1 30 21 ANB17287 TPO-nimetic 144 74.6 32 21 AAB17287 TPO-nimetic 39 144 74.6 32 21 AAB17287 TPO-nimetic 41 13.2 68.1 29 21 AAB17286 TPO-nimetic 42 131.5 68.1 29 21 AAB17285 TPO-nimetic 74 129.5 67.1 31 21 AAB16973 TPO-nimetic 74 129.5 65.0 29 21 AAB16974 TPO-nimetic 74 129.5 65.0 29 21 AAB16971 TPO-nimetic 74 129.5 65.0 29 21 AAB17901 TPO-nimetic 74 129.5 65.	36 145 75.1 30 21 AAB17287 38 144 74.6 32 21 AAB17287 38 144 74.6 32 21 AAB17287 39 144 74.6 32 21 AAB17287 40 138.5 71.8 29 21 AAB17286 41 132 68.4 2 29 21 AAB17286 42 131.5 68.1 29 21 AAB16970 44 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB16371 AAB17301 AAB17301 AAB17301 AAB17301, 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive pop. mon. Ann. Ann. Ann. Ann. Ann. Ann. Ann. A		51.5	78.5			AAB17288	Linear thrombopoi
37 144 74.6 32 21 AAB17297 TPO-mimetic 39 144 74.6 32 21 AAY96520 Thrombopoiet 40 138.5 71.8 29 21 AAY96520 Thrombopoiet 41 132 68.4 28 21 AAB17286 TPO-mimetic 52 21 AAB17285 TPO-mimetic 52 21 AAB16970 TPO-mimetic 52 21 AAB16970 TPO-mimetic 52 56.1 31 21 AAB16970 TPO-mimetic 52 56.1 31 21 AAB16970 TPO-mimetic 52 56.0 29 21 AAB16971 TPO-mimetic 52 56.0 29 21 AAB17301 TPO-mimetic 52 56.0 20 21 AAB17301 TPO-mimetic 52 56.0 20 21 AAB173	37 144 74.6 32 21 AAB17297 TPO-mimetic 39 144 74.6 32 21 AAY96520 Thrombopoiet 40 138.5 71.8 29 21 AAY96520 Thrombopoiet 41 132 68.4 28 21 AAB17285 TPO-mimetic 50.1 31 21 AAB17285 TPO-mimetic 50.1 31 21 AAB16970 TPO-mimetic 50.2 57.1 31 21 AAB16970 TPO-mimetic 50.2 57.1 31 21 AAB16970 TPO-mimetic 50.2 57.1 31 21 AAB16971 TPO-mimetic 50.2 57.1 AAB17301 AAB17301 TPO-mimetic 50.2 57.1 AAB17301 TPO-	37 144 74.6 32 21 AAB17297 38 144 74.6 32 21 AAB17297 39 144 74.6 32 21 AAP86520 39 144 74.6 34 21 AAP86520 40 138.5 71.8 29 21 AAB17286 42 131.5 68.4 28 21 AAB17286 43 129.5 67.1 31 21 AAB16974 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301 AAB17301 TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive For the contract of the contra		145	75.1			AAB17287	TPO-mimetic pepti
38 144 74.6 32 21 AAV96520 39 144 74.6 34 21 AAV96520 40 138.5 71.8 29 21 AAB17285 42 131.5 68.1 2.9 21 AAB16970 43 129.5 67.1 31 21 AAB16971 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB17301 AAB	38 144 74.6 32 21 AAV96520 39 144 74.6 34 21 AAV96520 40 138.5 71.8 29 21 AAB17286 42 131.5 68.1 29 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB17301 TPO-mimetic peptide sequence SEQ ID NO.357. Modified peptide; therapeutic agent; fusion; Fc domain; immunosuppressive; EPO; TPO; TPA, mimetic; thromboly immunoe disease; cytostatic; antiasthmatic; thromboly immunosuppressive; EPO; TPO; TPA, mimetic; thromboly immunosuppressive; EPO; TPO; TPA, mimetic; thromboly immunosuppressive; EPO; TPO; TPA; intraproxicatic; intrap	38 144 74.6 32 21 AAN96520 40 138.5 71.8 34 21 AAN96527 40 138.5 71.8 34 21 AAN17865 42 131.5 68.1 29.2 1 AAN1786 43 129.5 67.1 31 21 AAN16970 44 129.5 67.1 31 21 AAN16971 45 125.5 65.0 29 21 AAN16971 AAN17301		144	74.6			AAB17297	
39 144 74.6 34 21 AAN96527 40 138.5 71.8 29 21 AAB17286 41 131.6 68.4 29 21 AAB17285 42 131.5 68.1 29 21 AAB16970 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16974 45 125.5 65.0 29 21 AAB16974 ALIGNMENTS SULT 1 B17301 AAB17301 AAB17301 AAB17301 AAB17301 TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide: therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive; BPO: TPO: TPO: TPO: TPO: TPO: TPO: TPO: T	39 14 74.6 34 21 AAN96527 40 138.5 71.8 29 21 AAB17286 41 132 68.4 29 21 AAB17285 42 131.5 68.1 29 21 AAB16970 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16974 45 125.5 65.0 29 21 AAB16974 45 125.5 65.0 29 21 AAB16971 AAB17301 AAB17301 AAB17301 AAB17301 TPO-mimetic peptide; beptide; 36 AA. AAB17301 TOCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive; EDO; TPO; TEAA; mimetic; in 1:; TNF; MMP; inhibitor; ervthronietic thromboly thromboly thromboly through the contract thromboly thromb	39 144 74.6 34 21 AAP96527 40 138.5 71.8 29 21 AAB17286 41 132.5 68.4 28 21 AAB17285 43 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 AAB16971 AAB17301 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive Proc. and incompanies in the population of the populati		144	74.6			AAY96520	TPU-mimetic pepti
40 138.5 71.8 29 21 AAB17286 41 132 68.4 28 21 AAB17286 42 131.5 68.1 29 2 2 AAB17285 43 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive; EPO; TL-1; TNF; MMP; inhibitor; errorbooked.	40 138.5 71.8 29 21 AAB17286 41 132 68.4 28 21 AAB17285 42 131.5 68.1 29 2 21 AAB17285 43 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301 AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide; therapeutic agent; fusion; Fc domain; immunosuppressive; EPO; TPO; TPA, mimetic; thromboly immunoe disease; cytostatic; antiasthmatic; thromboly immunosuppressive; EPO; TPO; TPA, mimetic; thromboly immunosuppressive; EPO; TPO; TPO; TPA, mimetic; thromboly immunosuppressive; EPO; TPO; TPO; TPA, mimetic; thromboly immunosuppressive; EPO; TPO; TPO; TPO; TPO; TPO; TPO; TPO; T	40 138.5 71.8 29 21 AAB17286 41 132 68.4 28 21 AAB17286 42 131.5 68.1 29 2 21 AAB17286 43 129.5 67.1 31 21 AAB16970 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301 AAB17301 AAB17301 TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoolmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive Proc. Thro.		144	74.6			AAY96527	Inrompopoletin mi
41 132 68.4 28 21 AAB17285 TPO-mimetic 43 129.5 68.1 29 21 AAB16970 TPO-mimetic 43 129.5 67.1 31 21 AAB16970 TPO-mimetic 44 129.5 67.1 31 21 AAB16971 TPO-mimetic TPO-mimetic 45 125.5 65.0 29 21 AAB16971 TPO-mimetic TPO-mim	41 132 68.4 28 21 AAB17285 TPO-mimetic 43 129.5 68.1 29 21 AAB16970 TPO-mimetic 43 129.5 67.1 31 21 AAB16970 TPO-mimetic 44 129.5 67.1 31 21 AAB16971 TPO-mimetic TPO-mimetic 56.0 29 21 AAB16971 TPO-mimetic SEQ ID NO:357. Modified peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; auttoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; mwP; inhibitor; erythorocyte; thrombolytic; vegF; mWP; inhibitor; erythorocyte; thrombolytic; vegF;	41 132 68.4 28 21 AAB17285 43 131.5 68.1 29.21 AAB16970 44 129.5 67.1 31 21 AAB16971 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301 AAB		38.5	71.8			AAB17286	Inrombopoletin mi
42 131.5 68.1 29 21 AAB16970 TPO-mimetic 43 129.5 67.1 31 21 AAB16973 TPO-mimetic 44 129.5 67.1 31 21 AAB16973 TPO-mimetic 45 125.5 65.0 29 21 AAB16974 TPO-mimetic TPO-mimetic 56.0 29 21 AAB16974 TPO-mimetic TPO-mimetic 56.0 29 21 AAB16971 TPO-mimetic 56.0 50 50 50 50 50 50 50 50 50 50 50 50 50	42 131.5 68.1 29 21 AAB16970 TPO-mimetic 43 129.5 67.1 31 21 AAB16973 TPO-mimetic 44 129.5 67.1 31 21 AAB16973 TPO-mimetic 45 125.5 65.0 29 21 AAB16971 TPO-mimetic TPO-mimetic 57.0 29 21 AAB16971 TPO-mimetic TPO-mimetic 58.0 29 21 AAB16971 TPO-mimetic TPO-mimetic 58.0 29 21 AAB16971 TPO-mimetic 57.0 TPO-mimetic 57.0 AAB17301 AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; auttoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPOA; mimetic; LI:, TNF; antagonist; MMP; inhibitor; erythnosierin; thrombolytic; VEGF; MMP; inhibitor; erythnosierin; thrombolytic; TPOA; mimetic; thrombolytic; TPOA; mitagonist;	42 131.5 68.1 29 21 AAB16970 43 129.5 67.1 31 21 AAB16973 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301, 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive. Proc. Thro. Thro. Thro. Thro. Thro. Thro. Thro. Thromboly		132	68.4	28		AAB17285	
43 129.5 67.1 31 21 AAB16973 TPO-mimetic peptid 41 129.5 67.1 31 21 AAB16974 TPO-mimetic peptid 45 125.5 65.0 29 21 AAB16971 TPO-mimetic peptid 56.0 29 21 AAB16971 TPO-mimetic peptid 57.1 TPO-mimetic peptide; 36 AA. AAB17301 AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; immunosuppressive; EPO; TPO; CTLA4; mimetic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;	43 129.5 67.1 31 21 AAB16973 TPO-mimetic 45 125.5 65.0 29 21 AAB16971 TPO-mimetic TPO-mimetic 56.0 29 21 AAB16971 TPO-mimetic SGULT 1 AAB17301 AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiaathmatic; thrombolytic; VEGF; imwinosuppressive; EPO; TPOA; mimetic; LI-1; TNF; antagonist; MMP; inhibitor; erythnosic+ir, thrombolytic; VEGF; MMP; inhibitor; erythnosic+ir, thrombolytic; TLA; TNF; antagonist;	43 129.5 67.1 31 21 AAB16973 44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301; AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive. Por Port, Prop. TPO-mimetic; thromboly	_		68.1	29		AAB16970	pepti
44 129.5 67.1 31 21 AAB16974 TPO-mimetic 45 125.5 65.0 29 21 AAB16971 TPO-mimetic TPO-mime	44 129.5 67.1 31 21 AAB16974 TPO-mimetic 45 125.5 65.0 29 21 AAB16971 TPO-mimetic TPO-mime	44 129.5 67.1 31 21 AAB16974 45 125.5 65.0 29 21 AAB16971 ALIGNMENTS SULT 1 B17301 AAB17301; AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoAmmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive. For or o			67.1	31		AAB16973	
ALIGNMENTS ALIGNMENTS SULT 1 B17301 AAB17301; AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor: erythynoiciase;	ALIGNMENTS ALIGNMENTS SULT 1 B17301 AAB17301; AAB17301; AAB17301; TPO-mimetic AAB17301; TPO-mimetic AAB17301; TPO-mimetic AAB17301; TPO-mimetic AAB17301; AAB1730	ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS SULT 1 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmue disease; cytostatic; antiasthmatic; thrombolytic; VEGE; immunosuppressive; Pro-modified; worker, autiasthmatic; thrombolytic; VEGE;			67.1	31		597	
ALIGNMENTS SULT 1 B17301 B17301 AAB17301; AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor: erythmatic; IL-1; TNF; antagonist;	ALIGNMENTS SULF 1 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301; 31-OCT-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, mimetic; thrombolytic; VEGF; MMP; inhibitor; erythnosierin; thrombolytic; UL-1; TNF; antagonist;	ALIGNMENTS SULT 1 B17301 AAB17301 standard; Peptide; 36 AA. AAB17301; 31-ocr-2000 (first entry) TPO-mimetic peptide sequence SEQ ID NO:357. Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thromboly immunosuppressive: Pop. TPO. TRO. TRO. TRO. TRO. TRO. TRO. TRO. TR	_		0.59	29		597	
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			ESULT 1 AB17301						
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				nune d	lisease	CVTOR	uric tati	agent; fusion; Fc d	lomain; cancer;
				suppre	ssive;	EPO: T	 	TIA4. mimetic. II-1	rombolytic; VEGF;
				hibit	or; er	vthropo	, to	1 LAS MILMELLC; IL-1	, TNF; antagonist;
				T OT	Cerr	Vmphocv:	0	ation 1. timois see	

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vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
                                                                         99WO-US25044.
                                                                                         98US-0105371.
99US-0428082.
                                                                                                               (AMGE-) AMGEN INC.
                                        WO200024782-A2.
                                                                        25-OCT-1999;
                                                                                      23-OCT-1998;
                                                                                                 22-OCT-1999;
                                                        04-MAY-2000
                        Synthetic.
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WPI; 2000-350702/30.

Thrombopoietin mim Synthetic TMP-TMP-

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Matches
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                                                                                                          The present invention describes composition of matter (I) comprising an comparison, pharmacologically active peptides, and linkers. Where (I) is: F domain, pharmacologically active peptides, and linkers. Where (I) is: C (Xl)a-F1-(X2)b, where: F1 = an Fc domain; XI and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

CC (L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4

CC (L1)c-P1-(L2)d-P3-(L3)d-P3, or -(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "optionally modified by bromoacetyl or PEG"
                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 193; DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pred. No. 9.1e-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Scc. 100.0%; Pred. No. >.. 100.0%; Pred. No. >.. .. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                         Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96523 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100. Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96523;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
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                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 193; DB 21;
100.0%; Pred. No. 9.1e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16963 standard; Protein; 36 AA.
                                                                                                                                                   Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371
                           Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                           WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA;
(AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB16963;
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                                                                                                                                                                    The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is: independently selected from -(LI)--I)--[L2)d-P2.

(X1)a-F1-(X2)d-P2-(L3)e-P-3, or -(L1)--I)--[L1]--[L2)d-P2-(L3)d-P2-(L3)e-P3-(L4)-P2-(L3)d-P2-(L3)d-P3-(L4)-P3-(L3)d-P2-(L3)d-P3-(L4)-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 186; DB 21;
Pred. No. 6.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham J, Boone TC;
                                                                                                                                    Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17293 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 97.29 hes 35; Conservative
                                                                                                   autoimmune diseases -
                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present invention describes composition of matter (I) comprising an Fe domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently control of the composition of the converted conver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%; Score 186; DB 21; Length 36; 97.2%; Pred. No. 6.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin mimetic peptide compound 6.
                                                                                                                                                                                              Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96525 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jabel TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US24834.
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les 35; Conservative
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                                                                                                  autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024770-A2.
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(AMGE-) AMGEN INC.
23-OCT-1998;
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                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                      AAB17281
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                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              'note- "optionally linked to an Fc molecule"
                                                                                                                                                                                                                         96.4%; Score 186; DB 21; Length 36;
                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                              virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                Pred. No. 6.4e-16;
0; Mismatches 1.
                                                                                                                                                                                                                                                     Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     AAY96528 standard; peptide; 41 AA.
                                                                          Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                   28..41
/label- TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                              /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US24834.
                    Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                    97.28;
                                                                                                                                                                                                                                                                                                                                  04-SEP-2000 (first entry)
                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.2%
Matches 35; Conservative
                                  WPI; 2000-365108/31.
                                                                                                                                                                                                                36 AA;
        (AMGE-) AMGEN INC.
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Modified-site
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mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],

mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

is new. TMP_1 and TMP_2 are useful for increasing the production of thrombopoietin. The TMPs are useful for increasing the production of platelets or platelets are assetuled to mediates the production of the produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelets or platelet precursors (e.g. megakaryocytes) in a mammal, whit is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; munnosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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Pred. No. 7.3e-16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 65; 91pp; English.
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                                                                                                                                                                                    Liu C, Feige U, Cheetham J;
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98US-0105348
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nes 35; Conserva
                                                                                                                                                                                                                                                                                          WPI; 2000-365108/31.
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                                                                                                      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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The present invention describes composition of matter (I) comprising an (XI)a-F1-(XI)b, where: FI = an Fc domain, XI and X2 = are each independently selected from -(LI)c-P1-(LI)c-P1-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA69443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69226 and AAB16955 to AAB18003 represent nuclectide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide, therapeutic agent; fusion; Fc domain, cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; cytotoxic rell lymphooytein; thrombopoieth; interleukin ; cytotoxic real lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 186; DB 21; Length 42;
Pred. No. 7.5e-16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:338.
                                  Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                           Disclosure; Page 313; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%;
97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Conservative
                                                                                                                                                                           autoimmune diseases -
                                                                           WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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                          Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The present intrentation describes composition of marter (1) comprising an (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L3)e-P2-(L3)e-P2-(L3)e-P3-(L4)f-P4 (L1)c-P1-(L2)d-P2, (L3)e-P3-(L3)e-P3-(L4)f-P4 (P4)ere P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and and b is 1. The composition can cartivities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can cused for producing pharmaceutical compositions. The compositions are the used for producing pharmaceutical compositions. The compositions are the use of an Fc domain (rather than a Fab domain) can provide a longer (C be use of an Fc domain (rather than a Fab domain) can provide a longer that incorporate functions such as Fc receptor binding, protein CC A binding, complement fixation, and possibly placental transfer. AAA699443

CC sequences used in the exemplification of the present invention.
                                                                                                                                                     The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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Pred. No. 7.5e-16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                    Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17308 standard; Peptide; 42 AA.
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                                                                                      autoimmune diseases -
                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: Cr (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where (I) = an Fc domain; X1 and X4 = are each independently selected from (-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (-(L3)d-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; IgGl; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.4%; Score 186; DB 21; Length 42; 97.2%; Pred. No. 7.5e-16; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96530 standard; Protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA29225.
WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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Overlapping oligonucleotides were used to construct a synthetic connected that the defect of the defect of see encoding a thrombopoietin mimetic peptide (TMP), which connected the first of the first o
                                                                                                                                                                                                                                                                                                                                                                                                                                TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaemia, immune thrombocytopenia (ITP), human immu
associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.4%; Score 186; DB 21;
97.2%; Pred. No. 7.5e-16;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17311 standard; Peptide; 60 AA.
Example 2A; Page 48; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
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                                                 The present invention describes composition of matter (I) comprising in Fe domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-FI-(XI)b, where: FI = an Fc domain; XI and X2 = are each independently selected from -(LI)c-PI-(LI)c-PI-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-(LI)d-P2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autolnmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; munosoppressive; BPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; oytotoxic T cell lymphocyte antight 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.4%; Score 186; DB 21; Length 60; 97.2%; Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J, Boone TC;
                 Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB16960 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA69446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-P1-(L2)d-P2.

(L1)C-P1-(L2)d-P2-(L3)e-P^3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of independently linkers; and a, b, c, d, e, and f = are each independently inversion or 1. provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions.

CC os 1. provided that will be active the present invention can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions.

CC os 1. provided that will be active the composition can be used for producing pharmaceutical composition.

CC of the use of an FC domain (rather than a Fab domain) can provide a longer composition can be active to a producing cancer invention, and possibly placental transfer. AAA69443 cc sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.4%; Score 186; DB 21; Length 269; 97.2%; Pred. No. 5.2e-15; Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96531 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 1gG1 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, mimetic; IL-1; TRF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                 Length 269;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                               Pred. No. 5.2e-15;
                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                     Score 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                          AAB17303 standard; Peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0428082
                                                                                                                                                                                                                         96.4%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
                                                                                                                                                                                                                                   Best Local Similarity
Matches 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                  269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     AAB17303;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                           Query Match
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The present invention describes composition of matter (I) comprising an (X) are domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)C-F1, -(L1)C-F1 -(L2)d-F2, -(L3) -P-7, or -(L1)C-F1 -(L2)d-F2 -(L3) = P-7, or -(L1)C-F1 -(L2)d-F2 -(L3) = P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
pharmacologically active.peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently no or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer that incorporate functions such as Fc receptor binding, protein Abifalie or incorporate functions such as Fc receptor binding, protein to AAA69526 and AAB18033 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA#, mimetic; IL-1; TNF; antagonist; MRP; inhibitor; erythropoletin; thrombopoletin; interleuxin is cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                .:
                                                                                                                                                                                                                                                                                        95.9%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 8.5e-16;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                            TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17307 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                            35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
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                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17307;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                    Matches
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O or 1, provided that at least 1 of a and b is 1. The composition can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fcb domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein to Abinding, complement fixation, and possibly placental transfer. AA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemnic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                     Score 185; DB 21; Length 36;
Pred. No. 8.5e-16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15..22
/label= linker
                                                                                                                                                                                    95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105348
                                                                                                                                                                                                           35; Conservative
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365108/31.
                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                             AAY96524;
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                        RESULT 16
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10 to 14 residues in length comprising x_{-2} \cdot x_{-1} = 0, x_{-2} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, and x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, and x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, and x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_{-1} = 1, and x_{-1} \cdot x_{-1} = 1, x_{-1} \cdot x_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 185; DB 21; Length 36; Pred. No. 8.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17306 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similaricy
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive be used for producing pharmacoutical compositions. The compositions are be used for producing pharmacoutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC obmain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein Abinding, complement fixation, and possibly placental transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1],nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                              A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                           94.3%; Score 182; DB Z1
                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                            Thrombopoletin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                      Pred. No. 2e-1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96526 standard; peptide; 36 AA
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/label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US24834
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                                                                                                                                                                                                                                                                                                            94.48;
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                                                                                                                                                                                                                                                                                            94.33
Query Match
Best Local Similarity 94.43
Matches 34; Conservative
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                                                                                                                                                                                                                                                         36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96526;
                                                                                                                                                                                                                                                           Sequence
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CC X_1 = X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth interior matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 94.3%; Score 182; DB 21 Local Similarity 94.4%; Pred: No. 2e-15; les 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB16959 standard; Protein; 268 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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useful for treating cancer, astains, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive based to now wectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For domain, pharmacologically active peptides, and linkers. Where (I) i independently selected from -(L1)c-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

where P1, P2, P3, and P4 = are each independently sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiaschmatic; thrombolytic; VBGF; MMP: inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma: thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                  Score 182; DB 21; Length 268;
Pred. No. 1.6e-14;
0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARAGGGKGGGGIEGPTLROWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17304 standard; Peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                  94.38;
                                                                                                                                                                                                                                                                                                97.18;
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
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                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17304;
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                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
     888888888888888888888888888888888888
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can useful for breating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (tather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-TI-(X2)b. where: FI = an Fc domain; XI and X2 = are each independently selected from -(LI)c-PI-(LI)c-PI-(L2)d-P2. (L3)a-P3 -(L3)c-PI-(L2)d-P2. (L3)a-P3 -(L3)a-P3 -(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoinmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; munosoppressive; EPO; TPO; CTLA4; mimetic; IL-1; TMF; antagonist; cytotoxic reythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                           94.0%; Score 181.5; DB 21; Length 39; 92.3%; Pred. No. 2.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 181.3,
Pred. No. 2.4e-15;
....atches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGK---GGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17302 standard; Peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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FC domain, pharmacologically active peptides, and linkers. Where (I) is: FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b. where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L3)e-P3, r1, r1, r2-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 are each independently sequences of where P1, P2, P3, and P4 = are each independently pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
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O or 1, provided that at least 1 of a and b is 1. The composition can arterial solutions and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69226 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA, minetic; LT.1; TNF; antagonist; antwp; inhibitor; erythropoietin; thrombopoietin; interleukin is cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%; Score 181; DB 21; Length 40; 90.0%; Pred. No. 2.9e-15; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGK----GGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 317-318; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17292 standard; Peptide; 35 AA.
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99US-0428082.
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Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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Fc domain, pharmacologically active peptides, and linkers. Where (I) is: Fc domain, pharmacologically active peptides, and linkers. Where (I) is: Mand XI are each (XI)a-F1-(X2)b, where FI = an Fc domain; XI and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(
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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer than I rate of incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic: VEGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; wWRP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                        92.0%; Score 177.5; DB 21; Length 35; 97.2%; Pred. No. 6.7e-15; 1.1ve 0; Mismatches 0; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17294 standard; Peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17294;
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention describes composition of matter (I) comprising an (X1) are I (X2) b, where: F1 = an Fc domain; X1 and X2 = are each (X1) are I (X2) b, where: F1 = an Fc domain; X1 and X2 = are each (X1) b, where I b, P2 (X1) b, where (I) is: (X1) c-P1 (L2) d-P2 (L3) d-P
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; munosoppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF: antagonist; cytotoxic retythropoietin; thrombopoietin; interleukin; vascular endothelial ymphocyte antigen 4; tumour necrosis factor; asthmas; thrombosis; pharmaceutical; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                      90.9%; Score 175.5; DB 21; Length 37; 94.6%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARA-GGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17295 standard; Peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0428082
                                                                                                                                                                                                                                                      Local Similarity 94.69
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                     37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
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                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17295
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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; munosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; Cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                               90.7%; Score 175; DB 21; Length 38; 92.1%; Pred. No. 1.5e-14; Indels
                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARA--GGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17305 standard; Peptide; 39 AA.
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                                                                                                                                                                                                                   Best Local Similarity 92.1
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                            38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
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                                                                                                                                         Sequence
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                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
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            Sequence
                                                         Query Match
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                                                                                                                                                                                                                                                                     RESULT 27
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XX
So
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(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each (X1)a-F1-(L2)d-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P2-(L3)e-P3-(L3)e-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(
                                                                                                                                                                    ;;
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; autoimmunosuppressive; EPO; TPO; CTLAA; mimmetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                         3;
                                                                                                                              DB 21; Length 39;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGG---KGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                   90.4%; Score 174.5; DB 21
89.7%; Pred. No. 1.7e-14;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                            AAB17296 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                    Best Local Similarity 89.7
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                        39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-0CT-1999;
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                                                                                                           Sequence
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
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The present invention describes composition of matter (I) comprising an c. (XI)a-TH-(XZ)b, where: Fl = an Fr domain; X1 and X2 = are each C. (XI)a-TH-(XZ)b, where: Fl = an Fr domain; X1 and X2 = are each c. (II)c-TH-(IZ)b, where: Fl = an Fr domain; X1 and X2 = are each c. (II)c-PH-(IZ)d-P2. (IJ)d-P2. (IJ)d-P2. (IJ)d-P2. (IJ)d-P3. (IJ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiaathmatic; thrombolytic; VEGF; immunoSuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin is vascular cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                        9
89.6%; Score 173; DB 21; Length 42; 83.3%; Pred. No. 2.8e-14; Live 0; Mismatches 1; Indels
                                                                                                                                                                                1 IEGPTLRQWLAARA-----GGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17291 standard; Peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0105371.
99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                   Local Similarity 83.39
nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2000.
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34 AA;

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The present invention describes composition of matter (I) comprising an (X1)4-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)4-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)4-F1-(X2)b, where (I) is: independently selected from - (L1)c-P1, -(L1)c-P1-(L2)d-P2.

"Ul)c-P1-(L2)d-P2-(L3)d-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of independently linkers; and a, b, c, d, e, and I4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each invention can activities. DNAs, vectors and host cells from the present invention can useful for treating cancer, asthma, thrombosit.ons The compositions are the use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein can binding, complement fixation, and possibly placental transfer. AAA69443 exquences used in the exemplification of the present invention.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                        5;
                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
            DB 21; Length 34;
                          Pred. No. 4e-14;
0; Mismatches 0; Indels
                                                                           1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:346.
Ouery Match

Best Local Similarity 94.4%; Pred. No. 4e
Matches 34; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                          AAB17290 standard; Peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
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                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                   AAB17290;
                                                                                                                                                                    RESULT 28
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                                                                                                             С
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85.2%; Score 164.5; DB 21; Length 33;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; cytotoxic grythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacologically active peptides, useful for treating cancer and
                                              3;
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                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and
        Pred. No. 2.4e-13;
0; Mismatches 0;
                                                                       1 IEGPTLROWLAARAGGGKGGGGIEGPTLROWLAARA 36
                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                    AAB17298 standard; Peptide; 36 AA.
  91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases -
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                              AAB17298;
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                        Matches
                                                                                                                                                                                                      RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 82.9%; Score 160; DB 21; Length 36; 1 Similarity 91.7%; Pred. No. 9.1e-13; 33; Conservative 0; Mismatches 3; Indels
                  TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 320-321; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                           AAB17299 standard; Peptide; 36 AA.
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99US-0428082.
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Best Local Similarity
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                                                                                                                                                                                                                                                                             RESULT 30
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1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36

Matches

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Search completed: October 9, 2002, 08:58:57 Job time: 16.1874 secs

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e 17, Appl
185, Arr
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Sequence 13, Appl
Sequence 193, Appl
Sequence 13, Appl
Sequence 193, Appl
Sequence 193, Appl
Sequence 193, Appl
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Sequence 231, App
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Sequence 13, Appl
Sequence 13, Appl
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17, Appl
185, App
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185, App
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194, Appl
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Sequence 1
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                 1 IEGPTLROWLAARAGGGKGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                           231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                              OM protein - protein search, using sw model
                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                  US-09-422-838C-30
                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
                                                                                                                   BLOSUM62
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339.6

337.8

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                                                                                          Perfect score:
                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                        Score
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                                                                                                  Sequence:
                                                                                                                                            Searched:
                                                Run on:
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28 73 37.8 16 4 08-09-516-704-18 29 73 37.8 16 4 08-09-516-704-18 29 73 37.8 16 4 08-09-516-704-18 21 73 37.8 16 4 08-09-516-704-19 21 73 37.8 16 4 08-09-516-704-19 22 73 37.8 16 4 08-09-516-704-23 23 69 38.8 14 2 08-08-746-640-195 24 69 38.8 14 2 08-08-746-640-195 25 69 38.8 14 2 08-08-746-640-195 26 69 38.8 14 2 08-08-746-640-195 28 69 38.8 14 2 08-08-746-640-195 28 69 38.8 14 2 08-08-746-640-195 28 69 38.8 14 3 08-09-516-704-199 28 69 38.8 14 3 08-09-516-704-199 28 69 38.8 14 3 08-09-516-704-199 29 69 38.8 14 3 08-09-516-704-199 29 69 38.8 14 3 08-09-516-704-199 20 69 38.8 14 3 08-09-516-704-199 20 69 38.8 14 3 08-09-516-704-199 20 69 38.8 14 4 08-09-516-704-199 20 69 38.8 14 4 08-09-516-704-199 20 69 38.8 18 18 18 2 08-08-704-640-206 20 69 38.8 18 18 2 08-08-704-640-206 20 69 38.8 18 18 2 08-08-704-640-206 20 69 38.8 18 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 69 38.8 18 2 08-08-704-640-206 20 70 70 70 70 70 70 70 70 70 70 70 70 70			
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28 73 37.8 29 73 37.8 30 73 37.8 30 73 37.8 31 69 35.8 32 69 35.8 33 69 35.8 34 69 35.8 35 69 35.8 36 69 35.8 36 69 35.8 37 69 35.8 38 69 35.8 38 69 35.8 39 69 35.8 41 69 35.8 42 69 35.8 44 69 35.8 44 69 35.8 44 69 35.8 45 69 35.8 45 69 35.8 46 69 35.8 47 6640.231 58940ERG 231 APPLICANT APPLICANT: Balasul APPLICANT: Applica STRET: Five Moc CITY: Research T STRET: Five Moc CITY: Research T STRATE: II- COMPUTER REDABLE F APPLICATION NUMB REFERENCE/DOCKET TELECOMMUTCATION II TELECOMMUT		tion 37683 3	NUMBE NFORM 48-10 D NO: STICS acid
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28 29 31 31 32 33 34 44 44 44 45 40 41 41 42 42 43 44 44 44 45 40 40 40 40 40 40 40 40 40 40 40 40 40	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	440-2 231, 5831, 5840-2 231, 5840 5840 5840 5840 5840 5840 5840 5840	KENCE IMUNI HONE ON F ON F ON E H: A: A: A: DEDNI
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TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:

Sequence Sequence :|||||:|:: | :|||||:|:: 2 DGPTLREWISFXA-----DGPTLREWIS 24

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                 Query Match 39.6%; Score 76.5; DB 2; Length 25; Best Local Similarity 40.6%; Pred. No. 0.0037; Matches 13; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Five Moore Drive, P.O. Box 13398
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                          2 EGPTLRQWLAARAGGGKGGGGIEGPTLRQWLA 33
                                                                                                                                                                                           2 DGPTLREWISFXA------DGPTLREWIS 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/244,298A
DOCATION: 13
OTHER INFORMATION: /product= "Ava"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                Sequence 231, Application US/09244298A Sequence 131, Application US/09244298A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                  Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christlan
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hrubiec, Robert T
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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COUNTRY:
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APPLICANT:
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Gaps
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.6%; Score 76.5; DB 4; Length 25; llarity 40.6%; Pred. No. 0.0037; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 231:
                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: HILDIGG, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EGPTLRQWLAARAGGGKGGGGIEGPTLRQWLA 33
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08764640 Patent No. 5869411 Patent No. 5869451 5837683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Glaxo Wellcome
           Sequence 231, Application US/09516704 Patent No. 6251864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25 amino acids
                                                                                                                              Gates, Christian
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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Matches 13; Conserva
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                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NC
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US-08-764-640-13
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US-09-516-704-231
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NUMBER OF SEQUENCES:
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US-08-973-225-13
                                                                                                           COUNTRY:
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                                                                                                                                                              APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.8%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dower, William J.

Barrett, Ronald W.

Cwirla, Steven E.

Gates, Christian
Schatz, Peter J.

Balasubramaniahn, Palaniappan
Wagstrom, Christopher R.

Hendren, Richard W.
                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 193, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PK3281
                                                                                                                                Deprince, Randolph B.
Podduturi, Surekha
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Podduturi, Surekha
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STATE: NC
               Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION:
Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Glaxo Wellcome
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
COMPUTER READABLE FORM:
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; MOLECULE TYPE: peptide
US-08-764-640-13
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                ADDRESSEE:
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US-08-764-640-193
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APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.0053; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                 ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
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...ьек: US/08/764,640
11-DEC-1996
7N: 514
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; Patent No. 6083913
; GENERAL INFORMATION;
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 amino acids
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CORRESPONDENCE ADDRESS:
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Les 14; Conserv
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                                                                                                    USA
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US-08-973-225-193
                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                      37.8%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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FILING DATE: 04-Dec-1997
ATTORNEY AGENT INFORMATION:
NAME: HIDDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CRARACTERISTICS:
                                               RECISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
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Wagstrom, Christopher R.
Wrighton, Nicholas C.
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
         FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids
                                   ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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Matches 14; Conservative
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.8%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
37.8%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRUT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
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Balasubramanian, Palaniappan
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REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  ; sequence 13, Application US/09244298A ; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                    Deprince, Randolph B.
Podduturi, Surekha
Yin, Qun
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Matches 14; Conservative
          Query Match 37.89
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-09-244-298A-13
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APPLICANT: Dower,
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APPLICANT:
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NUMBER OF SEQUENCES: 244
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                                                                                                                                                       ZIP: 27709
                                                                                                             STATE: NC
COUNTRY: U
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                 APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.8%; Score 73; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.0053; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
                                 APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Schatz, Peter J.
APPLICANT: Schatz, Peter J.
APPLICANT: Wagstrom, Christian
APPLICANT: Wagstrom, Christopher R.
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Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                           : Wagstrom, Christopher R. : Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deprince, Randolph B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    27709
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                                                                                                                                                                           APPLICANT
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Podduturi, Surekha
TITLE OF INVENTION: PRETIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 14; Conservative 0; Mismatches 0,
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE, DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPROME: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 193, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J. Barrett, Ronald W.
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CORRESPONDENCE ADDRESS:
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APPLICANT: Dowert, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Handren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qui
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                                                                                                           Length 15;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,640
                                                                                                           37.8%; Score 73; DB 2; 1
100.0%; Pred. No. 0.0057;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         ; sequence 185, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,392
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INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                               Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-764-640-185
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CORRESPONDENCE ADDRESS:
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                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                   1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                             linear
TYPE: amino acid
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                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-764-640-185
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                                                                             US-08-764-640-17
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CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Mellcome STREET: Flve Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 37.8%; Score 73; DB 4; I
100.0%; Pred. No. 0.0053;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: CWirla, Steven E.
APPLICANT: CAITA, Steven E.
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendren, Richard W.
APPLICANT: Hendren, Richard W.
                                                                    ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
        APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLGGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-516-704-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08764640 Patent No. 5869451 Patent No. 5869451
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Matches 14; Conservative
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS_THAT BIND TO A
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                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                        THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/973,225A
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-08-973-225-185
                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schatz, Peter J. APPLICANT: Balasubramanian, Palaniappan
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Patent No. 6121238

GENERAL INFORMATION:

APPLICANT: Dower, William J.

APPLICANT: Cwirla, Steven E.

APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
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100.0%; Pre-
0; N
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Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
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                                                                    NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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Five Moore Drive,
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                   USA
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TITLE OF INVENTION: I
                                                                                                                                                                                                 ZIP: 27709
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                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                 COUNTRY:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.8%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.0057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
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APPLICATION NUMBER: US/08/973,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                          Wagstrom, Christopher R.
Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                           Research Triangle Park
                                                                                                   APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                Sequence 17, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 185, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
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                                 US-08-973-225-17
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               RESULT 14
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1 IEGPTLRQWLAARA 14
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                     Query Match
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.0057; tive 0; Mismatches 0; Indels
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                   COMPUTER: IBM PC compatible
OPERATING SYZEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSES: Glaxow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barrett, Ronald W. APPLICANT: Barrett, Ronald W. APPLICANT: CWILLA, Steven E. APPLICANT: Gates, Christian APPLICANT: Schatz, Peter J. APPLICANT: Balasubramanian, Palaniappan
                                                                                           APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W. APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
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             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEG ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                       amino acid
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                         37.8%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.0057; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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FILING DATE: 01-Mar-2000
CLASSIFICATION: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 98,3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ. ID NO: 17:
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Balasubramanian, Palaniappan
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                   US-09-516-704-17; Sequence 17, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                     Best Local Similarity 100.0
Matches 14; Conservative
LENGTH: 15 amino acids
                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-185
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                  amino acid
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HILDIEC, ROBERT 36,392
REFERENE/POCKET NUMBER: PK3281
                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Barret, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
           Balasubramanian, Palaniappan
                             Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                  Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 14; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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APPLICANT: Dower,
                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                           27709
                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                       STATE: NC
                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                                                     APPLICANT:
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           APPLICANT:
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                             APPLICANT:
APPLICANT:
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                                                                   APPLICANT:
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APPLICANT:
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.8%; Score 73; DB 4; I
100.0%; Pred. No. 0.0057;
tive 0; Mismatches 0;
                                                                                                                                                                                                                          Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PK3281 TELECOMMULCATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                 Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                         Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                            APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                        Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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ZIP: 27709
COMPUTER READABLE FORM:
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Matches 14; Conservative
1 IEGPTLRQWLAARA 14
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                                                                       US-09-516-704-185
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                       RESULT 19
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MOLECULE TYPE: peptide
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         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-973-225-18
                                                                         NAME:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HIDDIEC, ROBERT T.
REGISTRATION NUMBER: 95,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
LENGTH: 16 amino acids
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 73; DB 2; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 232, Application US/08764640 Patent No. 5869451 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 14; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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APPLICANT: DOWER,
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                                                                                         STATE:
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Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A
THTLE OF INVENTION: PEPTIDES AND THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                      37.8%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.0061; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PRICES: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSES: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PK3065USM TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HIUbiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
APPLICATION NUMBER: US/08/764,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08973225A; Patent No. 6083913; GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AppLICANT Bower, William J.
AppLICANT Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                              REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 232:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                   11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                              Hrubiec, Robert T
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.89
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-08-764-640-232
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WEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CORPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

ATTORNEY/AGENT INFORMATION:

NAME: HILDIGC, RODERT T.

NAME: HILDIGC, RODERT T.

REGISTRATION NUMBER: 36,392

RESTSTRATION NUMBER: 96,392

REPRENCE/DOCKET NUMBER: PR3065USW

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 144:

SEQUENCE CHARACTER STICS:
                                                                                                                                             37.8%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                             /product= "Beta-ala'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-973-225-194
                                     LOCATION: 15
OTHER INFORMATION: /product= "E
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                         14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27709
                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                      RESULT 24
US-08-973-225-194
FEATURE:
                                                                                                   US-08-973-225-18
                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 13398
                                                                                                                                                                                                                                                                                                                           THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower, William J.

Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-973-225-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Five Moore Drive, P.(CITY: Research Triangle Park
                                                                                                               Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                   Sequence 220, Application US/08973225A; Patent No. 6083913; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 18, Application US/09244298A
; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deprince, Randolph B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16 amino acids
                                                                                                                                                                                                                                             Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 14; Conservative
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ZIP: 27709
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APPLICANT: Dower,
                  US-08-973-225-220
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APPLICANT:
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APPLICANT:
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APPLICANT:
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RESULT 25
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STRANDEDNESS:
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US-09-244-298A-232
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                                                                                                                            SOFTWARE:
COUNTRY:
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                    APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.8%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                     COUNTRY: USEN 27709

COMPUTER READABLE FORM:
MEDIDUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: SI4
ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: PK3381
TELECOMMUNICATION INFORMATION:
TELECHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
FORMATION FOR SEQ ID NO: 18:
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwilla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 15
OTHER INFORMATION: /product- "Beta-ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 194, Application US/09244298A patent No. 6121238 GENERAL INFORMATION:
    APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glaxo Wellcome
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.8%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.O. Box 13398
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PPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILLIGO DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 232, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research Triangle Park
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                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Glaxo Wellcome
Five Moore Drive,
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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Matches 14; Conserv
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                           37.8%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
SIREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                      Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <u >Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-516-704-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hublec, Robert, T.9
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: October 9, 2002, 09:06:33 Job time : 5.98595 secs
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Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                           Sequence 194, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                      Query Match 37.8'
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                           COUNTRY: USA
                                                                                                                    1 IEGPTLRQWLAARA 14
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Matches 14; Conserva
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US-09-516-704-18
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                   37.8%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0061; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-Mar-2000 CLASSIFICATION: <Unknown>
  REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J. Barrett, Ronald W. Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                             LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                    MOLECULE TYPE: peptide US-09-244-298A-232
                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                 2 IEGPTLRQWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 27709
                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-516-704-18
                                                                                                                                                                                                                                                              Query Match
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October 9, 2002, 08:54:17; Search time 8.09368 Seconds (without alignments) 427.397 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                               283138
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               283138 seqs, 96089334 residues
                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                  US-09-422-838C-30
                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                             Sequence:
                                                                                            Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pir1:* pir2:* pir3:* pir4:* PIR_71:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		neurotrophin-4 pre	cal pr	probable ATP/GTP-b	hflX protein - Mvc	ш	neurotrophin-4 pre	hypothetical prote	conserved hypothet	insulin precursor	insulin precursor	probable Hflx - My	tei	hypothetical prote	hypothetical prote	ankyrin 3 homolog	splicing factor SF	hypothetical prote	hypothetical prote	Polyadenylate-bind	gag polyprotein -		laccase (EC 1.10.3	CREB-binding prote	protein K04G7.10 [hypothetical 20.2K	91ycine-rich prote	hypothetical prote	transcription fact phosphatidylinosit
SUMMARIES		BA2687	۴С	120301 087033	6270030	07000	F / 0 9 3 4	735116	100110 B71305	TNSH	TPBO	070505	520880	T47718	T49792	T04436	571185	T26807	126808	541644	FONTAIN	KCNCIO	FILMON	T13828	02021	101094	S34666	AG1974	A49447	T09084
	DB				۰,	٦,	۱ ۸	٠,	٠,		-	· C	٠.	2	2	N	· ^	· ~	1 ~	2		ا								
	Query Match Length	209	500	488	518	112	210	497	683	77	105	495	339	103	201	249	303	331	333	465	591	619	619	3190	328	201	271	327	445	490
dР	Query	32.4	31.6	31.3	31.3	30.8	30.8	30.6	30.6	30.3	30.3	30.3	30.1	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	28.8	28.5	28.5	28.5	28.5	28.5
	Score	62.5	61	60.5	60.5	59.5	59.5	59		58.5	ထ		28	26	26	26	99	26	26	26	26	56	26		55.5	55	55	22	22	22
	Result No.	Н	7	m	4	5	9	7	œ	σ,	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	. 52	5 2	17	28	29

A; Accession: JH0505
A; Accession: JH0505
A; Molecule type: mRNA
A; Ascession: JH0507
A; Molecule type: mRNA
A; Assidues: 1-176, 'P', 178-209 < BER1>
A; Rosidues: 1-176, 'P', 178-209 < BER1>
C; Comment: This protein is a targed-derived, diffusible neurotrophic factor.
C; Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro C; Superfamily: nerve growth factor beta chain
C; Superfamily: nerve growth factor beta chain
E; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-27/Domain: propeptide #status predicted <PRO>
E; 80-209/Product: neurotrophin-5 #status predicted <NEU>
E; 75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Gaps . ز

14; Indels

/ Match 32.4%; Score 62.5; DB 2; Length 209; Local Similarity 37.5%; Pred. No. 5.7; nes 15; Conservative 2; Mismatches 14; Indels ;

Query Match

Matches

RESULT 2

QΩ δ

hypothetical protein F15B9.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20961 R;Percy, C. submitted to the EMBL Data Library, August 1996

probable amidase - hypothetical glyci probable secreted probable polA prot LSR2 T-cell antige glutathione S-tran hypothetical prote probable lysyl-tRN protein F53C3.3 [i related to glycine hypothetical prote probable amidase [phosphoglucomutase numb protein - fru T-box protein 2 - dnaK-type molecula	ALIGNMENTS	RESULT 1 B42687 neutrotrophin-4 precursor - rat neutrotrophin-4 precursor - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Species: Laber-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999 R:CP, N.Y., Ibanez, T. Danez, T. Danez, T. Danez, T. Danez, D.R.; Belluscio, R:Telle: Mammalian neurotrophin-4: structure, chromosomal localization, tissue districtures preliminary A;Rcession: B42687 A;Status: preliminary A;Rocession: B42687 A;Status: preliminary A;Rcession: B42687 A;Resemeder, L.R.; Minslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenth A;Restemene number: JH0504 A;Reference number: JH0503; MUID:92075279 A;Recession: JH0504 A;Rec
E70948 E708958 C70559 B43601 C87617 C87617 C88115 T19389 T19389 T19389 A32466 G01840	ALIGN	ay rat) 5. 5. 7. McCla 3060-30 3060-30 2212967 2212967 2212967 2212967
папапапапапапапа		Norw reviews 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
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28.5 28.5 28.5 28.2 28.0 28.0 28.0 28.0 28.0 28.0 28.0		rrso brve #se #se #se ro ro ro ro ro ro ro ro ro ro ro ro ro
28		precursor us, norveg 2687, JH00 2688, JH00 2
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0 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9		RESULT 1 B42687 neurotrophin-4 precursor - rat C; Species: Rattus norvegiuss (Norway rat C; Date: 31-Dec-1993 #sequence_revision 3: C; Accession: B42687; JH0504; JH0505 R; Ip, N. Y; Ibanez, C.F; Nye, S.H; MCC Proc. Natl. Acad. Sci. U.S.A. 89; 3060-38 A; Title: Mammalian neurotrophin-4: struct A; Reference number: A42687; MUID:92212967 A; Status: preliminary A; Status: preliminary A; Status: preliminary A; Sesidues: 1-209 cIPA> A; Cross-references: GB: M86742; NID:920577 R; Berkemeier, L.R.; Winslow, J.W.; Kaptan A; Title: Neurotrophin-5: a novel neurotro A; Residues: 1-209 cBER> A; Residues: 1-209 cBER> A; Residues: 1-209 cBER> A; Residues: 1-209 cBER>

Gaps

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A;MOlecule type: DNA
A;Residues: 1-210 <BER>
C;Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro
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A;Cross-references: GB:1886528; NID:9190266 (NCBIN:91810, NCBID:93811)
A;Note: sequence extracted from NCBI backbone (NCBIN:91810, NCBID:93811)
A;Note: sequence extracted from NCBI backbone (NCBIN:91810, NCBID:91810, NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NyAlternate names: neurotrophin-5
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Accession: A42687; JH0503
F; Ip, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A; Accession: A42687; MUID:92212967
                                                                                                                                                                                                                                                                                                                                                                       probable lsr2 protein - Mycobacterium tuberculosis (strain H37RV)

C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Decession: F70954
R; Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
C; Accession: F70954
R; Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
C; Accession: F70954
R; Devilin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd,
C; Cole, S.T.; Brosch, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A; Leichors and College Colleg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.C.oss.references: GB:295557; GB:AL123456; NID:93242276; PIDN:CAB08947.1; PID:921139
A.Experimental source: strain H37Rv
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%; Score 59.5; DB 2; Length 112; 33.3%; Pred. No. 6.9;
                                8; Indels
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F:1-24/Domain: signal sequence #status predicted <PRO>
F:280/Domain: propeptide #status predicted <PRO>
F:28-80/Domain: propeptide #status predicted <NEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 IKOWWAAGRRYGGRRRGRSGSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
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A) Map position: 19pter-19qter
C; Superfamily: nerve growth factor beta chain
43.3%; Pred. No. 22;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                               219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                            4 PTLRQW-----LAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                              13; Conservative
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Best Local Similarity
                       Best Local Similarity
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                                                                                   Matches
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A. Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A; Title: Massive gene decay in the leprosy bacillus.
A. Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:U00019; NID:9467079; PIDN:AAA17274.1; PID:9467091
C;Genetics: GTG
A:Start Codon: GTG
C;Superfamily: GTP-binding protein hflx; translation elongation factor Tu homology
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hilx protein - Mycobacterium leprae
N;Alternate names: B2235_C2_202 protein
N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: 572938
R;Smith, D.R.; Robison, K.
A;Bescription: Mycobacterium leprae cosmid B2235.
A;Reference number: S72587
A;Accession: S72938
                                                                                                                                                                                                                                               A; residues: 1.500 <WIL>
A; Residues: Leferences: EMBL:278013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A; Cross-references: EMBL:278013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A; Experimental source: clone F15B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable ATP/GTP-binding protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: G87033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
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il Similarity 43.3%; Pred. No. 20; Length 488;
il Similarity 43.3%; Pred. No. 20; R. Indels 7
13; Conservative 2; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 61; DB 2; Length 500; 52.2%; Pred. No. 18; 7; Indels ative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
                                                                                                                       A; Accession: T20961
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PTLRQW-----LAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | ::|: | ||| ||||: |
429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPTLROWLAARAGGGKGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-518 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                            A; Reference number: 219351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
Molecule type: DNA
Residues: 1-488 <STO>
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:F15B9.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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A. Molecule type: protein
A. Residues: 1-30;57-77 CBRO>
B. Residues: 1-30;57-77 CBRO>
J. Biol. Chem. 247, 4866-4811, 1972
A. Title: Determination of the amino acid sequence of the monkey, sheep, and dog proin
A. Reference number: A92111; MUID:72258016
A.; Reference number: A92111; MUID:72258016
A.; Reference number: A92111; MUID:72258016
A.; Reference number: A92111; MUID:72258016
C.; Superfamily: Insulin
A.; Residues: 31-56 c/PET>
C.; Superfamily: Insulin
C.; Superfamily: Insulin
C.; Superfamily: Insulin status experimental cancer
F.1-30/Domain: Insulin chain # status experimental cancer
F.51-57/Domain: connecting peptide #status experimental cancer
F.57-77/Domain: insulin chain A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Bos primigenius taurus (cattle)
C; Date: 24 Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C; Accession: A40909; A9200; A92074; A91185; A90342; A90341; S48184; S48185; S46258;
Mol. Endocrinol 1, 327-331, 1987
A; Fitle: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic a A; Reference number: A40909; MUID: 88288209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Wolecule type: protein
A:Residues: 25-105 <NOL>
R;Residues: 25-105 <NOL>
A;Resider. D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
J. Biol. Chem. 246, 1365-1374, 1971
A;Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancre A/Reference number: A91185; MUID:71257721
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A.Residues: 57-82 <SAL>
R.Sanger, F.; Thompson, E.O.P.
Blochem J. 53, 366-374, 1953
A.Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation
A.Reference number: A90342
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A;Residues: 1-105 CDAA>
A;Cross-references: GB:M54979; NID:g163578; PIDN:AAA30722.1; PID:g163579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Experimental source: fetal pancreas
R:Nolan, C.; Margoliash, E.; Peterson, J.D.; Steiner, D.F.
J. Biol. Chem. 246, 2780-2795, 1971
A;Title: The structure of bovine proinsulin.
A;Reference number: A92080; MUID:71166442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F. Eur. J. Blochem. 20, 183-189, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.3%; Score 58.5; DJ
50.0%; Pred. No. 6.3;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 VEGP---QVGALELAGGPGAGGLEGP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.08
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 57-82 <STE>
                                                                                                                                                                                                            A; Accession: S16430
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R; Fraser, C.M.: Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin tson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Accession: B71325
A; Reference number: A71250; MUID: 98332770
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Residues: 1.683 <COL>
A: Residues: 1.683 <COL>
A: Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65409.1; PID:g332270
A: Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T35116
R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, March 1998
A; Reference number: 221568
A; Accession: T35116
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-497 <SEE.
A; Cross references: EMBL: AL022268; PIDN: CAA18333.1; GSPDB: GN00070; SCOEDB: SC4H2.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SCOEDB:SC4H2.17
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                      C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #Sequence_revision 05-Nov-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein TP0421 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                        6
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F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                 30.8%; Score 59.5; DB 2; Length 210; 35.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
                                                                                                                                                                                                                                                                                                                                            hypothetical protein SC4H2.17 SC4H2.17 - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.6%; Score 59; DB 2; Length 497;
51.9%; Pred. No. 30;
tive 2; Mismatches 7; Indels
                                                                                                                                     Indels
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                                                                                                                                14;
                                                                                                                                                                                                            129 GSPLROYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                                                                                                               3 GPTLRQWL------AARAGGGKGGGGIEGPTLRQWLA 33
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                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 PLILEWL---GNAYRSGIEGAALHQWGAAR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PTLRQWLAARAGGGKGGGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 PRLRGWGQSLSRQMGGGRGGGLATRGP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PTLRQW---LAARAGGGKGGG-GIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL022268; FA;Experimental source: strain A3(2) C;Genetics:
                                                                                  Best_Local Similarity 35.09
Matches 14; Conservative
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Best Local Similarity
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                                                        Query Match
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A; Cross-references: EMBL:AL161667
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A; Residues: 272-331 <DOL>
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A; Residues: 1-103 <BEN>
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. R;Cole, S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Centles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Autre 393, 537-544, 1998
A;Autre 393, 537-544, 1998
A;Aitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
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A;Cross-references: GB:298209; GB:AL123456; NID:g3261838; PIDN:CAB10901.1; PID:e332282;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Contents: annotation; amides; disulfides
R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
R;Wenzel, T.; Bckerskorn, C.; Lottspeich, F.; Baumeister, W.
A;Title: Asystence of a molecular ruler in proteasomes suggested by analysis of degradat A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degradat A;Reference number: S46258; MUID:94326921
A; Wolecule type: protein
A; Residues: 85-105 <SAN>
R; Sanger, F: Tuppy, H.
Biochem. J. 49, 481-496, 1951
Biochem. J. 49, 481-496, 1951
A; Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigat A; Reference number: A90341
A; Accession: A90341
A; Accession: A90341
                                                                                                                                                                                                                A.Molecule type: protein
A.Residues: 25-54 <SAS.
R.Chengy R.: Kawakishi, S.
Eur. J. Blochem. 223, 759-764, 1994
A.Title: Site-specific oxidation of histidine residues in glycated insulin mediated by
A.Fitle: Ste-specific oxidation of histidine residues in glycated insulin mediated by
A.Reference number: S48184: MUID:94333378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: insulin
C;Superfamily: insulin
C;Superfamily: insulin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54,85-105/product: insulin #status experimental <MAT>
F;55-54,85-105/product: insulin #status experimental <CPEP>
F;57-82/Domain: connecting peptide #status experimental <CPEP>
F;85-105/Domain: insulin chain A #status experimental <ACH>
F;85-105/Domain: insulin chain A #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 25-30, 'x', 32-42, 'x', 44-54 <CH2>
A; Residues: 25-30, 'x', 32-42, 'x', 44-54 <CH2>
R; Ryle, A.P., Sanger, F.; Smith, L.F.; Kitai,
B; Ryle, A.P., Sanger, F.; Smith, L.F.; Kitai,
B; Ryle, A.P., Sanger, F.; Smith, L.F.; Kitai,
A; Reference number: A90343
A; Reference number: A90343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 VEGP---QVGALELAGGPGAGGLEGP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 25-54 <WEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: S48184
A,Molecule type: protein
A,Residues: 85-105 <CHE>
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A; Status: preliminary
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C; Accession: T47718
C; Accession: T47718
R; Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, March 2000
A; Reference number: 224473
A; Accession: T47718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Two gene members of the murine HOX-5 complex show regional and cell-type spe A;Reference number: S09398; MUID:89356622 A;Accession: S09398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Nolecule type: DNA
A; Residues: 1-339 < REN>
A; Residues: 1-339 < REN>
A; Cross-references: EMBL:X62669; NID:951414; PIDN:CAA44542.1; PID:951416
A; Cross-references: EMBL:X62669; NID:951414; PIDN:CAA44542.1; PID:951416
B; Duboule, D: Dollar, P.
A; Title: The structural and functional organization of the murine HOX gene family res
A; Title: The structural and functional organization of the murine HOX gene family res
A; Accession: S09569; MID:89356621
A; Accession: S09569
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboul BMBO J. 11, 1459-1468, 1992
A;Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences in A;Reference number: $20879; MUID:92224884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cross-references: GB:X14714; GB:M21040; NID:951427; PIDN:CAB57813.1; PID:96015583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 272-331 < DUB>
A; Residues: 272-331 < DUB>
A; Cross_references: EMBL:X14714; NID:951427; PIDN:CAB57813.1; PID:96015583
B; Dobloule, D: Buboule, D: EMBO J: 8, 1507-1515, 1989
C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F1116.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr.2000 #sequence_revision 20-Apr.2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homeotic protein Hox 4.5 - mouse
c;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
C;Accession: S20880; S09569; S09398
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                                                                                                                                                        7;
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                                                                                       Length 495;
                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GRYVRSWMEPLPGFPGGAGGGGGGGGG 132
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                                                                                       Query Match 30.3%; Score 58.5; 1
Best Local Similarity 43.3%; Pred. No. 34;
Matches 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                             199 PRLRGWGESMSRQAGGRAGGSGGGVGLRGP 228
                                                                                                                                                                                                                                         4 PTLROW-----LAARAGGGKGGGGIEGP 26
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C; Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro F;8-72/Domain: ribonucleoprotein repeat homology <RRM1>F;120-183/Domain: ribonucleoprotein repeat homology <RRM2>
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                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y41C4A.4a - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 16-Feb-2001
C.Accession: T26807
R.Steward, C.
R.Steward, C.
R.Steward, C.
A.Reference number: 220269
A.Reference number: 220269
A.Status: preliminary: translated from GB/EMBL/DDBJ
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26808
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A;Accession: T26808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-333 <WIL>
A;Cross-references: EMBL:AL032627; PIDN:CAB54382.1; CESP:Y41C4A.4b
                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 2; Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
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                                                                                                                                                                                                                     A;Residues: 1-303 <LAZ>
A;Cross-references: EMBL:M98340; NID:g166843; PID:g166844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y41C4A.4b - Caenorhabditis elegans
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A/Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C:Superfamily: fos/jun DNA-binding domain homology
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                                                                                                                               submitted to the EMBL Data Library, October 1992 A; Reference number: S71185 A; Accession: S71185
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A;Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C;Superfamily: fos/jun DNA-binding domain homology
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                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 RGGGRGRGDGGSRGPSRRSEFRVLVTWLASSA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                              13 RAGG-GKGGGGIEGPTLRQ-----WLAARA 36
                           N; Alternate names: ribonucleoprotein
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                                                                                                                                                                                                                                                                                                                                                            29.0%;
                                                                                                                                                                                                                                                                                                                                                                                   43.8%;
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43.8 Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGGKGGGGIEGPT 27
                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-303 <LAZ>
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A; Residues: 1-331 <WIL>
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                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                             R; Lazar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T04436
R; Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A; Reference number: 215359
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
                                                                                                                                                                       Gaps
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A;Molecule type: DNA
A;Residues: 1-201 <SCH>
A;Cresives: Teferences: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A;Experimental source: BAC clone B9J10; strain OR74A
                                                                                                             29.0%; Score 56; DB 2; Length 103; 48.0%; Pred. No. 15; Live 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%; Score 56; DB 2; Length 201; 52.4%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.0%; Score 56; DB 2; Length 249; 69.2%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                     protein B9J10.290 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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A; Experimental source: cultivar Columbia; BAC clone FII16 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A: Experimental source: cultivar Columbia; BAC clone T18B16
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3; Mismatches
                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGKGGGGIEG 25
                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 RGGGGGGGGVNG----RWSA 90
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                                                                                                                                                         Conservative
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1 MAGRSGGGRGGGG 13
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                                                                                                                             Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: NCSP: B9J10.290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T49792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T04436
                                                                 A; Note: F1116.200
                                            A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: T18B16.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 27/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                     hypothetical
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                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-619 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
                                          RESULT 21
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                                                                                                                                                                                                                                                                                                              polyadenylate-binding protein - fruit fly (Drosophila melanogaster)

No.Alternate names: rox8 protein
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C; Accession: 841644; 841645
R; Brand, S.; Bourbon, H.M.
Nucleic Acids Res. 21, 3699-3704, 1993
A; Title: The developmentally-regulated Drosophila gene rox8 encodes an RRM-type RNA bind
A; Reference number: 841644; MuID:93376491
A; Accession: 841644
A; Residues: 1-465 < BRAA
A; Residues: 1-465 < BRAA
A; Recession: 841645
A; Accession: 841645
A; Molecule type: MRN
A; Residues: 1-465 < BRAA
A; Recession: 841645
A; Molecule type: mRNA
A; Residues: 1-465 < BRAA
A; Residues: 1-465 < BRAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: FlyBase:Rox8
A;Cross:references: FlyBase:FBgn0005649
A;Introns: 76/3; 379/3; 411/1
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein c;Superfamily: unassigned ribonucleoprotein repeat homology <RRMI>
F;8-72/Domain: ribonucleoprotein repeat homology <RRMI>
F;96-163/Domain: ribonucleoprotein repeat homology <RRM2>
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R; Moore, R.; Dixon, M.; Smith, R.; Peters, G.; Dickson, C.
J. Virol. 61, 480-499, 1987
A; Title: Complete nucleotide sequence of a milk-transmitted mouse mammary tumor virus: A; A; Reference number: A93030; MUID:87112944
A; Accession: A26795
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-591 <MOO>
A;Cross-references: EMBL:M15122; NID:9332127; PIDN:AAA46543.1; PID:9332130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:L13038; NID:g304799; PIDN:AAA02941.1; PID:g304800
C;Genetics:
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
DB 2; Length 333;
                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;86-163/Domain: ribonucleoprotein repeat homology <RRM2>
F;222-284/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: gag
(;Superfamily: mouse mammary tumor virus gag polyprotein
C;Keywords: core protein; DNA binding; polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 RQWIASRSIRTNWSTRKLPPPREPSKGGGGGGGGGGP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ROWLAARA------GGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.0%; Score 56; DB 83.3%; Pred. No. 74; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
29.0%; Score 56; DB;
Best Local Similarity 34.2%; Pred. No. 60;
Matches 13; Conservative 4; Mismatches
                                                                    2; Mismatches
                                   44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gag polyprotein - mouse mammary tumor virus
      Score 56;
Pred. No. 4
         29.0%;
69.2%;
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                                             Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 GGGKGGQGAEGP 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 GGGKGGGGIEGP 26
                                                                                                                                                                                                169 GGGGGGGGVPGPS 181
                                                                                                                                     15 GGGKGGGGIEGPT 27
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                      Query Match
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                                                                                                                                                                                                                                                                                              RESULT 19
S41644
                                                                              Matches
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C;Accession: B28523
R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
B. Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- a
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- a
A;Reference number: A28523; MUID:88087214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-619 <GER>
A;Cross-references: EMBL:M18334; NID:g168827; PIDN:AAA33592.1; PID:g168828
C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; increase (5. Keywords: copper: glycoprotein; oxidoreductase (5. Keywords: copper: glycoprotein; oxidoreductase (5. Keywords: copper: glycoprotein; status predicted <PRO> (5. Keywords: copper: glycoprotein; slynal sequence #status predicted <PRO> (5. C-2.49/Domain: slynal sequence #status predicted <PRO> (5. C-19/Pondin: arcase #status predicted <PRO> (5. C-19/Pondin: middle beta-barrel #status predicted <BB2> (5. 16. 372/Domain: middle beta-barrel #status predicted <BB2> (5. 16. 372/Domain: araboxyl-terminal beta-barrel #status predicted <BB2> (5. 319, 282, 293, 340, 422, 444/#sinding site: carbohydrate (Asn) (covalent) #status predicted  (7. 16. 180, 191, 482, 550/#sinding site: copper (His) (type 2) #status predicted  (7. 16. 180, 191, 482, 550/#sinding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 379-619 <GE2>
A;Crossreferences: GB:M14554; NID:g168823; PIDN:AAA33590.1; PID:g168824
C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquino
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBB:M14554
R;Germann, U.A.; Lerch, K.
Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
A;Title: Isolation and partial nucleotide sequence of the laccase gene from Neurospor A;Reference number: A29762; MUID:87067412
                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                            R:Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
J. Biol. Chem. 263, 885-896, 1988
J. Bitle: Characterization of two allelic forms of Neurospora crassa laccase. Amino-A; Fitle: Characterization of two allelic forms of Neurospora crassa laccase. Amino-A; Reference number: A28523; MUID:88087214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
                                                                                C;Species: Neurospora crassa
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C;Accession: A28523; A29762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . DB 1; Length 619; 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR) N,Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AERYGGG-GGGGCNSPINRQCW 64
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63.6%;
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Glycine-rich protein - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 13-3an-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S34666
R:Brady, K.; Darvill, A.G.; Albersheim, P.
submitted to the EMBL Data Library, July 1993
A:Description: Activation of a tobacco glycine-rich protein gene by a fungal glucan p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB:D12477; GB:D01129; NID:9222674; PIDN:BAA02044.1; PID:d1002526;
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A'Note: Anabaena sp.
A'Note: Anabaena sp.
A'Note: Anabaena sp.
A'Note: Anabaena sp.
C'Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C'Accession: AG1974
R'Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpoto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata A'Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A'Reference number: AB1807; MUD:21595285; PMID:11759840
A'Status: preliminary
A'Motession: AG1974
A'Status: preliminary
A'Motession: AG1974
A'Status: Preliminary
A'Motession: AG1974
A'Status: GB:BA000019; PIDN:BAB73303.1; PID:g17130693; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                   C.Species: tomato ringspot virus
C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C.Accession: J01094
J. Gen. Virol. 72, 1505-1514, 1991
A.Title: Nucleotide sequence of tomato ringspot virus RNA-2.
A.Reference number: J01093; MJID:91311402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X74106; NID:9395146; PIDN:CAAS2208.1; PID:9395147
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hypothetical protein alr1346 [imported] - Anabaena sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 201;
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                                                                   hypothetical 20.2K protein - tomato ringspot virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Phaseolus glycine-rich protein 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain raspberry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 RAGGGKGGGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 RAGGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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A; Residues: 1-201 <ROT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 RAGGGKGGGGIEG 25
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S34666
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F:84-215/Domain: amino-terminal beta-barrel #status predicted <BB1>
F:216-372/Domain: middle beta-barrel #status predicted <BB2>
F:316-372/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F:139, 282, 295, 340, 422, 444/Reinding site: carbohydrate (Asn) (covalent) #status predicted  F:144,480/Reinding site: copper (His) (type 2) #status predicted  F:146,189,191,482,548,550/Reinding site: 2Cu-O cluster (His) (copper type 3) #status predicted  F:477,549,554/Reinding site: copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13828
R;Akimaru, H; Chen, Y; Dai, P; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Gc Axtile: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
A;Reference number: 217785; MUID:97263578
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A; Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A; Residues: 1-328 <STO>
A; Cross-references: GB:chr_III; PIDN:AAA62536.1; PID:g687845; GSPDB:GN00021; CESP:K04G7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U88570; NID:g1916929; PID:g1916930; PIDN:AAB53050.1
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: G88499
C;Accession: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                      DB 1; Length 619;
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0; Mismatches
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32.6%; Pred. No. 49;
tive 1; Mismatches
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F;1723-1780/Domain: bromodomain homology <bre> <
                                                                                                                                                                                                                                                                                                                      Score 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
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A; Residues: 1-3190 <AKI>
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A;Accession: G88499
A;Status: preliminary
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C;Species: Chlamydomonas reinhardtii
C;Date: l.1-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09064
R;Molendijk, A.J.; Irvihe, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Thle: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
A;Reference number: 216411; MUID:98281574
                                                                                                                                                                                                                                                                                                                                                                         transcription factor Brn-2 - rat
N;Alternate names: class III POU domain protein brain-2
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: O7-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Feb-1998
C;Accession: A49447
R;Li, P.; He, X.; Gerrero, M.R.; Mok, M.; Aggarwal, A.; Rosenfeld, M.G.
Genes Dev. 7, 2483-2496, 1993
A;Tile: Spacing and orientation of bipartite DNA-binding motifs as potential functional A;Reference number: A49447; MUID:94102531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone (NCBIP:141696)
C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 68-90/Region: glycine-rich
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A;Experimental source: strain cw-15
C;Genetics:
A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Status: preliminary; not compared with conceptual translation A; Notecule type: mRNA A; Notecule type: mRNA A; Notecule type: mRNA A; Residues: 1-445 c.11>
A; Cross-references: GB:127663; NID:9443687
A; Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.5%; Score 55; DB 1; Length 445; 60.0%; Pred. No. 74;
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                                                                                                                                     28.5%; Score 55; DB 2; Length 327; 50.0%; Pred. No. 56;
                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQWLAARAGGGKGGGGI---EGPTLR--QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:125-1517Region: glutamine-rich
F:153-165/Region: histidine/proline-rich
F:131-261/Region: histidine/proline-rich
F:217-338/Domain: POU domain homology <POU>F:271-338/Domain: homeobox homology <POU>F:357-413/Domain: homeobox homology CHOX>
                                                A; Experimental source: strain PCC 7120 C; Genetics:
                                                                                                                                                                                                                                              10 LAARAGGGKGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                          36 LAARSGGRIGGGSFRAPSSRTY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                       Query Match
Best Local Similarity 50.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 OWLAARAGGGKGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 OWITALSHGGSGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T09084
                                                                                                           A;Gene: alr1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Pevlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Muthehead, S.; Barrell, B.G. A;Atter Decliphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MuID:98295987
A;Reference number: A70500; MuID:98295987
A;Accession: E70948
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                            probable amidase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 5%; Score 55; DB 2; Length 495; 55.0%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 9, 2002, 09:05:09 Job time: 9.09368 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: indoleacetamide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GRINNPWDAARTSGGSAGGG 166
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Gaps . 0

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds Run on:

(without alignments) 324.181 Million cell updates/sec

US-09-422-838C-30 Perfect score:

IEGPTLROWLAARAGGGKGGGGIEGPTLROWLAARA 36 Sequence:

BLOSUM62 Scoring table:

105224 seqs, 38719550 residues Gapop 10.0 , Gapext 0.5 Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		100	on mycon	Piomo	Otto Hollio	31/ DOS T	2 00 18	E CHOY		ASTION.		P10574 neurospora					_	-				P12795 schistosoma									0000	12252	13645
SUMMARIES		ID	NT5 RAT	LSR2 MYCTU	NTS HUMAN	FXD2 HIMAN	TNS BOUND	INS SHEED	HXD9 MOUSE		FZD8 HUMAN	GAG_MMTVB	LAC1_NEUCR	LAC2_NEUCR	YR21_TRSVR	DPO1_MYCTU	LSR2_MYCLE	SYK_AERPE	GATA_MYCLE	NUMB_DROME	TBX2_HUMAN	E2BE_RAT	AGO1_ARATH	HS70_SCHJA	PAC4_HUMAN	YACO_ALCEU	SIX3_MOUSE	FXD3_CHICK	HKLB_LYCES	OC3N_HUMAN	OC3N MOUSE	GATA_MYCTU	ATIN_HSVBP	CNA1_DROME	K1CJ_HUMAN
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de	Query	Match	32.4	30.8	30.8	30.6	30.3	30.3	30.1	29.8	29.5	29.0	29.0	29.0	28.5	28.5	28.2	28.2	28.0	28.0	28.0	28.0	28.0	27.7	27.7	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.5
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InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1. PRINTS; PR00268; NGF. ProDom; PD002052; NGF; 1. SMART; SM00140; NGF; 1.

HSSP; P34130; 1B8M.

drosophila acanthamoeb sorghum bic homo sapien rhodobacter homo sapien gallus gallus gallus gallus gallus mus musculu mus musculu mus musculu
094526 P10569 P10569 P48527 P29376 P29376 P29376 P29376 P49749 P008923 n
ORKI_DROME MYSC_ACACA PHYB_SORBI BAT2_HUMAN SSB_RHOSH KITK_HUMAN JUND_CHICK SXL_CERCA DCQ_DROME EVXZ_MOUSE KICZ_MOUSE KICZ_MOUSE
ппппппппппппппппппппппппппппппппппппппп
1000 1168 1178 2142 1742 1744 323 323 348 440 475 569
27.5 27.5 27.5 27.5 26.9 26.9 26.9 26.9
50 50 50 50 50 50 50 50 50 50 50 50 50 5
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ALIGNMENTS

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                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
NTF5 OR NTF4 OR NT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILNE-92212967; PubMed=1313578;
IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.;
Mammalian neurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92075279; PubMed=1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENSORY AND SYMPATHETIC NEURONS.
-!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuron 7:857-866(1991).
-!- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                             209 AA
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M86742; AAA41728.1; -.
EMBL; S69323; AAB20548.1; -.
PIR; JH0504; JH0504.
PIR; B4268?; B42687.
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_TaxID=10116;
RESULT 1
                              NT5_RAT
                                                                                                    DDR R DDR P DDR R DDR R
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EMBL; AE007170; AAK48061.1; -.
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                        RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Cole S. T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davier R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                    Score 62.5; DB 1; Length 209;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DOMINANT T-CELL ANTIGEN AND STIMULATES
-!- LYMPHOPROLIFERRATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POT:
R -> P (IN REF. 2).
W; DF5112C05C5D5B85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                   3 GPTLRQWL-----AARAGGGKGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                              NEUROTROPHIN-5.
                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSR2 protein precursor.
LSR2 OR RV3597C OR MT3704 OR MTCY07H7B.25.
                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 295557; CAB08947.1; -.
                                                                                                                                                                                                                             22332 MW;
                                                                                                                                                                                                                                                            32.4%;
milarity 37.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                           PROSITE; PS00248; NGF_1; 1. PROSITE; PS50270; NGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                              Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                              209 AA;
                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSR2_MYCTU
                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                         DISULFID
                                                                                                                                                         DISULFID
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                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ip N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H., Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20095835; PubMed=10631974; Robinson R.C., Radziejewski C., Spraggon G., Greenwald J., Robinson R.C., Radziejewski C., Strart D.I., Choe S., Jones E.Y.; Rostura M.R., Burtnick L.D., Stuart D.I., Choe S., Jones E.Y.; rythe structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92075279; PubMed=1742028; MEDLINE-92075279; PubMed=1742028; Nikolics K., Goeddel D.V., Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
(NT-4) (Neutrophic factor 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 8:2589-2597(1999).
-!- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribution, and receptor specificity."; proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                30.8%; Score 59.5; DB 1; Length 112; 33.3%; Pred. No. 3.9;
                                                                                                                                                                                                                                                     Indels
                                                                                           CHAIN 19 112 LSR2 PROTEIN.
SEQUENCE 112 AA; 12098 MW; A4B32E478CBAC3E4 CRC64;
                Antigen; Immune response; Signal; Complete proteome.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                          48 LKQWVAAGRRVGGRRRCRSGSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                               6 LRQWLAA------RAGGGKGGGGI---EGPTLRQW 31
                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Prostate;
MEDLINE=92212967; PubMed=1313578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
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                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuron 7:857-866(1991).
FIGR; MT3704; -.
Tuberculist; Rv3597c; -.
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTF5 OR NTF4
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INS_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D2 (Forkhead-related protein FKHLL17) (Forkhead-related FOXD2 OR FKHL17 OR FREAC9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98066765; PubMed-9403061; Ernstson C., Ericksson S., Ernstson S., Betz R., Lagercrantz S., Larsson C., Ericksson S., Caclerberg A., Carlsson P., Enerbaeck S.; "Cloning and characterization of freac-9 (FKHL17), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34."; Genomics 46:78-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCILON: FNOLTHON: Nuclear
-:- SUBCELULAR LOCATION: Nuclear
-:- TISSUE SPECIFICITY: KIDNEY SPECIFIC.
-:- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL). DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                            30.8%; Score 59.5; DB 1; Length 210; 35.0%; Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQWL-----AARAGGGKGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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                                                                                                                                                                                                                                             POTENTIAL.
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PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                            22426 MW;
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EMBL; M86528; AAA60154.1;
PIR; JH0503; JH0503.
PIR; A42687; A42687.
                                                                                                                                     PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
                                                                                                      InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1.
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Matches 14; Conservative
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                                               1B8M; 09-FEB-99.
1B98; 26-FEB-99.
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158
76
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Sanger F., Tuppy H.; "The phenylalanyl chain of insulin. 2. The mino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates."; Blochem. J. 49:481-490(1951).
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88288209; Pubmed-2456452;
D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid for bovine preproinsulin."; Mol. Endocrinol. 1:327-331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D., Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                  Score 59; DB 1; Length 497;
                                                                                                                                                                                                                                                                                                                              5; Indels
                                                          PRINTS; FKUUUCU, ...
SMART; SM00339; FH; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS50039; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
90 94 POLY-ALA.
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EAAF498D216BE019 CRC64;
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Nolam C., Margollash B., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 23, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AA
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Mismatches
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FORK-HEAD.
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POLY-GLY.
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                        nin, 00211,
InterPro: 187001766; Fork_head.
Pfam: PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
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                                                                                                                                                                                                                                                                                                                                                                                       385 PTALLRQGLKTDAGGGAGGGG 405
                                                                                                                                                                                                                                                                   49007 MW;
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                                                                                                                                                                                                                                                                                                  30.6%;
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Matches 14; Conservative
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217
250
306
409
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TRANSFAC; T02485; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin precursor.
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126
247
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               MIM; 602211;
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16-OCT-2001
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P01317;
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DNA_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal; 3D-structure.
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              Salokangas A., Smyth D.G., Markussen J., Sundby F.;
"Bovine proinsulin: amino acid sequence of the C-peptide isolated
from pancreas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                    Sanger F., Thompson E.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2.
investigation of peptides from enzymic hydrolysates.";
Biochem. J. 53:366-374(1953).
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-i- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
-i- DATABASE: NAME-Protein Spotlight;
NOTE-ISSUE 9 of April 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDES, SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS. Ryle A.P., Sanger F., Smith L.F., Kitai R.; "The disulphide bonds of insulin."; Biochem. J. 60:541-556(1955).
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INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The structure of des-Phe bl bovine insulin.";
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PDB: 1APH; 31-OCT-93.
PDB: 1BPH; 31-OCT-93.
PDB: 1DPH; 31-OCT-93.
PDB: 1DPH; 31-OCT-93.
PDB: 1PDD: OCT-93.
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                                                                                                                                                                            Eur. J. Biochem. 20:183-189(1971).
MEDLINE-71257721; PubMed-5105368;
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PIR; A40909; A40909.
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                                                                                                                                                                                                                                                                       SEQUENCE OF 85-105.
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Reynolds C.D.;
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                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94280618; PubMed-8011164; Ohlsen S.M., Lugenbeel K.A., Wong E.A.; (Characterization of the linked ovine insulin and insulin-like growth
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. Biol. Chem. 247:4866-4871(1972).

-i. FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYMTHESIS IN LIVER.

-i. SUBUNIT: HETEROLIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-72258016; PubMed=4626369; Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                      3;
                                                                                                                                       30.3%; Score 58.5; DB 1; Length 105; 50.0%; Pred. No. 4.7;
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
46
48
90
94
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103
104
1, 11393 MW; 75307CE78E61C06A CRC64;
                                                                                                                                                                        Indels
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Biochem. J. 60:556-565(1955).
                                                                                                                                                                                                                                                                                                                    PRT; 105 AA.
                                                                                                                                                                           2; Mismatches
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HSSP, P01315; 91NS.
Interpro; IPR000739; Insulin_IGF_relaxin.
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                                                                                                                                                                                                                                     58 VEGP---OVGALELAGGPGAGGLEGP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor-II genes.";
DNA Cell Biol. 13:377-388(1994).
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                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS
   33
48
86
91
97
102
104
105 AA;
                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procedure.";
                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                        INS_SHEEP
P01318;
                                                                                                                                              Query Match
                                                                                                              SEQUENCE
   HELIX
STRAND
HELIX
                                                                                                 STRAND
                                                                  HELIX
                                                 TURN
                                                                               TURN
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                         INS_SHEEP
                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                     FT
FT
FT
FT
SQ
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g
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                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 272-331 FROM N.A. MEDITE-8935622; Pubmed=2569970; Dolle P., Duboule D.; "Two gene members of the murine HOX-5 complex show regional and cell-
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renucci A.G.P., Zappavigna V., Zakany J., Izpisua-Belmonte J.-C., Buerki K., Douboule D.; "Comparison of mouse and human HOX-4 complexes defines conserved sequences involved in the regulation of Hox-4.4."; EMBO J. 11:1459-1468(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Nuclear.
-:- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
-:- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                       3;
                                                                                                                                                                                            30.3%; Score 58.5; DB 1; Length 105; 50.0%; Pred. No. 4.7;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                 105 AA; 11235 MW; 8B27C7FB9922BC7A CRC64;
                                                PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HOXD9 OR HOXD-9 (HOX-4.4) (HOX-5.2).
                                                                                                    C PEPTIDE.
INSULIN A CHAIN.
                                                                                        INSULIN B CHAIN.
                                                                                                                                                                                                                    2; Mismatches
                                                                                                                              INTERCHAIN.
                                                                                                                                          INTERCHAIN.
                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                          :||| | | | | || 11:11|
58 VEGP---QVGALELAGGPGAGGLEGP 80
                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92224884; Pubmed=1348690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X62669; CAA44542.1; -. EMBL; X14714; CAB57813.1; -.
            PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                     Conservative
                                     SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                   82
105
91
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509398; 509398.
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                      25
57
85
31
43
90
                                                                                                                                                                                                     Best Local Simi
Matches 13;
                                                                                                                                                                                                                                                                                                                                   HXD9_MOUSE
P28357;
                                                                                                                                       DISULFID
                                                                                                                             DISULFID
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                            Query Match
                                                                                                  PROPEP
                                                                           SIGNAL
                                     SMART;
                                                                                        CHAIN
                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                         HXD9_MOUSE
                                                                                                                                                                                                                                                                                                             RESULT 7
δŏ
                                                                                                                                                                                                                                                                    Q
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\$09569; \$09569. \$20880; \$20880.

PIR;

PIR; S20880; S20880 HSSP; P02834; 1B8I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-!- TISSUE SPECIFICITY: UBUIGUITOUS.
-!- DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE
CARDIOENCEHALOMYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS
CHARCTERIZED BY HYPERTROPHIC CARDIOMYOPATHY, LACTIC ACIDOSIS, AND
GLIOSIS. HEART AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX
ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
DEFICIENCIES.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20014747; PubMed=10545922.
MEDLINE=20014747; PubMed=10545922.
Papadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I., Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S., De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.; "Fatal infantile cardioencephalomyopathy with COX deficiency and mutations in SCO2, a COX assembly gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   .
8
                                                                                                                                                       Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.

GLY-RICH.

GLY-RICH.
                                                                                                                                                                                                                                                                                                                                     30.1%; Score 58; DB 1; Length 339; 40.6%; Pred. No. 15; 1ive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smink L.J., Burton J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             339 AA; 34992 MW; 370DC47C6929F7E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) SCO2 protein homolog, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 AA
                                                                                                                                                                                                                                  POLY-GLY.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GRYVRSWMEPLPGFPGGAGGGGGGGGGGGGT 132
                                                                                                                                                                                                                                                                                                                                                                                                                         3 GPTLRQWL-----AARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                            HOMEOBOX.
                                                                                                     SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCO2_HUMAN STANDARD; P 043819; 090K87; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequific-oct-2001 (Rel. 40, Last anno
                   MGD; MGI:96210; Hoxd9.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                             40.68;
                                                                                 PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                  131
176
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TRANSFAC; T01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Monocytes;
                                                                                                                                                                                                                                1119
163
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                              DOMAIN
DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCO2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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9

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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2000) to the beta-catenin canonical signaling pathway, which are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishvelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of wht target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by brain and lung. In adult tissues, expressed in kidney, heart, pancreas and skeletal muscle.

DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/Deta-catenin signaling pathway (By similarity).

DOMAIN: The fz domain is involved in binding with Wnt ligands (by
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21199598; PubMed=11295046;
Saitch T., Hirai M., Katch M.;
"Molecular cloning and characterization of human Frizzled-8 gene on chromosome 10p11.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    Interpro; IPR003782; SCO1_SenC.
Pfam; PF02630; SCO1-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation; Polymorphism.
TRANSIT 1 MITOCHONDRION (POTENTIAL).
CHAIN 42 266 SCO2 PROTEIN HOWOLGG.
VARIANT 20 20 R -> P (IN DBSNP:140523).
                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                   Score 57.5; DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                     3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                      6 LRQWLAARAGGGK--GGGGIEGPTLR-------QWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                          BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Frizzled 8 precursor (Frizzled-8) (Fz-8) (hFz8).
                                                                                                                                                                                          /FTId=VAR_011738.
E -> K (IN FIC).
/FTId=VAR_008874.
S -> F (IN FIC).
/FTId=VAR_008875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               694 AA
                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. J. Oncol. 18:991-996(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
                                                                                                                                                                                                                                                                                  266 AA; 29810 MW;
                                                                                                                                                                                                                                                                                                                     29.8%;
                                                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                 225
                                                     MIM; 604377; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FZD8_HUMAN
Q9H461;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heath P
                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FZD8_HUMAN
                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
6AG polyprotein (Contains: Protein P10; Phosphorylated protein PP21;
Protein P3; Protein P8; Major core protein P27; Nucleic acid binding protein P14].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ-11N.
PDZ-BINDING.
PDZ-BINDING.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                     SMART; SMUOUUS, ..... PROSTER, SECTED_F2_4; 1. PROSTER; PS50038; FZ; 1. PROSTER; PS50046; G_PROTEIN_RECEP_F2_4; 1. Multigene family; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.5%; Score 57; DB 1; Length 694; 32.6%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (P. E740CBFDA2A233EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYS-THR-X-X-X-TRP MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
         SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                             FRIZZLED 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY
                                                                                                                                                                               InterPro; IPR000539; Frizzled.
InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                             EMBL; AB043703; BAB41064.1; -. EMBL; AL121749; CAC10185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 32.6%;
nes 15; Conservative
                                                                                                                                                                                                                         Pfam; PF01534; Frizzled; 1. Pfam; PF01392; Fz; 1.
                                                                                                                                                                                                                                                  PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GPTLRQW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              694 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       533
585
585
606
30
168
194
 RECEPTORS
                                                                                                                                                                          MIM; 606146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAG_MMTVB
P10258;
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                            IRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
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Ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΠD
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us-09-422-838c-30.rsp

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Neurospora crassa.
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                             Hizi A., Henderson L.E., Copeland T.D., Sowder R.C., Krutzsch H.C.,
Oroszlan S.;
                                                                              Moore R., Dixon M., Smith R., Peters G., Dickson C.; "Complete nucleotide sequence of a milk-transmitted mouse mammary trumor virus: two frameshift suppression events are required for translation of gag and pol."; J. Virol. 61:480-490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN P3.

PROPEIN P8.

MAJOR CORE PROTEIN P27.

NUCLEIC ACID BINDING PROTEIN P14

CCHC-TYPE 1.
                                                                                                                                                                                                   "Analysis of gag proteins from mouse mammary tumor virus."; J. Virol. 63:2543-2549(1989).
-!- FUNCTION: P14 BINDS TO SINGLE STRANDED DNA.
-!- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
            Mouse mammary tumor virus (strain BR6).
Viruses; Retroid viruses; Retroviridae; Betaretrovirus.
NCBI_TaxID=11758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8A5C2212460864A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYRISTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                         SEQUENCE FROM N.A.
MEDLINE=87112944; PubMed=3027377;
                                                                                                                                                                 MEDLINE=89259031; PubMed=2542570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||| | |||||| 514 GGGKGGQGAEGP 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591 AA;
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2229
270
497
552
552
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ZN_FING
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LAC1_NEUCR
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01-JAN-1988 (Rel. 06, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
LACC.

STANDARD;

LAC1_NEUCR P06811;

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                                                                                                                                                                                                                                                                         human ceruloplasmin.";
Proco. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                           Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
Characteratization of two allelic forms of Neurospora crassa laccase.
Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:888-896(1988).
                                                                                                                                                                                                                        Germann U.A., Lerch K.; "Isolation and partial nucleotide sequence of the laccase gene from Neurospora crassa: amino acid sequence homology of the protein to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION. Secreted (Potential).
-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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FOCYANIN-LIKE 2.

STOCYANIN-LIKE 3.

PPER TYPE 3.

PPER TYPE 3.

COPPER TYPE 1.

COPPER TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88087214; PubMed=2961749;
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                           Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
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PIR; A29762; A29762.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; Multicu_oxidse2.
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                                                                                                                                                                                         SEQUENCE OF 379-619 FROM N.A. MEDLINE=87067412; PubMed=2947240;
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J. Biol. Chem. 263:885-896(1988).
--- FUNCTION. LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
--- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. PubMed-2961749; MEDLINE-88087214, PubMed-2961749; Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Characterization of two allelic forms of Neurospora crassa laccase.
                                                                                                                                                                                                                    P10574;
01-JUL-1989 (Rel. 11, Created)
01-FDB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; WULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; WULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLERAR (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted (Potential).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
  444 N-LINKED (GLCNAC. . .) (POTENTIAL).
68198 MW; FDED6D78B65048E3 CRC64;
                                                                       5;
                                                                                                                                                                                                                                                                                                          Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
                                          29.0%; Score 56; DB 1; Length 619; 63.6%; Pred. No. 42; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B28523; KSNCLT.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                    11 AARAGGGKGGGGIEGPTLRQ-W 31
                                                                                                                       44 AERYGGG-GGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M18334; AAA33592.1; -.
                                                                             14; Conservative
                                                                                                                                                                                                       STANDARD;
                     619 AA;
                                                              Best Local Similarity
                                                                                                                                                                                                       LAC2_NEUCR
                        SEQUENCE
          CARBOHYD
                                                   Query Match
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LAC2_NEUCR
                                                                                Matches
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                                                                                                                                                                                                                                                                                        5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                      Score 56; DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
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POLY-GLY.
POLY-GLY.
; 9038506E18D7B450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rott M.E., Tremaine J.H., Rochon D.M.; "Nucleotide sequence of tomato ringspot virus RNA-2."; J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                       OBB6CCDE18841145 CRC64;
                                                                                                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 20.2 kDa protein in RNA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91311402; Pubmed=1856689;
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                                                                                                                                                                                                                                                                                                                                                      44 AERYGGG-GGGGCNSPTNRQCW 64
                                                                                                                                                                                                                           68120 MW;
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                                                                                                                                                                                                                                                               29.0%;
                                                                                                                                                                                                                                                                             63.68;
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                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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66
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DOMAIN 15 2
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HSSP; P04002; 1WFA.
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619 AA;
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       480
482
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Best Local Similary
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P25245;
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CARBOHYD
CARBOHYD
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Best Local S
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YR21_TRSVR
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                                       METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CDC 1551 / Oshkosh, Fisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg &.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglineier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' AND 5' TO 3' EXONICLEASE ACTIVITY.
                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai \text{W}_{\cdot, j} "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                               MEDLINE-94124016; PubMed-8294019; Mizrahi V., Huberts P., Dawes S.S., Dudding L.R.; A PCR method for the sequence analysis of the gyrA, polA and rnhA gene segments from mycobacteria."; Gene 136:287-290(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
01-OCT-1994 (Rel. 30, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DOLA POLYMETASE I (EC 2.7.7.7) (POL I).
POLA OR RV1629 OR MT1665 OR MTCY01B2.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; MT1602, ...
TubercuList; Rv1629; -.
InterPro; IPR002562; 3_5_exonuclease.
Tron02421; 5_3_exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF01367; 5_3_exonuclease; 1. PF02739; 5_3_exonuc_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_poli.
DNA_pol_A.
Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11920; AAB46393.1; -.
EMBL; Z95554; CAB08882.1; -.
EMBL; AE007030; AAK45935.1; -.
                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002298;
InterPro; IPR001098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000513;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19821; 1BGX.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + [DNA](N)
                                                                                                                                                                                                               STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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                                                                                                                                                                                                                                                             Transferase, DNA directed DNA polymerase; DNA replication; DNA repair;
Hydrolase; Exonuclease; DNA-binding; Complete proteome.
SEQUENCE 904 AA; 98471 MW; 1C8E560FE5F74323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92040086; Pubmed=1840579;
MEDLINE=92040086; Pubmed=1840579;
Thole J.E., Ottenhoff T.H., Clark-Curtiss J.E.;
Tidentification of Mycobacterium leprae antiqens from a cosmid
library: characterization of a 15-kilodalton antigen that is
recognized by both the humoral and cellular immune systems in leprosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.; Woodward J.R., Marrell B.G.; Woodward J.R., Rajandream G., Woodward J.R., Razerell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-115 FROM N.A. MEDLINE-91126054; PubMed-1992456; Laal S., Sharma Y.D., Prasad H.K., Murtaza A., Singh S., Tangri S., Mara R.S., Nath I.; "Recombinant fusion protein identified by lepromatous sera mimics native Mycobacterium leprae in T-cell responses across the leprosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DISEASE: MOST PROBABLY CAUSES THE LYMPHOPROLIFERATIVE RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 1; Length 904;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 88:1054-1058(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1872 protein precursor (15 kDa antigen) (A15).
LSR2 OR ML0234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
Pfam; PF00476; DNA_pol_A; 1.
PRIMYS; PR00868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00279; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 59:4117-4124(1991).
                                                                                                                                                                                                                                                                                                                                                                                                      28.5%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 TVROWLAEHAGDGRRAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TLRQWLAARAGGGKGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OCCURRING IN LEPROSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYMPHOPROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSR2_MYCLE
P24094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TN;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spectrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
LSR2_MYCLE
LD LSR2_MYCLE
LD 1-MAR.
DT 01-MAR.
DT 16-OCT-
DT 16-OCT-
DT 18-CCT-
OC Bacter:
OC Acting
OX NCBLING
RX MEDLINN
RX MEDLINN
RX MEDLIN
RY Teccogn
RT IDEAT:
RT INFECT
RY MASSI
RA MUNDAY
RA MUNDAY
RA MUNDAY
RA MUNDAY
RA BATTEI
RA BATTEI
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"KMSKS" REGION.

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01921; tRNA-synt_1f; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nomura N., Sako Y., Kikuchi H.; Rubota K., Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + L-lysyl-trna(Lys).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS).
LYSS OR APEO161.
                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                          DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                       B4CD4D7C0D9F00A1 CRC64;
                                                                                                                                                                                                                                    Antigen; Immune response; Signal; Complete proteome.
SIGNAL 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               .;
9
                                                                                                                                                                                                                                                                                                                                                                                                  6 LRQWLAA--RAGG-----GKGGGGI---EGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                       48 LROWVSAGRRVGGRRRGRSNSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                          Score 54.5; 1
Pred. No. 13;
                                                                                                                                                                                                                                                                       LSR2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002904; tRNA-synt_lys_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99310339; PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                     EMBL, AL589917; CAC29742.1; --
EMBL, X53487; CAA37572.1; --
PIR; S14407; S14407.
                                                                                                                                                                                                                                                                                           SEQUENCE 112 AA; 12164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP000058; BAA79072.1; -
                                                                                                                                         EMBL; M67510; AAA25351.1; -.
                                                                                                                                                                                                                                                                                                                                28.2%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 35.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SITE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYK_AERPE
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                            SIGNAL
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                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE - ADP + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMATE.
-!- SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wheeler P.R., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Whogeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED GLN-TRRA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINYL-TRNA SYNTHETASE. THE REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium leprae.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineee; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) (Glu-ADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                3;
                                           Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%; Score 54; DB 1; Length 497; 52.6%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein biosynthesis, Ligase, Complete proteome.
SEOURNCE 497 AA; 51536 MW; D3723D871518BDC7 CRC64;
     753664E2937FBF27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                      497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                               Score 54.5; I
Pred. No. 55;
                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                            293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                         8 QWLAARAGGGK---GGGGIEGPTLRQWL 32
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00571; AMIDASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000120; Amidase.
           65114 MW;
                                                                                                                                                                                                                                                                                                                                                                        subunit A).
GATA OR ML1702 OR MLCB637.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z99263; CAB16428.1; -. EMBL; AL583923; CAC30655.1;
                                               28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01425; Amidase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                        11; Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserv
               562 AA;
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leproma; ML1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                          GATA_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
             SEQUENCE
                                                                                                                                                                                                                                         GATA_MYCLE
                                                                                            Matches
                                                                                                                                                                                                                           RESULT 17
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DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                       TBX2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99061335; Pubmed-9846878;
Li S.-C., Zwahlen C., Vincent S.J., McGlade C.J., Kay L.E., Pawson T.,
                                                                                                                                                                                                                                                                    Eukaryota; Metazoā; Arthropoda; Trācheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forman-Kay J.D.;
"Structure of a Numb PTB domain-peptide complex suggests a basis for
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89324081; PubMed=2752427; Uemura T., Shepherd S., Ackerman L., Jan L.Y., Jan Y.N.; "Numb, a gene required in determination of cell fate during sensory organ formation in Drosophila embryos.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diverse binding specificity.";
Nat. Struct. Biol. 5:1075-1083(1998).
-!- FUNCTION: NUMB IS REQUIRED IN DETERMINATION OF CELL FATE DURING SERSORY ORGAN FORMATION IN DROSOPHILA EMBRYOS. IT FUNCTIONS IN NUCLEI AND SEEMS TO INTERACT WITH NUCLEIC ACIDS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 PID DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; ATP-binding; Alternative initiation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMB PROTEIN, ZYGOTIC ISOFORM. NUMB PROTEIN, MATERNAL ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 1; Length 556;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4FECAAE9C98FEE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR MATERNAL ISOFORM.

ATP (POTENTIAL).

ARG/LYS-RICH (BASIC).
                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROBABLE)
                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 OTLASGTGAAVGGGGPDDPFDAEWVA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QWLAARAGGGKGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0002973; numb.
InterPro; IPR000050; PID_domain.
Pfam; PF00640; PID; 1.
145 GPTRNPWNVDRVPGGSGGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M27815; AAA28730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 64-210.
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00462; PTB; 1.
PROSITE; PS01179; PID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 58:349-360(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A32466; A32466.
PDB; 2NMB; 04-NOV-98.
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22
25
81
81 2
556 AA;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                                                                                       Numb protein.
                                                                                                   NUMB_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                         P16554;
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DOMAIN
                                                                                NUMB_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                     SOTITITITITIES OF SOCIOUS COURTES AND SECOND SECOND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Fetal kidney;

WEDLINE=96169568; PubMed=8597636;

MEDLINE=96169568; PubMed=8597636;

Law D.J., Gebuhr T., Garrey N., Agulnik S.I., Silver L.M.;

Identification, characterization, and localization to chromosome

I 7421-22 of the human TBX2 homolog, member of a conserved

developmental gene family.";

Mamm. Genome 6:793-797(1955).

-1- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES

REQUIRED FOR MESODERM DIFFERENTIATION. PROBABLY PLAYS A ROLE IN

LIMB PATTERN FORMATION.

-1- SUBCELLULAR LOCATION: Nuclear (Potential).

-1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN ADULT IN KIDNEY, LUNG,

AND PLACEMTA. WEAK EXPRESSION IN HEART AND OVARY.

-1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Fetal kidney;
MEDLINE-96015055; PubWed-8530034;
Campbell C., Goodrich K., Casey G., Beatty B.;
"Cloning and mapping of a human gene (TBX2) sharing a highly conserved protein motif with the Drosophila omb gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding; Nuclear protein; Developmental protein.

POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y -> D (IN REF. 2).
AGKA -> TDKT (IN REF. 2).
C6477134C69D7C2C CRC64;
               013207; Q16424;

OLNOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

T-box transcription factor TBX2 (T-box protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
   702 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 76;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 152-245 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74194 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U28049; AAA73861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01283; TBOX_1; 1
PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS50252; TBOX_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S81264; AAB36216.1; -. HSSP; P24781; 1XBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001699; T-box.
Pfam; PF00907; T-box; 1.
PRINTS; PR00937; TBOX.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00425; TBOX: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571
585
155
165
702 AA;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 600747; -
TBX2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Query Match
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qq
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1307:318-324(1996).
-1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOFIC INITIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
                                                                                                                                01-NOV-1999 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP
                                                                                                                                                                                                                                                                      MEDLINE-9FRAGUE-DAWLEY;
MEDLINE-96305355; PubMed-8688467;
MEDLINE-96305355; PubMed-8688467;
Flowers K.M., Mellor H., Matts R.L., Kimball S.R., Jefferson L.S.;
Flowers K.M., Mellor H., Matts R.L., Kimball S.R., Jefferson L.S.;
"Cloning and characterization of complementary and genomic DNAs encoding the epsilon-subunit of rat translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.0%; Score 54; DB 1; Length 716; Best Local Similarity 43.3%; Pred. No. 77; Matches 13; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C6E4BFCE060AF6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino-acid biosynthesis; Translation regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argonaute protein.
AGO1 OR ATIG48410 OR F11A17.3.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AARAGGGKGGGGIEG-----PTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 ANKRGGGSGGGGTQGAEEEPPPPLQAVLVA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003307; eIF5C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 716 AA; 80240 MW;
                                                                                                                         01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U19516; AAB17690.1; -. EMBL; U19511; AAB17691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00132; haxapep; 3.
Pfam; PF02020; W2; 1.
SMART; SM00515; eIF5C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                   502 LASVAGGGNGGGG--GP 516
          10 LAARAGGGKGGGGIEGP 26
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 2-BOUND GDP FOR GIP
                                                                                                                                                                                                                                                                                                                                                                                                           DELTA AND EPSILON.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGO1_ARATH
004379;
                                                                                                                                                                                                                                                                                                                                               factor-2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGO1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 21
                                                                                         E2BE_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Theologis A., Ecker J.R., Palm C.J.; Federspiel N.A., Kaul S.,
RA Theologis A., Ecker J.R., Palm C.J.; Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,
RA Hunter J.L., Jonkins J., Johnson Hopson C., Khan S., Khaykin E.,
RA Lim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lin S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Lin S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                             STRAIN=CV. COLUMBIA; TISSUE-Leaf;
MEDLINE-88090460; PubMed-9427751;
Bohmert K., Camus I., Bellini C., Bouchez D., Caboche M., Benning C.;
"AGOI defines a novel locus of Arabidopsis controlling leaf
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000).

-i - FUNCTION: ESSENTIAL FOR PROPER DEVELOPMENT OF LEAVES AND FLORAL ORGARD.

-i - SUBCELLULAR LOCATION OF AXILLARY MERISTEMS.

-i - SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-i - TISSUE SPECIFICITY: WIDELY EXPRESSED AT LOW LEVELS.

-i - DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT ALL DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.0%; Score 54; DB 1; Length 104 62.5%; Pred. No. 1.1e+02; .ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN 13 104 GLY-RICH.
SEQUENCE 1048 AA; 116190 MW; 3E5146343A09C541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE ARGONAUTE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendel; 24973; Arath;3192;24973.
InterPro; IPR003100; PAZ.
InterPro; IPR003165; Piwi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC007932; AAD49755.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 GGGRGGGPSSGPPORQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U91995; AAC18440.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GGGKGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02170; PAZ; 1.
Pfam; PF02171; Piwi; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 17:170-180(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                          development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAGES
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DNA Cell Biol. 10:757-769(1991).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels 11; Gaps
                             01-077-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
01-077-1989 (Rel. 12, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Fragment).
Echistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of a second human subtilisin-like protease gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            Hedstrom R., Culpepper J., Schinski V., Agabian N., Newport G., "Schistosome heat-shock proteins are immunologically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAC4_HUMAN STANDARD; PRT; 969 AA. P29122; Q15099; Q15100; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ7; Q9UEJ9; Q9UEZ7; Q9Y4G9; Q9Y4H0; Q9Y4H1;
                                                                                                                                                                                                                                                                                                             . Biochem. Parasitol. 29:275-282(1988).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%; Score 53.5; DB 1; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 AA; 21845 MW; 800F8586046D5313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the fes/fps region of chromosome 15.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 RAGG-----GKGGGGIEGPTLRQ 30
         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00297; HSP70_1; PARTIAL. PROSITE; PS00329; HSP70_2; PARTIAL. PROSITE; PS01036; HSP70_3; PARTIAL. ATP-binding; Heat shock.
                                                                                                                                                                                                                                        MEDLINE=88318804; PubMed=2457805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M21011; AAA29897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A54507; A54507.
HSSP; P08109; ICKR.
InterPro; IPR001023; HSP70.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                              host-like antigens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                         NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local S...
   HS70_SCHJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PACE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
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Mori K., Kil S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.; "A novel human PACE4 isoform, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

1- COFACTOR: PACE4A IS PROBABLY CALCIUM-DEPENDENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), J. Blochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K., Tsuji A., Matsuda Y.;
"Bloosyntheric processing and quaternary interactions of proprotein convertase Spc4 (PACE4) ";
FEBS Lett. 434:155-159(1998).
-!- FUNCTION: LIKELY TO REPRESENT AN ENDOPROTEASE ACTIVITY WITHIN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                              "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                          Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                              Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.,
                                                                                                                                                                                                                                                                                                                                                                                                  Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
MEDLINE-98021085; PubMed-9378725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Eurotional analysis of human PACE4-A and PACE4-C isoforms: ifentification of a new PACE4-CS isoform."; FEBS Lett. 396:31-36(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II)
                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
                                                                                                                                                                      Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                      SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING (ISOFORM PACEACS).
                                                                      MEDLINE=94235049; PubMed=8179631;
                                                                                                                                                                                                                          MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99233559; PubMed=10215603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97335942; PubMed=9192737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98408849; PubMed=9738469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
                                                                                                                                                    PACE4 isoforms.
                                                                                                                                                                                                                                                                                                      PACE4 isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moehring T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROCESSING.
                                                                                                                                                                                                            ERRATUM
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-1- SUBBNIT: THE PACE4A-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX WHEREAS MATURE PACE4A-I ENSISTS ONLY AS A MONOMER, SUGGESTING THAT PROPERTIES CLEAVAGE AFFECTS ITS TERRITARY OR QUATERNARY STRUCTURE.
-1- SUBCELLULAR LOCATION: PACE4A-I AND PACE4-AIL ARE SECRETED. PACE4CA AND PACE4CS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM IN ENDOPLASMIC RETICULUM. PACE4E-I AND PACE4E-II ARE RETAINED INTRACELLULARIX PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
```

TERMINUS. PACCAGE MIGHT BE SECRETED.

--- ALTERNATUS. PACCAGE MIGHT BE SECRETED.

--- ALTERNATUS PRODUCTS: 8 ISOFORMS; PACCAG-I/PACCA (SHOWN HERE),

PACCAG-II, PACCAGE PACCA I, PACCAG', PACCAG'S, PACCAD.

--- PACCAG-II, PACCAGE BY ALTERNATUSE SPLICING. ISOFORMS PACCAGE.

C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.

--- TISSUE SPECIFICITY: EACH PACCA ISOFORM EXHIBITS A UNIQUE

RESTRACTED DISTRIBUTION. PACCAGA ISOFORM EXHIBITS A UNIQUE

RESTRACTED DISTRIBUTION. PACCAGE ISOFORM EXHIBITS A LEAST

COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACCAGA-II IS AND EACH

KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACCAC AND PACCAGE ARE

EXPRESSED IN PLACETHY PACCAGE. IS EXPRESSED IN CEREBELLUM,

PLACEMYA AND PITUITARY. PACCAGE-II IS AT LEAST

PLACEMYA AND PITUITARY. PACCAGE-II IS AT LEAST PRESENT IN

-i- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTIN: THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY CEREBELLUM.

-! - SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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A80482; AAA59990...,
AB001914; BAA21620.1; -A8001898; BAA21620.1; JOINED.
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EMBL; M97217; AAA21946.1; -.

AB001903;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDITINE-9301571; MEDITINE-93015711; Pubmed=1356967; Priefert H., Steinbuechel A.; Priefert H., Steinbuechel A.; Fidentification and molecular characterization of the acetyl coenzyme identification and molecular characterization of the acetyl coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A synthetase gene (accb) of Alaaligenes eutrophus.";
J. Bacteriol. 174:6590-6599(1922).
-i. SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i. SIMILARITY: BELONGS TO THE SODIUM:SOLUTE SYMPORTER FAMILY (SSF).
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in acoE 3'region (OFF2) (Fragment).
Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
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AB001907; BAA21625.1;
AB001908; BAA21625.1;
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BAA21624.1;
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                                                                                     AB001908;
AB001909;
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AB001898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Development 121:4045-4055(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SIX/SINE OCULIS FAMILY OF HOMEODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.,
                                                                                                                                                                                                                                                Hypothetical protein; Transport; Transmembrane; Sodium transport;
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MEDLINE-96125147; PubMed-8575305;
Oliver G., Mailhos A., Wehr R., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIX3_MOUSE STANDARD, PRT; 333 AA.
062233; P70176; P70177;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-Momeobox protein SIX3 (Sine oculis homeobox homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                        332 AA; 37031 MW; CB8F4471BD7341C8 CRC64;
                                                         InterPro; IPR001734; Na_solut_symport.
PROSITE; PS00456; Na_SOLUT_SYMP_1; PARTIAL.
PROSITE; PS00457; Na_SOLUT_SYMP_2; PARTIAL.
PROSITE; PS50283; Na_SOLUT_SYMP_3; 1.
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Pred. No. 50;
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EMBL; D83144; BAA11822.1; -.
EMBL; D83145; BAA11823.1; -.
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137 GYTIPDFLAARYGNGKPGGNL 157
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Matches 11; Concornation
                                                                                                                                                                                                                                                                                                                                                              332
PIR; B45736; B45736.
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                                                                                                                                                                                                                                                                       VA -> WP (IN REF. 1).
PSGMRSLAEPGCPTHGSAESPSTAASPTTSVSSLTERADTG
TSILSVTSSDSECDV -> ERDALPGRARLPHARLSRVTVH
GGQPDHQCVQPDGARGHRHEDPLGNLQRLGM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.; "Aberrant cell growth induced by avian winged helix proteins.";
                                                                                                                                                                                                               LOHQAIGPSGMRSLAE -> SVAGTAARPPQA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                  PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
Developmental protein; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 1; Length 333;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                              ISOFORM SIX3A).
MISSING (IN ISOFORM SIX3A).
G -> GG (IN REF. 1).
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                    HOMEOBOX.
POLY-ALA.
                                                                                                                                                                      GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDLINE=97141794; PubMed=8988052;
                                         MGD; MGT:102764; Six3.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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HSSP; 063245; 2HFH.
1702405; 2HFH.
InterPro; IPR001766; Fork_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                   333 AA; 35592 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 AGGAGGGSGGGSRAP 74
                                                                                                                                     Developmental F-1
Alternative splicing.
                                                                                                                                                                                 266
267
286
                                                                                        SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             helix protein CWH-3).
               TRANSFAC; T03263; -.
TRANSFAC; T03270; -.
HSSP; P40427; 1B8I.
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                               264 271
                                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FXD3_CHICK
P79772;
                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                   ONA_BIND
                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FXD3_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26
   DR
DR
DR
DR
KKW
KKW
KKW
KKW
FT
FT
FT
FT
FT
SO
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1;

5

3; Indels

DR DR DR DR FT FT SQ

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: MAY HAVE A ROLE TO PLAY IN FORMATIVE EVENTS IN OVULE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBRYO MORPHOGENESIS.
-- SUBCELLULAR LOCATION: Nuclear (Probable).
-- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN THE MATURE PLANT.
-- SIMILARITY: BELONGS TO THE TALE/KNOX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. VFNT CHERRY:
MEDLINE-98145476; PubMed-9484482;
Janssen B.J., Williams A., Chen J.J., Mathern J., Hake S., Sinha N.;
"Isolation and characterization of two knotted-like homeobox genes
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. NCBI_TaxID=4081;
                                                                                                                                                   ;
                                                                                                                            Score 53; DB 1; Length 394;
Pred. No. 58;
                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMEOBOX (TALE-TYPE).
5B52B9E0A34A86BC CRC64;
                      PROSITE; PS00657; FORK HEAD_1; 1.
PROSITE; PS00658; FORK HEAD_2; 1.
PROSITE; PS50039; FORK HEAD_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
DOMAIN
67 70
POLY-ALA.
                                                                                                         324A4B36B9E31899 CRC64;
                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                   PRT; 426 AA.
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELK DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLN.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ASN
                                                                                                 FORK-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-ASP
                                                                  POLY-ALA.
POLY-GLY.
                                                                                                                                                                                                                                                                                                      Homeobox protein knotted-1 like LET12
                                                                                      POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 36:417-425(1998)
                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF000142; AAC49918.1; -. InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47581 MW;
                                                                                                           40995 MW;
                                                                                                                                27.5%;
                                                                                                                                           76.98;
    PRINTS; PR00053; FORKHEAD.
                                                                                                                                            Local Similarity 76.9
es 10; Conservative
                                                                                                                                                                                                                                                    STANDARD;
                                                                            91
106
211
                                                                                                                                                                           13 RAGGGKGGGGIEG 25
                                                                                                                                                                                                 82 RGGGGGGGGEEG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
283
325
349
426 AA;
                                                                            80
100
117
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
               SMART; SM00339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 from tomato.
                                                                                                                                                                                                                                                       HKLB_LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
SEQUENCE
                                                                                                   DNA_BIND
SEQUENCE
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIWOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                        DOMAIN
                                                                   DOMAIN
                                                                               DOMAIN
                                                                                                                                                                                                                                              HKLB_LYCES
                                                                                                                                                         Matches
                                                                                                                                                                                                                                  RESULT 27
                                                                                                                                                                                                                                                       g
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Score 53; DB 1; Length 426; Pred. No. 62;

27.58;

Query Match Best Local Similarity

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-:- SUBCELLUIAR LOCATION: NUCLEAR.

-:- ALTERNATIVE PRODUCTS: 3 ISOFORMS; N-OCT 3 (SHOWN HERE), N-OCT 5A

AND N-OCT 5B; ARE PRODUCED BY ALTERNATIVE INITIATION.

-:- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL

CELL LINEAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression of a large family of POU-domain regulatory genes in mammalian brain development.";

Nature 340:35-42(1989).

-i- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO THE FECGRITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, (GCAT') AND ("TAAT'), SEPRARTED BY A NONCONSERVED SPACER REGION OF 0, 2, OR 3 NUCLEGITLES. POSITITVELY REGULATES THE GENES UNDER THE CONTROL OF CONTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The brn-2 gene regulates the melanocytic phenotype and tumorigenic potential of human melanoma cells."; oncogene 11:691-700(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schreiber E., Tobler A., Malipiero U., Schaffner W., Fontana A.; "CDNA cloning of human N.Oct3, a nervous-system specific POU domain transcription factor binding to the octamer DNA motif."; Nucleic Acids Res. 21:253-258(1993).
                                                                                                                                                                                                                                                                                                                           P20265; 014960;
01-FEB-1991 (Rel. 17, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nervous-system specific octamer-binding transcription factor N-OCT
(Brain-specific homeobox/POU domain protein 2) (BRN-2 protein)
(Contains: N-OCT 5A; N-OCT 5B].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treacy M.N., Simmons D.M., Ingraham H.A., Swanson L.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angus J., Thomson F., Murphy K., Baker E., Sutherland G.R., Parsons P.G., Sturm R.A.;
                                                                                                                                                                                                                                                                                                         443 AA
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=93181199; PubMed=8441633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=89295573; PubMed=2739723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95380176; PubMed=7651733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POU3F2 OR BRN2 OR OTF7 OR OCT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 280-404 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z11933; CAA77990.1; -. EMBL; L37868; AAB59611.1; -.
                                                                                                                                 96 OWLSPTAAAGGGSNGGG 112
                                                                    8 QWLA--ARAGGGKGGGG 22
   11; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S05043; S05043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          He X., Treacy
Rosenfeld M.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver
                                                                                                                                                                                                                                                                                                                OC3N_HUMAN
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HSSP; P14859; 10CT
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    68
125
268
356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATA_MYCTU
                                                                                                                                                                                                                                                                                       Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit A).
                                                                                                                                                                                                                                                                                                                         DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
GATA_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                           Matches
        òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1998 (Rel. 36, Last annotation update)
Nervous-system specific octamer-binding transcription factor N-OCT 3
(Brain-specific homeobox/POU domain protein 2) (BRN-2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 89:3280-3284(1992)

-!- FUNCTION: TRANSCRIPTION FACTOR THAI BINDS PREFERENTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, ('GCAT') AND ('TAAT'), SEPRAFED BY A NONCONSERVED SPACER REGION OF 0, 2, OR 3 NUCLEOTIDES. POSITIVELY REGULATES THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II PROMOFERS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hara Y., Rovescalli C., Kim Y., Nirenberg M.; "Structure and evolution of four POU domain genes expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                                                   PROSITE; PS00465; P00_2; 1.
PROSITE: PS50071; HOMBOBOX,2; 1.
DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                         DB 1; Length 443;
                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                      A -> G (IN REF. 2).
2CAC852328334A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 AA.
                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Pred. No. 64;
                                                                                                                                                                                                                                      FOR N-OCT 5A.
                                                                                                                                                                                                                                                                                                                                        Score 53;
                                                                                                                                                                                                    N-OCT 3.
N-OCT 5A.
N-OCT 5B.
                                                                                                                                                                                                                                                                       POLY-GLN.
                                                                                                                                                                                                                                                             POLY-GLY.
                                                                                                                                                                                                                                                                                              HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                       Activator; Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDLINE=92228768; PubMed=1565620;
                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
                                          InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; Pou; 1.
                                                                                                                                                                                                                                                                                                                  46921 MW;
                                                                                                                                                                                                                                                                                                                                        27.5%;
                                                                                    PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                           SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                 8 QWLAARAGGGKGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                      60 OWITALSHGGGGGG 74
         HSSP; P14859; 10CT.
TRANSFAC; T00630; -.
PIR; S29334; S29334
                                                                                                                                                                                                                                                                                         354
26
443 AA;
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL LINEAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                MIM; 600494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OC3N_MOUSE
                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                   INIT_MET INIT_MET
                                                                                                                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OC3N_MOUSE
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
DR
DR
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Cole S. T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) (Glu-ADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.5%; Score 53; DB 1; Length 445; 60.0%; Pred. No. 64; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AA; 47149 MW; 1A47F10950EECE8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATA OR RV3011C OR MT3091 OR MTV012.25C.
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POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                  MGD; MGI:101895; Pou3f2.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; Pou.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                     EMBL; M88300; AAA39961.1; -.
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QWLAARAGGGKGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 QWITALSHGGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
149
338
                                                                                                                                                                                                           S31224; S31224.
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Figure 1. White 0., Alland D., Eisen J.A., Carpenter L., White 0., Ra Reterson J., Dedson R., Garin M.L., Haft D., Hickey E., E. Rollonay J.F., Natson W.C., Unayam L.A., Ermolaeva M.D., Salaberg S.L., Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Blishal W.; Randlaw M. R. Salaberg S.L., Mikula M., Ralson W.C., Unayam L.A., Ermolaeva M.D., Salaberg S.L., Rollonay J.F., Natson W.C., Unayam L.A., Ermolaeva M.D., Salaberg S.L., R. Bishal W.; Randlaw M. R. Salaberg S.L., Salaberg S.L., R. Bishal W.; Randlaw M. Salaberg S.L., Salaberg S.L
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Search completed: October 9, 2002, 09:00:18 Job time : 6.3831 secs

8 6

Rhabditidae; Peloderinae; Caenorhabditis.

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SEQUENCE FROM N.A.
MEDLINE-92375684; PubMed-1354852;
Iwasaki M., Okumura K., Kondo Y., Igarashi H., Tanaka T.;
Iwasaki M. okumura K., Kondo Y., Igarashi H., Tanaka T.;
"cDNA cloning of a novel heterogeneous nuclear ribonucleoprotein gene
homologue in Caenorhabditis elegans using hamster prion protein cDNA
as a hybridization probe.";
"ucleic Acids Res. 20:4001-4007(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. BEDLINE-97320490; PubMed=9177341; SEGUENCE FROM N.A. MEDLINE-97320490; PubMed=9177341; Sudo S., Fujikawa T., Nagakura T., Ohkubo T., Sakaguchi K., Tanaha M., Nakashima K., Takahashi T.; Stuctures of mollusc shell framework proteins."; Setuctures of mollusc shell framework proteins."; Nature 387.563-564(1997). EMBL; D86074; BAA20466.1; SEQUENCE 738 AA: 61723 MW; FDF984139BF3BA59 CRC64; SEQUENCE 738 AA: 61723 MW; FDF984139BF3BA59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pterioida;
Pterioidea; Pteriidae; Pinctada.
NCBI_TaxID=50426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 74.5; DB 5; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%; Score 74.5; DB 5; Length 738; 55.0%; Pred. No. 5.4; tive 0; Mismatches 15; Indels 3
                                                                                                                                                                                     STRAIN-BRISTOL N2;
Du Z., Scheet P., Andrews S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; D10877; BAA01645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 346 AA; 36344 MW; 48B95818D8BB9A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGGIEGPTLRQ---WLAARAGGGGGGGGGIEGPTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGIEGPTLRQWLAARAGGG-GGGGGGIEGPTLRQWLAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: October 9, 2002, 09:03:18 Job time : 16.7742 secs
                                                                                                                                                                                                                                               EMBL: AF038613; AAB92051.1; --
HSSP: P09651; 1UP1.
InterPro: IPR002952; Eggshell.
InterPro: IPR000504; RRM.
Pfam; PF00076; rrm; 2.
PRINYS; PR01228; EGGSHELL.
SMART: SW00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.3%;
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.08
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSOLUBLE PROTEIN.
                NCBI_TaxID=6239;
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FlyBase;
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Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Rukarvota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74.5; DB 5; Length 308; Pred. No. 2.3;
                                     Score 74.5; DB 5; Length 147;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
Du Z., Scheet P., Andrews S.;
"The sequence of C. elegans cosmid F42A6.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038613; AAL02515.1; -.
                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEOUENCE 308 AA; 32323 MW; C3F172FDD75A1E45 CRC64;
             147 147
147 AA; 13179 MW; DF945751D333CE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 32.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLRQ----WLAARAGGGGGGGGGGIEGPTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                   PRT; 308 AA
                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequ
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                                                                                            1 GGGGGIEGPTLROWLAARAGGGGGGG 27
                                                                                                           24 GGGGGFRG------RGGGGGGGG 41
                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
                                              33.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 43.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                             Best Local Similarity 55.69
Matches 15; Conservative
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
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              NON_TER
SEQUENCE
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                                                  Query Match
                                                                                                                                                                                         095X69
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                                                                           Matches
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RE SEQUENCE FROM N.A.

RA Admis M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admis M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admis M.D. Celniker S.E., Holt R.A., Henderson S.N.,

RA George R.A. Lewis S.E., Richards S., Sabhurner M. Henderson S.N.,

RA Sutron G.G., Worthman J.E., Richards S., Sabhurner M. Henderson S.N.,

RA Ballew R.M. Edsul W. Halt G., Mahape M., Pfeiffer B.D.,

RA Abril J.E., Agbayani A., An H.-J., Andrews Pichankon C.E., Baldwin D.,

RA Abril J.E., Agbayani A., Baxendale J., Bayraktaroglu L., Basaley E.M.,

RA Ballew R.M. Basul A., Baxendale J., Bayraktaroglu L., Basaley E.M.,

RA Becson K.Y., Bernos P.V., Berman B.P. Bhandari D., Bolahakov S.,

RA Berson K.Y., Bernos P.V., Berman B.P. Bhandari D., Bolahakov S.,

RA Gerigs S.D., Botchan M.R., Bouck J., Brivstein P., Brottier P.,

RA Gerigs S.D., Botchan M.R., Bouck J., Brivstein P., Brottier P.,

RA Gerigs S.D., Botchan M.R., Bouck J., Brivstein P., Brottier P.,

RA Gerigs S.D., Delloher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Gerigs S.D., Botchan M.R., Garg N.S., Galbart W.M., Glasser K.,

RA Good K., Doup L.E., Gorrell J.H., Gu Z., Gann P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Heisser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Heisser K.,

RA Harris N.L., Mattel B., McIntooh T.C., Moll. J. M., McDarry C., Morris J., Woshrefi A.,

RA Jalain M. Xallush E., Karapen G.H., Ke Z., Kannison J.A.,

RA Jalain M. Xallush E., Karapen G.H., Ke Z., Kannison J.A.,

RA Jasko D., Lei Y., Levitsky A.A., Howland J.Y., Maller N., Saller R.,

RA, Mencol O., Millshina N.V., Mobbrity U., Muzny D.M., Millshina N., Wobbrity U., Muzny D.M., Millshina N., Strong R., Sun R.,

RA, Melson D.R., Pittan G.S., Pan S., Pollard J., Pull S., Shu R.,

RA, Ranger E., Spradling A.C., Stapleton M., Strong S., Yao O., Zhong Y., Shu R.,

RA, Millshina N., Weinstein S., Wang S., Zhu D., J., Wang X., Shu R., Myezser M., Ranger E., Spradling A., Weinstein D., Wang X., Shu R., Myezser R., Rang
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55.6%; Pred. No. 2...
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
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PRINTS; PRO1228; EGGSHELL.
ProDom; PD004637; Fibrillarin; 1.
PROSITE; PS00566; FIBRILLARIN; 1.
SEQUENCE 344 AA; 34637 MW; 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002952; Eggshell.
Interpro; IPR000692; Fibrillarin.
Pfam; PF01269; Fibrillarin; 1.
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Query Match
Best Local Similarity 55.65
Matches 15; Conservative
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Caenorhabditis elegans.
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RA Adams W.D., Celniker S.E., LIPW., Foshins R.A., Gocayne J.D., RA Adams W.D., Celniker S.E., LIPW., Boskins R.A., Galle R.F., Reparatides S., Ashburner M., Henderson S.N., Sutton G.C., Worter S.E., Holt R. B. Ashburner M., Henderson S.N., Sutton G.C., Worter S.E., Richards S., Ashburner M., Henderson S.N., Ra Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Radradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Radradon R.W., Basu A., Baxendal J., Baytaktaroglu L., Bessley E.M., Ballew R.W., Backen B.P., Bhandari D., Boshahavo S., Radravia B. Bernan B.P., Bhandari D., Boshahavo S., Radravia S.C., Burler H., Cadler E., Center A., Chandra I., Radery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. M., Dodson K., Doup L.E., Dounces M., Dugan-Pocha S., Plates R.A., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. M., Dodson K., Doup L.E., Dounces M., Dugan-Pocha S., Plates R.A., Chorg E., Gabrielista C.C., Ferraz C., Ferriaz C., Gabrielista C.C., Ferraz C., Ferriaz C., Gabrielista C.C., Ferraz C., Gabrielista C.C., Ferraz C., Ferrias D.H., Harvey D., Hahman T.J., Hernandez J.R., Houck J., Harvey D., Hahman T.J., Hernandez J.R., Houck J., R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C., Raballi M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., Raballi M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., Mattas N.L., Mattshina N.V., Wobarry C., Morris J., Moshrefi A., Moy M., Moy M., Moy M., Nelson D.L., Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A., Moy M., Wilshina N.V., Wobarry C., Worter S., Shen H., Rabiato D.R., Nelson K.A., Nixon K., Wolly W., Weitsenbach J., Wang Z.Y., Wassarman D.A., Weinsenbach J., Wang Z.Y., Wassarman D.A., Weinsenbach J., Wang Z.Y., Wassarman D.A., Silperow K., Shingson M., Skupski M.P., Smith H.O., A., Shing K., Wolly M., Wollson D.S., Zhan M., Zhuo S., Zhan M., Zhuo S., Zhan M., Zhuo S., Zhan M., Zhuo S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu N., 
                                                                                                                                                                                                                                                                                                                                                        Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, Nosophila, NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Y, CN BW SP.
STRAIN=Y, CN BW SP.
STRAIN=Y, CN BW SP.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Goralez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Yu C., Lewis S.E., Rubin G.M., Celliker S.; Phouanenavong S., Wan K., Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003703; ARF55026.1; --
EMBL, AT058341, AAL135701; --
EMBL, ROSSECTE CONTRACTOR CONTRACTO
                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75; DB 5; Length 1024;
Pred. No. 6.6;
1; Mismatches 10; Indels
                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                             PRT; 1024 AA.
                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
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58.1%;
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CG14355.
                                                                      PRELIMINARY;
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                                                               O9VFM5
RESULT 24
                                   Q9VFM5
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4; Indels 13; Gaps
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Score 74.5; DB 10; Length 113; 45.7%; Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003272; BAB67948.1; -
SEQUENCE 113 AA; 11708 MW; 26D9B2C86935BC0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavell A.J., Dyson J., Ish-Horowicz D., "A novel GC-rich dispersed repeat sequence in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Royker-Pokora B.,
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                       113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 GGGGG-------GGGGGGGGGGGBPPLRE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
               1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGP 31
                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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FlyBase; FBgn0003062; Fib.
InterPro; IPR000692; Fibrillarin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD004637; Fibrillarin; 1.
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                 STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRILLARIN (FRAGMENT).
                                                                                                                                                      01-DEC-2001 (Tremblie P0506E04.26 PROTEIN. P0506E04.26.
                                                                                                                                                                                                Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                              clone: P0506E04.
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NCBI_TaxID=7227;
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                                                                                                              0942U6;
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                                                                   RESULT 25
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δy
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3

Gaps

2;

10; Indels

18; Conservative

Best Local Similarity

Matches

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SEQUENCE FROM N.A.
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09N6M8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90164534; PubMed-8587504; MEDLINE-90164534; PubMed S.R.; Palumbi S.R.; Palumbi S.R.; Palumbi S.R.; Polymorphism in the gamete recognition protein bindin."; polymorphism in the gamete recognition protein bindin."; Mol. Biol. Evol. 13:397-406(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinosoa; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinosoa; Ec
        Lampetra fluviatilis (River lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
                                                                                                                              SEQUENCE FROM N.A. Kao H. H. H. S., Stefani G., Pieribone V.A., Kao H.-T., Porton B., Hilfiker S., Stefani G., Pieribone V.A., Desalle R., Greengard P., "Molecular Evolution of the Synapsin Gene Family.";
                                                                                                                                                                                                                                                                                                                                                                                                       33.7%; Score 75.5; DB 13; Length 687;
45.7%; Pred. No. 4;
tive 2; Mismatches 6; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; DB 5; Length 250;
Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metz E.C., Palumbi S.R.;
Metz E.C., Palumbi S.R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 035514; AmB00415:1; -.
Interpro; IFR000775; Bindin.
Pfam; PF02084; Bindin.
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                                                                                                                                                                                               J. Exp. 2001. 0:0-0(2000).

J. Exp. 2001. 0:0-0(2000).

HSSP; P17599: 1AUX.

INCEPTO: IPRO01359; Synapsin.

Pfam; PF02750; Synapsin. 2.

Pfam; PF02750; Synapsin. 2.

PRINTS; PR001468; SYNAPSIN.

SEQUENCE 687 AA; 71320 MW; D2D917A69FBDBABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 GGGGG-----PRPGGSGGGGMVGPQTQQ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 GGGGGAGG----MGMAGGRGGGGGGGGMMG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGIEGPTLROWLAARAGGGGGGGGIEG 30
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1 Similarity 53.3%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 45.7% tes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=43350;
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                                                                                         NCBI_TaxID=7748;
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Q9N6M8
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                                                                                                                                                                                                                                            Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=10185351: TULNING=1101827:

Begun D.J., Whitley P.;

Begun D.J., Whitley P.;

Reduced X-linked nucleotide polymorphism in Drosophila simulans.";

Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).

Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).

EMBL; AF252749; AAF68523.1; ---

EMBL; AF252745; AAF68529.1; ---

EMBL; AF252747; AAF68529.1; ---

EMBL; AF252747; AAF68530.1; ---

EMBL; AF252749; AAF68530.1; ---

EMBL; AF252749; PAG68531.1; ---

EMBL; AF252749; PAG68531.1; ---

EMBL; AF252749; PAG68531.1; ---

EMBL; AF252749; PAG68531.1; ---

EMBL; BEG02952; EGG5HELL.

PRINTS; PRO1228; EGGSHELL.
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MEDLINE-98335676; PubMed=9724735;
Qin X.X., Waite J.H.;
Qin X.X., waite J.H.;
A potential mediator of collagenous block copolymer gradients in muscal byssal threads.";
Proc. Natl. Acad. Sci. U.S.A. 95:10517-10522(1998).

PROC. Natl. Acad. Sci. U.S.A. 95:10517-10522(1998).

EMBL; AP043944; AAC33847.1; --
EMBL; Prol3915; Collagen.

Pfam; PP01391; Collagen.

Pfam; PP01391; Collagen.

SEQUENCE 904 AA; 77883 MW; 5529135651AD4C40 CRC64;
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Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilidae; Mytiloidea; Mytiloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75; DB 5; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 AA; 46322 MW; 32677BA0F49648FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) NONGRADIENT BYSSAL.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SIM7, SIM2, SIM3, SIM4, SIM5, AND SIM6;
MEDLINE-20283933; PubMed=10823947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 GGGGASGP--GGGPSANSGGGGGGGGXNG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 GGGLGGGLGGGLGGGLGGGGGGGL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.5%;
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                              OVO PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453
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SYNAPSIN IB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09PUD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PUD9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PUD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PUD9
                           RP RA RA RE RE RA RE RE RA RE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Óλ
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barlot W., Becker A., Boistard P., Bothe G., Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P., Cowie A., Davis R.W., Dream G., Federspiel N.A., Fisher R., Chain P., Glows S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn M.L., Kalman S., Keating D.H., Kiss B., Komp C., Lelaure V., Ramsperger U., Surzycki R., Thebault P., Vandenhol M., Veh K.-C., Batut J.; "The composite genome of the lequme symbiont Sinorhizobium mellioti.";
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                 33.9%; Score 76; DB 13; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%; Score 76; DB 16; Length 1610; 53.3%; Pred. No. 8.2;
                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 293 668-672(2001).
EMBL; AL591783; CAC41893.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 1610 AA: 163768 MW; BOAAFC5E64B47886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                           SMART: SM0389; HOX; 1.
PROSITE; PS0027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 377 AA; 37998 MW; C2DBC19402D3A172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) GLYCINE-RICH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1610 AA
                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                  259 GGYGPPQGYTAASYYGVECGGGGGGGGGGGGPYL 291
                                                                                                                                                                                                                                                        1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260 GGGGGTSLALGGTTVLKAGGGGGGGGAAG 1289
                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21368234; PubMed=11474104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN SMC01710.
                                                                                                                                                                                          ilarity 48.5%;
Conservative
  Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F1N20.120 OR AT4G22020.
                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                       092KQ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                065450;
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                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                 092KQ8
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SEQUENCE FROM N.A.
Bevan M., Wedler H., Wambutt R., Bancroft I., Mewes H.W., Mayer K.,
Schueller C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kao H.-T., Porton B., Hilfiker S., Stefani G., Pieribone V.A., DeSalle R., Greengard P.; "Molecular Evolution of the Synapsin Gene Family."; Lsrp. 2001. 0:0-0(2000).
EMBL, AF192748; AAF108806.1; -. HSSP; P17599; 1AUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                               33.7%; Score 75.5; DB 10; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.7%; Score 75.5; DB 13; Length 642;
45.7%; Pred. No. 3.7;
tive 2; Mismatches 6; Indels 11
                                                                                                                                        Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL02140; CAA18105.1;
EMBL; AL161556; CAB79157.1;
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
SEQUENCE 396 AA; 31470 MW; 1CDCD0FFBE337CAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOSE; FLOSS, LECON.
InterPro; IPRO01359; Synapsin.
Plan; PF02776; Synapsin.C: 1.
Pfam; PF02750; Synapsin.C: 1.
PRINTS; PR01368; SYNAPSIN.
PROSITE; PS00415; SYNAPSIN.
SEQUENCE 642 AA; 66448 MW; BE3FDB68A3A89CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
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ULMAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SYNAPSIN 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      642 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 GGGG-----PRPGGSGGGGMVGPQTQQ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGEFTLRQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GAGGGVSG-----AAGGGGGGGGGGGG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lampetra fluviatilis (River lamprey).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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09YHD0
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                                                                                                                                                                                                                                            RESULT 15
096853
                                                                                                                                      Matches
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E.,

RA Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,

RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Mandon R.C., Rogers Y.H.C. Blazel R.G., Clampe M., Pfeiffer B.D.,

RA Mandon R.C., Rogers W.H.C., Balacel R.G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M. Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,

Ra Ballew R.M. Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,

RA Beson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolthakov S.,

RA Berky J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,

RA Buttis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Cosoler G., Downes M., Dugan Rocha S., Dunkov B.C., Duun P.,

RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Plackorhman M.,

RA Codek A., Gong F., Gorrell J.H., Gu Z., Gun P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., I. Degwam C.,

RA Harris N.L., Harvey D., Helman T.J., Mei M.-H., I. Degwam C.,

RA Jalali M., Kalush F., Karpen G.H., Kavitz S., Kulp D., Lai Z.,

RA Mimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Merkulov G., Milshian N.V., Mobrary C., Morris J., Meison D.L.,

RA Merkulov G., Milshian N.V., Mobrary C., Morris J., Mandon J., Meison D.R.,

RA Balazzolo M., Pittmen G.S., Pan N., Subseh W., Shu B.,

Ra Syler E., Spradling A.C., Stanbetor E., Wang A.H., Wang X.,

RA Syler E., Spradling A.C., Zhan M., Stuong S., Yao Q.A.,

RA Walliams S.M., Woodage T., Worley K.C., Mu Shu S., Zhu X., Smith H.O.,

RA Shong S.-Y., Woodage T., Worley K.C., Mu Weissenbach J.,

RA Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                           4; Gaps
                                                                                                                                             34.4%; Score 77; DB 5; Length 265; 63.0%; Pred. No. 1.1;
                                                                                                                                                                           5; Indels
   Waterston R.;
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submitted (JUN-2010.";
EMBL, U40802, AAK19014.2; -.
InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
Hypothetical protein.

Hypothetical protein.

-- The F. Length 20
                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                       PRT; 679 AA
                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                233 GGGGGIPG----QSVYMGAGGGGGGG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                            1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                    Ouery Match
Best Local Similarity 63.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     CG1521 PROTEIN.
                                                                                                                                                                                                                                                                                                                              09W3E3
                                                                                                                                                                                                                                                                                                RESULT 14
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                  RA
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DR
DR
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomsa J.M., Langeland J.A.;
Tomsa J.M., Langeland J.A.;
botx expression during lamprey embryogenesis provides insights into
the evolution of the vertebrate head and jaw.";
Dev. biol. 0:0-0(1998).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- SUBCELLULAR WITH OTHER HOMEOBOX PROTEINS.
--- SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels 11; Gaps
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76.5; DB 5; Length 194;
Pred. No. 0.9;
                                                                                                                                       34.4%; Score 77; DB 5; Length 679; 56.7%; Pred. No. 2.8; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17667 MW; 9F40A4430BB3E52C CRC64;
                                                                                                71601 MW; E5A5183B36B02FD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AA.
                                                                                                                                                                                                                                                                                                                                                                                         PRT; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GGGGGGGG-----AGGGGGGGGGG 220
                                                                                                                                                                                                                                     1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schistosoma haematobium (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89137380; PubMed-2917627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.";
Exp. Parasitol. 68:17-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
SEQUENCE 194 AA: 17667 MW;
Science 287:2185-2195(2000).
EMBL; AE003444; AAF46385.1: -.
FlyBase; FB9n0030046; CG1521.
InterPro: IPR002665; MgtE.
Pfam; PF01769; MgtE; 2.
SEQUENCE 679 AA; 71601 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M27658; AAA29878.1;
HSSP; P02876; 9WGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 16; Conserv
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                  SEQUENCE
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035295
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                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                   035295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%; Score 78; DB 10; Length 253;
35.0%; Pred. No. 0.82;
tive 3; Mismatches 10; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGIEG------PTLRQW------LAARAGGGGGGGGGFEPTLR 34
                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidea; Oryzeae; Oryza.
                                                                      9
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                          Score 79; DB 5; Length 650;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 308;
                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003235; BAB64100.1; -.
SEQUENCE 253 AA: 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002817; BAB03442.1; -
InterPro; IPR003015; HLH_Myc.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SEQUENCE 308 AA; 33320 MW; 4A3A3B83E66DE468 CRC64;
Pfam; PF00932; IF_tail; 1.
SEQUENCE 650 AA; 70492 MW; 3F45D74AAC220CE9 CRC64;
                                                                                      1 GGGGGIEGPTLRQWLAARAGGGGG----GGGIEGPTLRQWLAA 39
                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ESTS AU029606(E31139).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 34.8%; Score 78; DB 10; Best Local Similarity 54.8%; Pred. No. 1; Matches 17; Conservative 3; Mismatches 5,
                                                                                                                                                                                     253 A.A.
                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 308 AA.
                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                  PRT;
                                                   46.5%;
                                          35.3%;
                                              Best Local Similarity 46.59
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
                                                                                                                                                                                                                                          P0039A07.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone: P0699D11."
                                                                                                                                                                                                                                                       P0039A07.6
                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                             Q943K0
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                                                                                                                                                    RESULT 10
Q943K0
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Q9LG49
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Gaps

9;

5; Indels

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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                Kelm R.J. Jr., Elder P.K., Strauch A.R., Getz M.J., "Sequence of cDNAs encoding components of vascular actin single-stranded DNA-binding factor 2 establish identity to Puralpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.8%; Score 78; DB 11; Length 324; 52.5%; Pred. No. 1.1; tive 2; Mismatches 15; Indels
                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VASCULAR ACTIN SINGLE-STRANDED DNA-BINDING FACTOR 2 P44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The sequence of C. elegans cosmid 20477.", Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding.
SPOUENCE 324 AA; 33901 MW; 5CB70CCE3FDB7913 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN ZC477.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAAR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 AA.
1 GGGGGI-EGPTLRQWLAARAGGGGGGGGGIEG 30
                       Purbeta.";
J. Biol. Chem. 272:26727-26733(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=B6/CBAF1J; TISSUE-LUNG;
MEDLINE=97476282; Pubmed=9334258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF017630; AAB71859.1; -.
                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1338779; Purb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                            (Mouse).
                                                                                                                                                                                                                                                     PURB OR PURB BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          Mus musculus
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TISSUE=MALE FLOWER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P0416G11.17.
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9AS28;
                                                                                                                                                                                                                                                                                                                                                                                                                                           09AS28
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                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                         09AS28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                             δ
         Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels 14; Gaps
                                                                                                                                                                                     26; Gaps
                                                                                                                                          1 GGGGGIEGPTLRQWLAARA-----PTLR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silene latifolia.
Sukaryota; Viridlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Caryophyllaceae; Sllene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L "qBrain-2, a POU-box gene expressed in quail embryos.";
"qBrain-2, a POU-box gene expressed in quail embryos.";
"qBrain-2, a POU-box gene expressed in quail embryos.";
"gbrain-2, a POU-box gene expressed in quail embryos.";
"gbrain-2, a POU-box gene expressed in quail embryos.";
"gbrain-2, a POU-Box gene expressed in quail embryos.";
"l-1 - SUMICARITY: WITH OTHER HOMEOBOX PROTEINS.
"I - SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
"R HSSP; P14859; 10CT.
"R HSSP; P14859; 10CT.
"InterPro; IPR001357; POU.
"InterPro; IPR000327; POU.
"Pfam; PPF00045; Pomeobox: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%; Score 80; DB 13; Length 431; 48.8%; Pred. No. 0.87;
                                                         36.2%; Score 81; DB 5; Length 422; 36.7%; Pred. No. 0.68;
                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein.
722 MW; 1DC47E53F9ACC7D5 CRC64;
             422 AA; 44892 MW; 85FE742F07751B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TIEMBLIEL 19, Last sequence update) POU-BOX PROTEIN BRAIN-2. Coturn's Actual Decounts of the coturn of the coturn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GGGGGGGGGGGGGGGGGGBAP----WAAAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Pred. w...
                                                                                                                                                                                                                                                                                                        PRT; 431 AA
                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
MEN-4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                    Q9PVG9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRINTS; PROMOSES; POUDOMAIN.
PRODOM; PROMOSES; POUDOMAIN.
SWART; SM00389; POX; 1.
SWART; SM00382; POX; 1.
SMRAT; SM00352; POX; 1.
PROSITE; PS00037; HOMEOBOX_2; 1.
PROSITE; PS00037; POUL; 1.
PROSITE; PS00045; POUL; 1.
DNA binding; Homeobox; Nuclear prosecure 431 AA; 43722 MW; 1DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                         Best Local Similarity 36.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-37657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                           SEQUENCE
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   024352
                                                                                                                                                                                                                                                                                                                 09PVG9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                      RESULT 6
Q9PVG9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
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Gaps
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Brber A., Riemer D., Bovenschulte M., Weber K.;

Brber A., Riemer D., Bovenschulte M., Weber K.;

Molecular Phylogeny of metazoan intermediate filament proteins.";

J. Mol. Evol. 47:751-762(1998).

BrML, AJ004932; CAB38182.1; -..

Interpro; IPR001664; IF.

Interpro; IPR001322; IF_tail.

Pfam; PF00038; filament; 2.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Vidiojantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
        Scutt C.P., Li Y., Robertson S.E., Willis M.E., Gilmartin P.M.; Sx determination in Silene latifolia: Y chromosome- and Ustilago violacea-mediated effects during dioecious flower development."; plant Physiol. 114:969-979(1997).

EMBL; Y08776; CAA700221: --
SEQUENCE 187 AA: 18357 MW; FAFC6B5E7F7DFEEI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CY. INTERPONDERE;
STRAIN-CY. MATPONDERE;
Sasaki T., Matsumoto T., Yamamoto K.;
Soraki T., Matsumoto T., Yamamoto K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 167 AA; 17271 MW; 770BB98A7294CC43 CRC64;
                                                                                                                                                                                                          35.5%; Score 79.5; DB 10; Length 187; 43.2%; Pred. No. 0.43; tive 1; Mismatches 9; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.3%; Score 79; DB 10; Length 167; Best Local Similarity 40.5%; Pred. No. 0.43:
                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) INTERWEDIATE FILAMENT PROTEIN IF1.
                                                                                                                                                                                                                                                                                                                            1 GGGGGIEGPTLRQWLAARAGGGGGGGGI------EGPTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
p0416G11.17 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGGIEGPTLRQWLAARAGGGGGGGGGIEG--PTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE=97377129; PubMed=9232878;
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                                                                                                                                                                                                                                                                                   19; Conservative
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NCBI_TaxID=10231;
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                                                                                                                                                                                                                                                      Best Local Similarity
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Query Match
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                          023062;
            023062
                                                                                    T28H11
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                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                               Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Pred. No. 0.32;
2; Mismatches 10; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0465H08."
                                                                                                                                                                                                                                                                                                                   37.9%; Score 85; DB 5; Length 500; 55.2%; Pred. No. 0.31;
                                                                                                                                                                                                           'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                        Percy C.M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (UNN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002525; BAB07996.1; -. InterPro; IRR000571; 2f-CCCH. FROM PFO0052; zf-CCCH; 4. SWART; SM00356; ZnF_CSH1; 4. SEQUENCE 360 AA; 37368 MW; 5105598D7E1C77B2 CRC64;
                                                                                                                                                                                                                                                      InterPro; IPR001254; Trypsin.
PROSITE; PS50240; TRYPSIN.DOM; 1.
Hydrolase; Serine protease.
SEQUENCE 500 AA; 53946 MW; 1416327086FE7CF6 CRC64;
       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 360 AA
                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                             2 GGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; 278013; CAB01420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUTATIVE ZINC FINGER PROTEIN.
P0462H08.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.3%;
51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.3%
Best Local Similarity 51.4%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.2<sup>8</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=6239;
                                            F15B9.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
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RESULT 4

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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karabinos A., Riemer D., Erber A., Weber K.; "Homologues of vertebrate type I, II and III intermediate filament (IF) proteins in an invertebrate: the IF multigene family of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERNEDIATE FILAMENT PROTEIN EL.
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Brkartyota: Metazoa; Chordata; Cephalochordata; Branchiostoma.
Branchiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Nolson J., Wohldmann P.;
"The sequence of C. elegans cosmid T28H11.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
"Direct Submission.";
"Direct Submission.";
Submitted (JUL 742040) to the EMBL/GenBank/DDBJ databases.
EMBL; U64609; AAA6604.2; -
Hypothetical protein.
eroureNCE 374 AA; 32630 MW; CBOD4ECD7519D997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 83; DB 5; 59.3%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340'GGGGGIPGQSV--YMGAGGGGGGGGG 364
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGGIEGPTLRQWLAARAGGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 437:15-18(1998).

EMBL; AJ010294; CAA09068.1;
InterPro; IPR002952; Eggshell.

InterPro; IPR001664; IF.

InterPro; IPR002957; Keratin_I.

InterPro; IPR003489; Ribosomal_S30.
                                                                                                                                                                                                                                                                         STRAIN=BRISTOL N2;
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-99019308; Pubmed-9804163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cephalochordate Branchiostoma.";
                                                                                                    HYPOTHETICAL 32.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01228; EGGSHELL.
PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 16; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=6239;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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October 9, 2002, 08:52:16; Search time 14.6909 Seconds (without alignments) 482.803 Million cell updates/sec OM protein - protein search, using sw model Run on:

224 1 GGGGGIEGPTLRQWLAARAG......GGGGGGGIEGPTLRQWLAARA 41 US-09-422-838C-34 Perfect score:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

562222 seqs, 172994929 residues Searched: 562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SPTREMBL_19:* Database :

sp_vertebrate:*
sp_unclassified:* sp_human:* sp_invertebrate:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_archeap:* sp_rodent:* sp_rvirus:* sp_mammal:* sp_plant:* sp_virus:* sp_fung1:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q9ase5 oryza sativ	Q19476 caenorhabdi	Q91gc9 oryza sativ	Q23062 caenorhabdi	096755 branchiosto	Q9pvg9 coturnix co	024352 silene lati	Q9as28 oryza sativ	097344 sagitta ele	Q943kO oryza sativ	Q91g49 oryza sativ	O35295 mus musculu	Q23347 caenorhabdi	Q9w3e3 drosophila	096853 schistosoma	Q9yhd0 petromyzon
COLUMNICO		ID	Q9ASE5	019476	630160	Q23062	096755	09PVG9								Q9W3E3	096853	09хнр0
		DB	10	S	10	ഹ	Ŋ	13	10	10	വ	10	10	11	വ	Ŋ	ស	13
		Query Match Length DB	529	200	360	374	422	431	187	167	650	253	308	324	265	619	194	377
	æ	Query Match	38.6	37.9	37.3	37.1	36.2	35.7	35.5	35.3	35.3	34.8	34.8	34.8	34.4	34.4	34.2	33.9
		Score	86.5	85	83.5	83	81	80	79.5	79	79	7.8	78	7.8	77	77	76.5	16
		Result No.		5	m	4	ı.	9	, ,	. α	σ	, ,	:-	12	3.	14	15	16

500 AA.

PRT;

· PRELIMINARY;

019476

Q19476 ID Q1

RESULT 2

	-		σ.			076271 mytilus edu	Q9vfm5 drosophila	Q942u6 oryza sativ	Q24348 drosophila			Q22037 caenorhabdi	002402 pinctada fu	Q9c7r3 arabidopsis	Q94hz3 oryza sativ	Q9w323 drosophila	Q942q2 oryza sativ		ω		Q9xhc4 arabidopsis	Q9sdk6 oryza sativ				ന	Q9w218 drosophila	Q9vx65 drosophila	
Q92KQ8	065450	Q9PUD8	09PUD9	024917	9M9N60	076271	09VFM5	094206	024348	95x69	9W1V3	022037	002402	09C7R3	Q94HZ3	Q9W323	094202	620960	024874	09SKZ1	09XHC4	09SDK6	O9NGF6	09VBK9	0960C1	090MH3	09W2T.8	59XA60	
16	10	13	13	5	2	2	'n	10	2	2	2	2	2	10	10	5	0		ın.	10	10	10	_	_	ı,	C	ľ	ı ru)
1610	396	642	687	250	453	904	1024	113	147	308	344	346	738	228	822	277	535	827	236	270	296	439	453	454	455	667	237	173	1
33.9	33.7	33.7	33.7	33.5	33.5	33.5	33.5	33.3	33	33.3	33.3	33.3	33.3	33.0	33.0	32.8	32.8	32.8	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	30.0	32.1	1.1
16	75.5	75.5	75.5	7.5	7.5	7.0	75	74.5	74.5	74.5	74.5	74.5			7.4	73.5	73.5	73.5	7.3	73	73	73	73	73	7.3		7.07	2.3	4
17	18	19	200	2 6	100	3 6	, C	. C	90	27	280	000	200	3.5	3.5	33	3.6		9 6	3.7	, cc	000	0 4	• •	1 0			* v	7

ALIGNMENTS

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Gaps
                                                                                                                                    Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                             Match 38.6%; Score 86.5; DB 10; Length 529; Local Similarity 59.4%; Pred. No. 0.23; Local 19; Conservative 3; Mismatches 7; Indels 3;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Supras astiva nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0456F08.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002901; BAB39414.1;
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR002055; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01593; Amino_oxidase; 1.
SEQUENCE 529 AA; 55981 MW; 0A5DA55CDD076D24 CRC64;
                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
P0456F08.14 PROTEIN.
                          529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                            PRELIMINARY;
                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                             Q9ASE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                          MEDLINE-92155707; PubMed-1740329;
Ghanshani S., Pak M., McPherson J.D., Strong M., Dethlefs B.,
Wasmuth J.J., Salkoff L.A., Gutman G.A., Chandy G.K.;
"Genomic organization, nucleotide sequence, and cellular distribution of a Shaw-related potassium channel gene, Kv3.3, and mapping of Kv3.3 and Mapping of Kv3.3
                                                                                                                    MEDLINE-94132879; PUDNEd-8301351;
GOldman-Wohl D.S., Chan E., Baird D., Heintz N.;
"Kv3.3b: a novel Shaw type potassium channel expressed in terminally
differentiated cerebellar Purkinje cells and deep cerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVERY THIRD POSITION.
-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
                                                Mus musculus (Mouse).
EuKaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
15-DEC-1998 (Rel. 37, Last annotation update)
Voltage-gated potassium channel protein Kv3.3 (KSHIIID).
                                                                                                                                                                                                                                               SEQUENCE OF 78-769 FROM N.A. (ISOFORM KV3.3A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000210; BTB_POZ.
InterPro; IPR000636; Cation_chan_non_lig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001622; Channel_pore_K.
Interpro; IPR001301; K_channel.
Interpro; IPR001311; K_tetra.
Interpro; IPR003968; Kv_channel.
Interpro; IPR003968; Kv_channel.
Pfam; PF00520; ion_trans; 1.
Pfam; PF002214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60796; CAA43209.1; -
EMBL; X60797; CAA43209.1; JOINED.
                                                                                                                                                                                                                   Neurosci. 14:511-522(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S69381; AAC60679.1; -.
                                                                                                                                                                                                                                                                                                                                                                       Genomics 12:190-196(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:96669; Kcnc3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPARTMENTS.
                                                                                                                                                                                                                                                                  STRAIN=AKR/J;
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PRINTS: FRALE-C.
SMART; SM00225; BTB: 1.
Ionic channel, Transmembrane; Ion transport; Voltage-gated channel;
Glycoprotein; Multigene family; Alternative splicing; PhosphoryLation.
DOMAIN 1 290 CYTOPLASMIC (POTENTIAL).
SECMENT 3 (POTENTIAL).
                                                                                                                                                                                                                                                                POLY-PRO.
POLY-ALA.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
VDPRPWGDPAAAALAHEDCPAIDOPAMSPEDKSPITPGSRG
                                                                                                                                                                                                                                                                                                                                              SLRLAPLATPPGSPRATRRAPPTLBSIL -> GEAGARIGG
VGRSGGKVAGLEGMGGGFLGSGRVGWEATADRRDKNLEGW
TPGTKSHRNKIPRTRACEHGFQPGCSQRPLVRSSRVRIFGE
                                                                                                                                                                                                                                                                                                                                  RYSRDRACFLVTDYAPSPDGSIRKGYEKSRSLSSIVGLSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 769;
                                                                                                                                                                                                                                                                                                                                                                                RDSETQV (IN ISOFORM KV3.3A).
6 -> D (IN REF. 2).
GGGGGG -> ARAGGA (IN REF. 2).
BCACD5AB2D66D9EC CRC64;
                                                                                                                                      EXTRACELLULAR (FOTENTIAL)
SEGMENT 34 (POTENTIAL)
CYTOPLASMIC (FOTENTIAL)
SEGMENT S5 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches 13; Indels
                                                                                           EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S3 (POTENTIAL).
                                                                                                                                                                                                SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 GGGGLDGAGGELKRLCFQDAGGGAGGLPGGAGGAGGTWWRRW 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGGGIEGP--TLRQWLAARAGGG-----GGGGGGIEGPTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68.5;
Pred. No. 9.
                                                                                                                                                                                                                                POLY-GLY.
POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                       POLY-GLN.
            PR01491; KVCHANNEL.
PR01498; SHAWCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                82116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%;
40.5%;
PRINTS; PR00169; KCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 40.59 hes 17; Conservative
                                                                                           350
370
379
3398
4411
447
469
769
769
                                                                                                                                                                                                                                                                                                                                                                                                               769 AA;
                                                                                                                                                                                  470
518
540
                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                           CARBOHYD
VARSPLIC
                                                                                                                          PRANSMEM
                                                                                                                                                 TRANSMEM
                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                        PRINTS;
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Search completed: October 9, 2002, 09:00:22 Job time : 6.98029 secs

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Lee J.E., Garbutt J.H., Phillips K.L., Roses A.D.;
"A human chromosome 19 shaw type potassium channel gene.";
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLITAGE-DEPENDENT POTASSIUM
CONFORMATIONS IN RESPONSE TO THE VOLITAGE DEFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
MHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
                                                                                                                                                                                                                                                                                          COMPARTMENTS.
-!- SIMILARITY: THIS CHANNEL PROFEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
                                                                                                                                                                                                                             EVERY THIRD POSITION.

1. DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0169; KCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01498; SIAMCHANNEL.
SWART; SM00225; BTB: 1
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                             HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
-: SUBCELLULAR LOCATION: Integral membrane protein.
-: DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                   SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEGMENT S3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SEGMENT S4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEGMENT S5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266F6B2BB2AC5A52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IODIC CHANNEL, ILLUMENCALONIO, Phosphorylation.
Glycoprotein; Multigene family; Phosphorylation.
DOMAIN 290 CYTOPLASMIC (POTENTIAL).
SEGMENT S1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000636; Cation_chan_non_lig.
Interpro; IPR001622; Channel_pore_K.
Interpro; IPR003091; K_channel.
Interpro; IPR003131; K_tetra.
Interpro; IPR003968; Kv_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY - GLY .
POLY - PRO .
POLY - PRO .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF055989; AAC24118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00520; ion_trans; 2. Pfam; PF02214; K_tetra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 211585; CAA77671.1; -. HSSP; Q63734; 12TN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000210; BTB_POZ.
InterPro; IPR000636; Cation_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483
757 AA;
                                                                                                                                                 GRADIENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 176264;
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                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
-!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Kim Y.-C., Koo H.-S.; "CDNA cloning and overexpression of Caenorhabditis elegans DNA topoisomerase III.";
                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA CLEÁVAGE (BY SIMILARITY).
3D862412D72946BD CRC64;
30.6%; Score 68.5; DB 1; Length 757;
40.5%; Pred. No. 9.2;
tive 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                   231 GGGCLDGAGGELKRLCFQDAGGGAGGPPGGAGGAGGTWWRRW 272
                                                                   2 GGGGIEGP--TLRQWLAARAGGG-----GGGGGIEGPTLRQW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.5; DB 1;
Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; pr01131; Topoisom_bac; 1.
pfam; pr01751; Toprim; 1.
pr1NTS; PR00417; PRTPISMRASEI.
SWART; SW00437; TOP1AC; 1.
SWART; SW00436; TOP1BC; 1.
SWART; PS00396; TOPRIM; 1.
PROSITE; PS00396; TOPRIM; 1.
PROSITE; PS00396; TOPRIM; 1.
PROSITE; PS00396; TOPRIM; 1.
PROSITE; PROSIDSOMERASE_L_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIKE_MOUSE STANDARD: PRT: 769 AA. 063959; 065088; 15-101-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA topoisomerase III (EC 5.99.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51,6%; Pred. No. -
                                                                                                                                                                                           759 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619 GCPGGGGGP-----PRGPGGGGGGFTGP 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF057032; AAC13567.1; -. TP_bind.
InterPro; IPR003601; DNAtopI_DNA_bind.
InterPro; IPR0003602; DNAtopI_DNA_bind.
InterPro; IPR000380; Pro_topolsomerase.
InterPro; IPR002936; Toprim.
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 759 AA; 85438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                              Best Local Similarity 40.5
Matches 17; Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
                                                                                                                                                                                              TOP3_CAEEL
061660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                Query Match
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                                                                                                                                                                                  TOP3_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-895(1988).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
-!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                                                                                       Gaps
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88087214; PubMed-2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
"Characterization of two allelic forms of Neurospora crassa laccase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted (Potential).

-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                             DB 1; Length 619;
                                                                                                       COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ) (PC
FDED6D78B65048E3 CRC64;
                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
                                                                       PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                               5 GIEGPTL-----RQWLAARAGGGGGGGGGIEGPTLRQ-W 36
                                                                                                                                                                                                                                                                                                                                                                                              26 GTEGVNLLTPVDKRQDSQAERYGGGGGGCNSPTNRQCW 64
                                                                                                                                                                                                                                                                                                                                                        7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 619 AA.
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Score 68.5;
                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                  68198 MW;
                                                                                                                                                                                                                                                                                                                                        30.6%;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
             Glycoprotein; Repeat
                                                                                                                                                                                                                                                                                                               619 AA;
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAC2_NEUCR
                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                   DOMAIN
DOMAIN
                                   PROPEP
                                                        PROPEP
                         SIGNAL
                                                                                           DOMAIN
                                                                                                                         METAL
                                                                                                                                                            METAL
                                                                                                                 METAL
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                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                           Pfam; PF00394; Cu-oxidase; 3. PROSITE: PS0079; MULTICOPPER_OXIDASE1; 1. PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1. Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation; SIGNAL. 1. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                    COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
N-LINKED (GLONAC...) (POTERTIAL).
N-LINKED) (GLONAC...) (POTERTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. ) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68.5; DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-gated potassium channel protein Kv3.3 (KSHIIID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Kv3.3 potassium channels in lens epithelium and corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBB6CCDE18841145 CRC64;
                                                                                                                                                                                                                                                                                                                                 PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GIEGPTL-----RQWLAARAGGGGGGGGGEGPTLRQ-W 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GTEGVNLLTPVDKRQDSQAERYGGGGGGCNSPTNRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                    InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; Multicu_oxidse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Lens epithellum;
MEDLINE=20179629; PubMed=10712820;
Rae J.L., Shepard A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exp. Eye Res. 70:339-348(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68120 MW;
                                                                                         EMBL; M18334; AAA33592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 291-651 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444
619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query ...
Best Local Similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIKF_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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InterPro;
                                                                                                                                                                                               LAC1_NEUCR
P06811;
                                                       SEQUENCE
DOMAIN
DOMAIN
                                DOMAIN
DOMAIN
                      DOMAIN
                                                                                                                                                                                      LAC1_NEUCR
                                                                                                  Matches
                                                                                                                                                                          RESULT 26
                                                                                                                                                                                                            FT
FT
FT
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               the X chromosome.";

Genomics 29:471-477(1995).

-i- FUNCTION: POSSIBLE REGULATOR OF LYMPHOCYTE AND PLATELET FUNCTION

-i- FUNCTION: POSSIBLE REGULATOR OF LYMPHOCYTE AND PLATELET FUNCTION

MAY BE INVOLVED IN SIGNALING PATHWAYS WITH CYTOSKELETAL FUNCTION

(BY SIMILARITY).
                                                            7; Gaps
                                                                                                                                                                                                                                                                                                                          Derry J.M.J., Wiedemann P., Blair P., Wang Y., Kerns J.A.,
Lemahieu V., Godfrey V.L., Wilkinson J.E., Francke U.;
"The mouse homolog of the Wiskott-Aldrich syndrome protein (WASP)
gene is highly conserved and maps near the scurfy (sf) mutation on
                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musia
                                                                                                                                                                                                                                                                                                                                                                                                                          -i- DOMAIN: THE WHÎ (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH
                                      Score 68.5; DB 1; Length 369;
Pred. No. 5;
                                                             6; Indels
                  288E464708DA6C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRSGPLPPXP MOTIF 1. GRSGPLPPXP MOTIF 2.
                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Wiskott-Aldrich syndrome protein homolog (WASP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000095; PAK_box_P21_Rho_bindng.
Interpro; IPR000697; RanBP1_WASP.
Interpro; IPR001960; WH1.
Interpro; IPR003124; WH2.
          LEUCINE-ZIPPER.
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -: SIMILARITY: CONTAINS 1 GBD DOMAIN.
                                                                                                         215 GAGGG--GPA----SAGGGGGGGGGGTAG 237
                                                                                    1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C;
MEDLINE=96115600; PubMed=8666397;
           312 333 E. 369 AA; 38457 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U54788; AAC52556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02205; WH2; I.
SMART; SM00265; PBD; I.
SMART; SM00461; WH1; I.
SMART; SM00246; WH2; I.
PROSITE; PS50108; GBD; I.
                                            30.6%;
53.3%;
                                                        Best Local Similarity 53.33
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00786; PBD; 1.
Pfam; PF00568; WH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
2559
363
402
1167
3321
341
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:105059; Was.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                   WAS OR WASP.
                                                                                                                                                                    WASP_MOUSE
                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                               Query Match
                                                                                                                                                RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
-1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Crarecterization of two allelic forms of Neurospora crassa laccase. Amino- and carboxyl terminal processing of a precursor."; J. Biol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germann U.A., Lerch K.; "Isolation and partial nucleotide sequence of the laccase gene from "Isolation and partial nucleotide sequence homology of the protein to Neurospora crassa: amino acid sequence
                                                                                                                                                                                                                              Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:-CONTROL BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERE KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

-:-SUBCELLULAR LOCATION: Secreted (Potential).

-:-SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

-:-SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                            Score 68.5; DB 1; Length 520;
                                                                                                                         9C223733C59F0C8A CRC64;
                                                                                               ASP/GLU-RICH (ACIDIC)
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                                                                                                                                                                                                                                                                                                                                                  325 GGGGG------GGGGGGGGGGGPLR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 AA
                                                                                                                                                                                                               No. 6.7;
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                             1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=88087214; PubMed=2961749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                    POLY-PRO.
POLY-PRO.
                                                                             POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 379-619 FROM N.A. MEDLINE=87067412; PubMed=2947240;
                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M14554; AAA33590.1; -. EMBL; M18333; AAA33591.1; -.
                                                                                                                                     54191 MW;
                                                                                                                                                                                              30.68;
                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A28523; KSNCLO.
PIR; A29762; A29762.
379
390
403
424
520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human ceruloplasmin.
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                        520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5141;
                                                                                   408
503
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Hederson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Addrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Bornes P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA BOrkova D., Detchan M.R., Bouch J., Envisten D., Bolshakov S.,
RA BORKOVA D., Detchan M.R., Bouch J., Envisten P., Brottier P.,
RA Burtis K.C., Busam D.A., Burller H., Cadieu E., Center A., Chandra I.,
RA George R., Doug L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Davies P.,
RA Horbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C.,
RA Hostin D., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Hostin D., Houston K.A., Havyey D., Heiman T.J., Herrandez J.R., Hookey B.C.,
A Julai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Julai M., Matles B., Kaft C., Meritz S., Kalp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
A Huu X., Mattel B., Molintoh T.G., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Blazzolo M., Pittman G.S., Pan S., Pollard J., Walsserbed T.W.,
Shine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shire E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Hang Z.-Y. Wassarman D.A., Weinstoner E., Wang A.H., Wang Y.,
RA Hilams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zhao Q., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-free European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - FUNCTION: WEAKLY RELAXES NEGATIVE SUPERCOILS AND DISPLAYS A DISTINCT PREFERENCE FOR BINDING SINGLE-STRANDED DNA.
- CATALYTIC ACTIVITY: AFP-independent breakage of single-stranded DNA, followed by passage and rejoining.
- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME IS JOINED TO A DNA PHOSPHORUS.
- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                           Plank J.L., Reineke J.C., Wilson T.M., Hsieh T.-S., "Drosophila melanogaster topoisomerase III alpha."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0040268; Top3-alpha.
InterPro; IPR003601; DNAtopI_ATP_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF255733; AAF71288.1; -.
EMBL; AE003663; AAF53813.1; ALT_SEQ.
                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakai M., Imaki J., Yoshida K., Ogata A., Matsushima-Hibaya Y.,
Kuboki Y., Nishizawa M., Nishi S.;
"Rat maf related genes: specific expression in chondrocytes, lens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proto-oncogene; Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 69; DB 1; Length 1250;
                                                                                                                                                                                                                                                                                                                                                                           356 356 DNA CLEAVAGE (BY SIMILARITY).
1250 AA; 136137 MW; 28809F770B3DB75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 14:745-750(1997).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor MAF2 (Proto-oncogene C-MAF).
                                       InterPro; Irrovosco; Irolandericase.
InterPro; Irroposcom, Irroposcom; Irr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 780 GGGGSGRGAGSGGWSSGPGGGGGGGGGG 809
                              InterPro; IPR000380; Pro_topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
  InterPro; IPR003602; DNAtopI_DNA_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97190228; PubMed=9038383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U56242; AAB50063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03131; bZIP_Maf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.73
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P05412; 1JUN.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00338; BRLZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spinal cord.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAF2 OR MAF
                                                                                                                                                                                                                                                                                                                                                                                                  SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAF2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P54844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 24
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BASIC MOTIF.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES.
-:- DEVELOPMENTAL STAGE: ABUNDANT IN EMBRYOS YOUNGER THAN 50% OF EMBRYONIC DEVELOPMENT.
-:- SIMILARITY: BELONGS TO THE A/B GROUP OF HNRNP, WHICH ARE BASIC AND GLY-RICH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91195067; Pubmed-1901646;
Ball E.E., Rehm E.J., Goodman C.S.;
"Cloning of a grasshopper coding for a protein homologous to the Al, A2/B1 proteins of mammalian hnRNP.";
Nucleic Acids Res. 19:397-397(1991).
       Oncogene; Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Schistocerca.
                                                                                                                                       Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69; DB 1; Length 342; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                  01-WAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heterogeneous nuclear ribonucleoprotein A1, A2/B1 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pram., Pram., Pram., Pram., Pram., Pram., Pram., Prosite; Ps50102; RRM; 2. PROSITE; Ps00030; RRM_RNP_1; 2. PROSITE; Ps00030; RRM_RNP_1; 2. In Protein; RnA-binding; Ribonucleoprotein; Repeat. 1 1 193 RNA-BINDING (RRM) 1. In RNA-BINDING (RRM) 2. In RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                 8: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35404 MW; F8426A21C8125DD8 CRC64;
                                                                                                              F386B220ACE50FF6 CRC64;
                                                                                                                                         DB 1;
                                                                                                                                                                                                       1 GGGGGIEG------PTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                      Schistocerca americana (American grasshopper).
                                                                                                   LEUCINE-ZIPPER
                                                                                                                                                                 2; Mismatches
                                                                                                                                         Score 69.5;
                                                                                      BASIC MOTIF.
                                                                                                                                                      Pred. No.
                         POLY-ALA
                                  HIS-RICH
                                                          POLY-GLY
                                                 POLY-GLY
                                                                          POLY-GLY
                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                               38892 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X54670; CAA38481.1; -.
                                                                                                                                         31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S13513; S13513.
PIR; S14432; S14432.
HSSP; P09651; 1UP1.
InterPro; IPR000504; RRM.
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00076; rrm; 2.
SMART; SM00360; RRM; 2.
                                                                         240
300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 AA;
                                                                                                              369 AA;
                                                                                                                                                     Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7009;
                                               184
                                                                                                                                                                                                                                                                              ROA1_SCHAM
P21522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                       DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                 SEQUENCE
                                                                                                                                           Query Match
                                                              DOMAIN
                                      DOMAIN
                                                   DOMAIN
                                                                                                                                                                                                                                                                      ROA1_SCHAM
                                                                                                                                                                                                                                                         RESULT 21
                                                                                                                                                                                                                                                                                               g
  NKW
KW
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ή
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                     Petunia hybrida (Petunia).
Rukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TP3A_DROME STANDARD; PRT; 1250 AA.
09NG98; 09VIV1;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA topoisomerase III alpha (EC 5.99.1.2).
TOP3-ALPHA OR CG10123.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%; Score 69; DB 1; Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLY-RICH.
C8541C549417D18C CRC64;
                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MG-1992 (Rel. 23, Last annotation update)
01-AVG-1992 (Rel. 23, Last annotation update)
01-AVG-1992 (Rel. wall structural protein 1 precursor.
  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell wall; Structural protein; Repeat; Signal.
                                                                                                                                                                                        384 AA
                                                                                 223 GGGGGWGGAD--PWENGRGGGGDRWGGGGGGMGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
      1; Mismatches
                                          1 GGGGGIEGPTLRQWLAARAGG----GGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X04335; CAA27866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.85
Best Local Similarity 46.75
Matches 14; Conservative
      Matches 17; Conservative
                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A26099; A26099.
HSSP; P30129; 4DPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4102;
                                                                                                                                                                                        GRP1_PETHY P09789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP3A_DROME
                                                                                                                                                                         GRP1_PETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
                                                                                                                                                   RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC
DT
DT
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DT
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPROTEIN.
                                                                                                              EMBL; X62636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMAF_AVIS4 P23091;
                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              TMAF_AVIS4
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEIC ACIDS RES. 19:4909-4914(1991).

-I'FUNCTION: THIS PROTEIN IS A COMFONENT OF RIBONUCLEOSOMES. COULD BE NEEDED TO ORGANIZE A CONFENTRATION GRADIENT OF A DORSALIZING MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.

-I'S SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.

-I SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=OREGON-R, AND CANTON-S; TISSUE-Ovary;
MEDLINE-91187645; PubMed-1849257;
Haynes S.R., Johnson D., Raychaudhuri G., Beyer A.L.;
"The Drosophila Hrb87F gene encodes a new member of the A and B hnRNP
                                                                                                     MISSING (IN ISOFORM SHOX2B).
E -> EGRRKPTKAEVQATLLLPGEAFRFL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CANTON-S; TISSUE-Embryo; MEDLINE-92020124; PubMed-L717937; Hovemann B.T., Dessen E., Mechler H., Mack E.; "Drosophila snRNP associated protein P11 which specifically binds to heat shock puff 93D reveals strong homology with hnRNP core protein
                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Heterogeneous nuclear ribonucleoprotein 87F (HRP36.1 protein) (P11
                                                                                                                                                                                                                                          10;
                                     Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matunis E.L., Matunis M.J., Dreyfuss G.; "Characterization of the major hnRNP proteins from Drosophila
                                                                                                                          2).
E -> D (IN REF. 1; CAA05341).
P -> S (IN REF. 2).
D -> N (IN REF. 2 AND 3).
H -> L (IN REF. 3; AAC39663).
MW; 55431B073B3B2250 CRC64;
                                                                                                                                                                                                                Score 70; DB 1; Length 331;
                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                      386 AA.
                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                            1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEG 30
                                                                   HOMEOBOX.
                                                                                                                                                                                                                                                                                  61 GGGGGGG------GGGGGGGGGVGG 80
                                                                                           POLY-GLY
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein group.";
Nucleic Acids Res. 19:25-31(1991).
PS00027; HOMEOBOX_1; 1. PS50071; HOMEOBOX_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92112968; PubMed=1730754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.";
J. Cell Biol. 116:257-269(1992).
                                                                                                                                                                                       34964 MW;
                                                                                                                                                                                                               31.2%;
50.0%;
                            OAR; 1.
                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                 199
326
86
246
115
                                                      Alternative splicing.
                                                                                                                                                                                     331 AA;
                                                                                                                                                                                                                         Best Local Similarity
                PS50071;
PS50803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  OR HRP36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CANTON-S
                                                                                                                                                                                                                                                                                                                                                  RB87_DROME
                                                                                                                                                                         CONFLICT
     PROSITE;
                                                                 DNA_BIND
                                                                                                    VARSPLIC
                                                                                                                                                             CONFLICT
                                                                                                                CONFLICT
                                                                                                                                   CONFLICT
                                                                                                                                                                                                             Query Match
                            PROSITE
                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                             P48810:
                                                                                                                                                                                                                                                                                                                                    RB87_DROME
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                        RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian musculoaponeurotic fibrosarcoma virus AS42.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DISEASE: INDUCES MUSCULOAPONEUROTIC FIBROSARCOMA IN CHICKENS.
-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                               RNA-BINDING (RRM) 2.
MISSING (IN ISOFORM HRP36.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 1; Length 386;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                  RNA-binding; Nuclear protein; Ribonucleoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 S -> T (IN REF. 3).
2036C04D01E3AFD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                RNA-BINDING (RRM) 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 20, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 GGGGGYGGGNSNGSWGGNGGGGGGGGG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                          115 192 RN7
315 374 MI5
271 271 S
386 AA; 39557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                FlyBase; FBgn0004237; Hrb87F.
                                                                                                                               EMBL; X54803; CAA38574.1; -.
                                                                                                                                                     CAA44502.1; -.
                                                                                                                                                                     EMBL; X59691; CAA42212.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26769; AAA42377.1; -.
                                                                                                                                                                                                                          InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; TO1430; -.
InterPro; IPR001871; bZIP.
Pfam; PF03131; bZIP_Maf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming protein Maf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                        Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B33975; TVFVAF.
                                                                                                                                                                                     HSSP; P09651; 1UP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05412; 1JUN.
TRANSFAC; T01430; -
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                                                                                                                                                                                                                                                                                                   MEDLINE-90215256; PubMed-2576652;
MEDLINE-90215256; PubMed-2576652;
MEDLINE-90215256; PubMed-2576652;
MEDLINE-90215256; PubMed-2576652;
Gaudino G., Stornatiuolo A., Cafiero M., Faiella A., Simeone A.;
Organization of human class I homeobox genes.";
Organization of human class I homeobox genes.";
I- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSTITIONAL DENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
I- SUBCELLULAR LOCATION: Nuclear.
I- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT 5-9 WEEKS FROM CONCEPTION.
I- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Kidd J.R., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V., Kidd J.R., Pakstis A.J.; "Overall linkage disequilibrium in 33 populations for highly informative multisite haplotypes spanning the HOXB gene cluster."; Am. J. Hum. Genet. 67:235-235(2000).
                                                                                                                                                            Giampaolo A., Acampora D., Zappavigna V., Pannese M., D'Esposito M., Care A., Faiella A., Stornaiuolo A., Russo G., Simeone A., Boncinelli E., Peschle C.; "Differential expression of human HOX-2 genes along the anterior-posterior axis in embryonic central nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QL -> HV (IN REF. 2).
941706EDCC2975E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 GGGGGGGG-----GSGGGGGGGGGCKSP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLROWLAARAGGGGGGGGGIEGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred
                                                                                                                                                    MEDLINE=89378558; PubMed=2570724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF287967, AAG31255.1; --
EMBL, X16175, CAA34297.1; --
PIR, S07543; WJHU26.
PIR, D37042; D37042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X16667; CAA34657.1; -. EMBL; U59298; AAD10852.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    illarity 48.4%;
Conservative
                                                                                                                    SEQUENCE OF 188-253 FROM N.A.
                                                                                                                                                                                                                                                                                               SEQUENCE OF 188-253 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; PO2833; 1SAN.
TRANSFAC; T01723; -.
MIM; 142966; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                           TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- ATTERNATURE PRODUCTS: 2 isoforms; 1/SHOX2A/SHOTA (shown here) and 2/SHOX2B/SHOTB/OG12XB; are produced by alternative splicing.
-i- TISSUE SPECIFICITY: Expressed in heart, skeletal muscle, liver, lung, bone marrow fibroblast, pancreas and placenta.
-i- DEVELOPMENTAL STAGE: Expressed during cranofacial development as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i-- FUNCTION: May be a growth regulator and have a role in specifying neural systems involved in processing somatosensory information, as well as in face and body structure formation.
                                                                                                                                                                                                                                                                                                Blaschke R.J., Monaghan A.P., Schiller S., Schechinger B., Rao E., Padilla-Nash H., Ried T., Rappold G.A.; Padilla-Nash H., Ried T., Rappold G.A.; SHOY, a SHOX-related homeobox gene, is implicated in craniofacial, brain, heart, and limb development."; Proc. Natl. Acad. Sci. U.S.A. 95:2406-2411(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Semina E.V., Reiter R.S., Murray J.C.; "A new human homeobox gene OG12X is a member of the most conserved homeobox gene family and is expressed during heart development in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            well as in heart.
             SHX2_HUMAN STANDARD;
PRT; 331 AA.
SHX2_HUMAN STANDARD;
060902; 060902; 060465; 060467;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Short stature homeobox protein 2 (Paired-related homeobox protein SHOT) (Homeobox protein 0912X).
SHOT) (Homeobox protein 0912X).
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 116-331 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ002367; CAA05341.1; ALT_INIT.
EMBL; AJ002368; CAA05342.1; ALT_INIT.
EMBL; BC008829; AAH08829.1; -1.
EMBL; AF022654; AAC39662.1; ALT_INIT.
EMBL; AF023203; AAC39663.1; -1.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Craniofacial;
MEDLINE=98133920; PubMed=9466998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Mol. Genet. 7:415-422(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003654; OAR_domain.
                                                                                                                                                                                                                                                                            TISSUE=Fibroblast;
MEDLINE=98151525; PubMed=9482898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BICOID" SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06601; 1FJL.
                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 602504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSD;
SHX2_HUMAN
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SMART; SM00389; HOX; 1.

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                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC.
DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE
M-DOMAIN BINDS THE 7S RNA IN PRESENCE OF SRP19 AND ALSO BINDS THE
SEQUENCE FROM N.A.
MEDLINE=96144300; PubMed=8566805;
MEDLINE=96144300; PubMed=8566805;
Nucleotide sequence of the Aspergillus niger srpA gene.";
Gene 167:337-338(1995).
I- FUNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROPEIN WHEN THEY EMERGE FROM THE RIBOSOMES AND TRANSFERS THEM TO TRAM (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROPEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-91117256; PubMed-1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Eisenberg M.T.; "The Drosophila suppressor of sable gene encodes a polypeptide with regions similar to those of RNA-binding proteins."; Mol. Cell. Biol. 11:894-905(1991).
                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 71; DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        GTP-binding; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1B21E3A48CCB3BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 GGGGGLPGLGGMDLQSMMSQMSGLMGGGGGGG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGGIEG-----PTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                    G-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 M-DOMAIN.
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InterPro; IPR00125; SRP54.
InterPro; IPR004125; SRP_SPB.
Fram; PR014881; SRP54. 1.
Fram; PR02881; SRP54. 1.
ProDom; PD000819; SRP54. 1.
PROSITE; PS00300; SRP54; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57117 MW;
                                                                                                                                                                                                                                                                                  EMBL; L38317; AAB04946.1; -. HSSP; 007347; 2FFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.79
Best Local Similarity 42.49
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
249
468
493
522
534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUS_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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             1- DEVELOPMENTAL STAGE: AT ALL STAGES.
1- SIMILARITY: HAS REGIONS SIMILAR TO THOSE OF RNA-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thorsteinsdottir U., Hough M.R., Hugo P., Lawrence H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E.,
Morelli F., Stornaluolo A., Nigro V., Simeone A., Boncinelli E.;
"The human HOX gene family";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Largman C., Humphries R.K.;
"Deregulated expression of HoxB3 in hematopoietic cells causes defective development of alpha beta T Lymphocytes and progressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.7%; Score 71; DB 1; Length 1322; 47.1%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLN-RICH (OPA-REPEAT).
RNA-BINDING (BY SIMILARITY).
MW; D5F534EB5702EA08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIGHLY CHARGED DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14651; P17484; O95615; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 01-ARR-2002 (Rel. 14, Last sequence update) HOMEGODOX protein HOX-B3 (HOX-2G) (HOX-2C) (HOX-2C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1149 GGGGDSG-----GGVGGGGGGGVVLPNLSQ 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 17:10385-10402(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90098876; PubMed=2574852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1322 AA; 143555 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         Flybase; FBgn0003575; su(s).
InterPro; IPR000571; zf-CCCH.
Pfam. PF00642; zf-CCCH; 2.
RNA-binding; Nuclear protein.
DOMAIN 138 327
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M57889; AAA28920.1; -. EMBL; X59364; CAA42010.1; -.
SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.19
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474
1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A39612; A39612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sauvageau G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HXB3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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DT DT DT OC OC OC OC OC OC OC OC
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RA Adams M.D., Celniker S.E., Hill R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hill P.W., Hoskins R.A., Galle R.F.,
RA Struck G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.B.,
RA Struck G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pefeiffer B.D.,
RA Bank K.H., Doyle C., Baxter E.G., Helf G., Nelson C.K., Miklos G.L.G.,
RA Ballew R.M. Basu A. Baxendale J., Baytakarogiu L., Beasley E.M.,
RA Beson K.Y. Benos P.V., Berman B.P., Bhandari D., Botshakov S.
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothafter P.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchafter P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothafter P.,
RA Borkova D., Botchan M.R., Doug L.E., Owneport L.B., Davies P.,
RA Borson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Celbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Celbart W.M., Glasser K.,
RA Hostin D., Harkop D., Heiman T.J., Hernandez J.R., Beuck J.,
RA Hostin D., Harkop D., Heiman T.J., Hernandez J.R., Beuck J.,
RA Hostin D., Harkop D., Heiman T.J., Hernandez J.R., Beuck J.,
RA Kimmel B.E., Rodire C.D., Kraft C., McLendor S., Dinny D., Lai Z.,
RA Kimmel B.E., Rodire C.D., Kraft C., McLendor S., Liang Y., Lin X.,
RA Hoston D.W., Pituma G.S., Pollard J., Murph L., Murph D., Lai Z.,
RA Hoston D.W., Murphy B., Murph L., Murph S., McCheeler F., Shen H.,
RA Relson D.W., Murphy B., Murph C., Scheeler F., Shen H.,
RA Relson D., Weller B., Wenter E., Wang X.,
RA Relson D., Weller E., Standers R.D., Purl V., Wang X.,
RA Relson D., Weller R., Venter E., Wang S., Yao Q.A.,
RA Relson D., Weller R., Venter E., Wang S., Yao Q.A.,
RA Relson R.A., Myers E.W., Weller R., Venter E., Stand S., Shen S., How B.C., Stand M., Pitum G. C., Stand M., Stung G., Shen S., Shen S., Shen S., Shen S., Shen S., Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBCELLULAR LOCATION: Nuclear.
-:- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 AND 2 (SHOWN HERE);
MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: UBIQUITOUS, ENRICHED IN THE BRAIN AND CENTRAL
NERVOUS SYSTEM DURING EMBRYOGENESIS. ENRICHED IN THE ADULT HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haynes S.R., Rebbert M.L., Mozer B.A., Forquignon F., Dawid I.B.; "Pen repeat sequences are GGN clusters and encode a glycine-rich domain in a Drosophila cDNA homologous to the rat helix destabilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 84:1819-1823(1987).
-1- FUNCTION: MAY PARTICIPATE IN A FUNCTION COMMON TO THE EXPRESSION
OF MOST GENES TRANSCRIBED BY RNA POLYMERASE II.
                                                                                              Stolow D.T., Haynes S.R.; "Cabeza, a Drosophila gene encoding a novel RNA binding protein, cabeza, a Drosophila gene encoding a novel shares homology with EWS and TLS, two genes involved in human sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      Nucleic Acids Res. 23:835-843(1995).
          Mol. Cell. Biol. 15:4562-4571(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87175568; PubMed-3031652;
                                                                 STRAIN-CANTON-S;
MEDLINE-95223793; PubMed-7708500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 212-261 FROM N.A.
                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 39-404 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-OREGON-R;
Haynes S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=OREGON-R.
                                                                                                                                                                                                                STRAIN-BERKELEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
EMBRYOS CONTAIN BOTH TYPE 1 AND TYPE 2 ISOFORMS, WHEREAS LATER IN DEFELOPMENT (HEADS AND TORSOS) ONLY THE TYPE 2 ISOFORM IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
                                                                               -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING EMBRYO FROM THE EARLIEST STAGES OF CELLULARIZATION AND IS SUBSEQUENTLY FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGGPMRNDGG -> MVDQEKRWS (IN REF. 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                       -:- MISCELLANEOUS: 'CABEZA' MEANS 'HEAD' IN SPANISH.
-:- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
-:- SIMILARITY: CONTAINS 1 RANBP2-TYPE ZINC FINGER.
-:- SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENART; SM00360; RRM; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; 1.
PROSITE; PS01030; RRM; 1.
PROSITE; PS01935; ZE_RANBP2_1; 1.
PROSITE; PS0199; ZE_RANBP2_2; 1.
Nuclear protein; Zinc-finger; Metal-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7062A0446BEA5984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM 1).
PNY -> LFI (IN REF. 4).
p -> H (IN REF. 3).
G -> GG (IN REF. 3).
MISSING (IN REF. 3).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Signal recognition particle 54 kDa protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-BINDING (RRM). GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANBP2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLY-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GGGGGGGG---RGGFGGRRGGGGGGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, L37083; AAC41563.1; --
EMBL, AE003501; AAF48578.1; --
EMBL; M15765; AAA70425.1; --
FlyBase; FBGn0011571; Caz.
InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-RanBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U13178; AAA86955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00076; rrm; 1.
PF00641; zf-RanBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.3%
Matches 16; Conservative
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283
283
389
3404 AA;
                                                                                                                                                  MANY CELL TYPES.
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              DOR NO DO
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                                                                                                                                                                                                                                                                       S -> L (IN REF. 3).
GAYGTPIMQGSPVIVGGGGY -> APTGRPPCRAVRCMWAG
                                                                                                                                  G -> C (IN REF. 1).
A -> S (IN REF. 1).
GCGGGGGGGGGGGG -> RLWWWRPAVVAAAAAVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
-i- SUBCELLULAR LOCATION: Nuclear (Poctential).
-i- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN THE EGG, BUT IS RAPIDIX LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=OREGON-R;
MEDLINE=91293102; PubMed=1712294;
MEDLINE=91293102; PubMed=1712294;

MEVEL-INIO.M.T.M., Terracol R., Kafatos F.C.;

"The ovo gene of Drosophila encodes a zinc finger protein required for female germ line development.";

EMBO J. 10:2259-2266(1991).
  HOMEOBOX_2; 1.
ling; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                 VAT (IN REF. 3).
9AD3C922663612A6 CRC64;
                                                                       ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                    (IN REF. 3).
D -> N (IN REF. 4).
LC -> FV (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OVO_DROME STANDARD; PRT; 1028 AA. P51521; 09XZU4; 10.CGT-1996 (Rel. 34, Last sequence update) 10-CGT-1996 (Rel. 34, Last sequence update) 16-CGT-2001 (Rel. 40, Last annotation update) OVO protein (Shaven baby protein).
                                                                                                                                                                                                                                                                                                                                                                 Score 72; DB 1;
NO. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 GGGGSSG------GGGGGGGGGDKSP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGP 31
                                                                                            GLY-RICH.
                                                                                                                 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95021209; PubMed=7935398;
                                                                                                                                                                                                                                                                                                                                       433 AA; 44353 MW;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.1%;
Best Local Similarity 48.4%;
Matches 15; Conservative 1
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                                             ranscription regulation.
PROSITE; PS50071; HOMEC
Homeobox; DNA-binding;
                                                                                          181
250
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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CONFLICT
CONFLICT
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Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota: Neotera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immanuel D., Zinszner H., Ron D.; "Association of SARFH (sarcoma-associated RNA-binding fly homolog) with regions of chromatin transcribed by RNA polymerase II.";
                                                                                                            PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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027294; 024445; 09VX14;
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
NNA-Linding protein cabeza (Sarcoma-associated RNA-binding fly homolog) (P19).
CAZ OR SARFH OR CG3606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72; DB 1; Length 1028; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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; D7068BBZBC0F6F77 CRC64;
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POLY-GLN.
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POLY-GLN.
POLY-GLN.
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POLY-SER.
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POLY-GLN.
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                                                                                                                                                                                                                                                       POLY-HIS
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                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
EMBL; X59772; CAB36921.1; ALT_SEQ.
HSSP; P25490; 12NM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95349623; PubMed=7623847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110620 MW;
                                FlyBase; FBgn0003028; ovo.
InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; zf-C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.1%;
55.2%;
                                                                                 PRINTS; PR00048; ZINCFINGER.
                                                                                                SMART; SM00355; ZnF_C2H2; 4
                                                                                                                                                                     regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                   Pranscription
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HXB3_MOUSE
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                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
                                                                                                                                   "The crystal structure of calcium-free human m-calpain suggests an electrostatic switch mechanism for activation by calcium."; proc. Natl. Acad. Sci. U.S.A. 97:588-592(2000).

-i-FUNCTION: Calcium-regulated non-lysosomal thiol-procease which
                                                                 X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=20105516; PubMed=10639123;
Strobl S., Fernandez-Catalan C., Braun M., Huber R., Masumoto H.,
Nakagawa K., Irie A., Sorimachi H., Bourenkow G., Bartunik H.,
Suzuki K., Bode W.
                                                                                                                                                                                                                                2;
                                                                                                                                                                                       catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.1%; Score 72; DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                        Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17B87A8E47A90632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLY-RICH (HYDROPHOBIC). CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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EF-HAND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 3.
PROSITE; PS00018; EF HAND; 2.
Calcium-binding; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M31505; AAA35646.1; JOINED.
M31506; AAA35646.1; JOINED.
M31508; AAA35646.1; JOINED.
M31508; AAA35646.1; JOINED.
M31510; AAA35646.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                     M31511; AAA35646.1; ..
M31502; AAA35646.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                               M31503; AAA35646.1; JOINED. M31504; AAA35646.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 AA; 28316 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC007779; AAH07779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X04106; CAA27726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                  TISSUE-Skin, and Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A23650; CIHUL
        SEQUENCE FROM N.A
                                 Strausberg R
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CA_BIND
CA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila Deformed gene.";
Genes Dev. 2:1424-1438(1998)
-i- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
-i- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WITH
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
-i- SUBCELLULAR LOCATION: Nuclear:
-i- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with differential distributions in the nervous system and the potential for shared regulatory regions."; EMBO J. 11:1825-1836(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of a murine homeo box gene, Hox-2.6, related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown W.M., Taylor G.R.;
"The 5'-sequence of the murine Hox-b3 (Hox-2.7) gene and its intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graham A., Papalopulu N., Lorimer J., McVey J.H., Tuddenham E.G.D.,
Krumlauf R.;
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 152-361 FROM N.A.
MEDLINE-88054465; PubMed-2890503;
Lonai P., Arman E., Czosnek H., Fuddle F.H., Blatt C.;
Lonai P., Arman E., Czosnek H., chromosomal assignment, and differential expression in adult erythropolesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92258392; PubMed=1582411;
Sham M.H., Hunt P., Nonchev S., Papalopulu N., Graham A.,
Boncinelli E., Krumlauf R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contain multiple transcription-regulatory elements.";
Int. J. Biochem. 26:1403-1409(1994).
HXB3 MOUSE STANDARD; PRT; 433 AA. p09026; P10285; Q61680; 01-NOY-1988 (Rel. 09, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) HOXB3 OR HOXB-3 OR HOX-2.7; (MH-23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 181-265 FROM N.A. MEDLINE-89091992; PubMed=2463210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X66177; CAA46951.1; -. EMBL; U02278; AAB60496.1; -. EMBL; M18168; AAA37840.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:96184; Hoxb3.
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PIR; C29585; C29585.
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                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protease, small subunit (Calpain regulatory subunit)
(Calcium-activated neutral proteinase) (CANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86250903; PubMed=3013892; Emori Y., Kawasaki H., Imajoh S., Kawashima S., Suzuki K.; "Isolation and sequence analysis of cDNA clones for the small subunit of rabbit calcium-dependent protease."; J. Biol. Chem. 261:9472-9476(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                    GLY-RICH (HYDROPHOBIC).
CALCIUM-BINDING.
BF-HAND 1 (POTENTIAL).
FF-HAND 2 (POTENTIAL).
ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CANP) can bind Ca2+ ions.";
J. Biochem. 101:889-895(1987).
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (regulatory) subunit.
-!- SUBCELDILAR LOCATION: Oytoplasmic; Translocates to the plasma
membrane upon Ca++ binding (By similarity).
-!- PTM: The N-terminus is blocked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-67279982; PubMed=3038855;
Minami Y., Emori Y., Kawasaki H., Suzuki K.;
"E-F hand structure-domain of calcium-activated neutral protease
                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 1; Length 266;
Pred. No. 1.8:
                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                               3FA81023EDC4141A CRC64;
                                                                                                                                                                                                         Calcium-binding; Repeat; Acetylation; 3D-structure. MOD_RES 1 1 ACETYLATION.
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POLY-GLY.
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                                                                                                                                    PDB; 1ALV; 03-JUN-98.
PDB; 1ALW; 10-JUN-98.
InterPro; 1PR002048; EF-hand.
PEAM; PF00036; efhand; 3.
PROSITE; PS00018; EF_HAND; 2.
                                                                                             EMBL; M11778; AAA31010.1; -.
EMBL; M11779; AAA31011.1; -.
PIR; A25166; CIPGL.
                                                                                                                                                                                                                                                                                                                                                                                         32.1%;
55.2%;
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                                                                                                                                                                                                                                                                                                                                                               266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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01-MAR-2002 (Rel. 41, Last annotation update)
Calcium-dependent protease, small subunit (Calpain regulatory subunit)
(Calcium-activated neutral proteinase) (CANP).
CAPNA OR CAPNSI OR CAPNS.
HOMO sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF-HAND 1 (POTENTIAL).
BF-HAND 2 (POTENTIAL).
BC-STRAL CALCIUM SITE 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K., Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O., Carrano A.V.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 1; Length 266;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLY-RICH (HYDROPHOBIC).
CALCIUM-BINDING.
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Nucleic Acids Res. 14:8805-8817(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium-dependent protease.";
Nucleic Acids Res. 14:5559-5559(1986).
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MEDLINE=87066759; PubMed=3024120;
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161
161
191
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PC
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HSSP; P04632; 1DKV.
InterPro; IPR002048; EF-hand.
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PROSITE; PS00018; EF_HAND; 2.
Calcium-binding; Repeat.
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180
215
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0AN-1990 (Rel. 13, Created)
01-0AN-1990 (Rel. 13, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
Calcium-dependent protease, small subunit (Calpain regulatory subunit).
(Calcium-activated neutral proteinase) (CANP).
                                                                                                                                                                                                                                                                                                                                                            ADULT-SPECIFIC CUTICULAR PROTEIN ACP-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McClelland P., Lash J.A., Hathaway D.R.; "Identification of major autolytic cleavage sites in the regulatory subunit of vascular calpain II. A comparison of partial amino-terminal sequences to deduced sequence from complementary
DETERMINING THE PHYSICAL PROPERTIES OF CUTICLES.
-!- TISSUE SPECIFICITY: EPIDERMAL REGIONS SYNTHESIZING HARD CUTICLE.
-!- DEVELOPMENTAL STAGE: PREECDYSIAL ADULT CUTICLE DEPOSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Calcium regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane upon Ca++ binding (By similarity).
-!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 1; Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> Y (IN REF. 2).
1EBF2D1DBEC6739F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGGIEGPTLRQW-----LAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 264:17428-17431(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY
                                                           -!- INDUCTION: BY 20-HYDROXYECDYSONE.
                                                                                                                                                                                                                                                                                     InterPro; IPR000618; Insect_cuticle. Pfam; PF00379; Insect_cuticle; 1.
                                                                                                                                                                                                                                                                                                                            Structural protein; Cuticle; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90008911; PubMed=2551902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20710 MW;
                                                                                                                                                                                                                                     EMBL; X60455; CAA42985.1; -. EMBL; X72783; CAA51290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                          S16063; S16063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANS_BOVIN
P13135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                               PIR;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-Cclcium-dependent protease, small subunit (Calpain regulatory subunit)
(Calcium-activated neutral proteinase) (CANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85298299; PubbMed-2994060; MEDLINE-85298299; PubbMed-2994060; Yumoto N., Kikuchi T., Sasaki T., Sakihama T., Kakidani H., Zenita K., Yumoto N., Titani K., Murachi T., Kannagi R., Nakanishi S., Ohmori M., Takio K., Titani K., Murachi T.; "A putative Ca2+-binding protein: structure of the light subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-FAX CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 94-266.
MEDLINE-97372891; PubMed-9228946;
Lin G.D., Chatcopadhyay D., Maki M., Wang K.K., Carson M., Jin L.,
Yuen P.W., Takano E., Hatanaka M., Delucas L.J., Narayana S.V.;
"Crystal structure of calcium bound domain VI of calpain at 1.9-A
resolution and its role in enzyme assembly, regulation, and inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   porcine calpain elucidated by molecular cloning and protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Struct. Biol. 4:539-547(1997).
FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM BINDING.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma membrane upon Ca++ binding (By similarity).
-!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 72; DB 1; Length 263; 55.2%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9427925D5284CE1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                 GLY-RICH (HYDROPHOBIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 82:6075-6079(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEG--PTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GGGGGLGGGLGNVLGGLISGAGGGGGGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27931 MW;
                                                                                                                                                                                                                                           Interpro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 3.
PROSITE; PS00018; EF_HAND; 2.
                                                                                                                                                           EMBL; J05065; AAA30422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                         Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                263
158
188
223
255
255
                                                                                                                                                                                                PIR; A34466; A34466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                         HSSP; P04574; 1ALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANS_PIG
P04574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CA_BIND
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                             TISSUE-Fetal brain;
MDDLINE-99452997; PubMed=10521492;
MOVINEN T.P., Ardley H.C., Nubber U., Rose S.A., Jones P.F.,
Markham A.F., Schefner M., Robinson P.A.;
"The ubiquitin-conjugating enzymes UbcH7 and UbcH8 interact with RING finger/IBR motif-containing domains of HHARI and H7-AP1.";
J. Biol. Chem. 274:30963-30968(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aguilera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.; "Ariadne-1: a vital Drosophila gene is required in development and defines a new conserved family of ring-finger proteins."; Genetics 155:1231-1244(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MIGHT ACT AS AN E3 UBIQUITIN-PROTEIN LICASE, OR AS PART OF THE E3 COMPLEX, WHICH ACCEPTS UBIQUITIN FROM SPECIFIC E2 UBIQUITIN CONJUGATING ENZYMES, SUCH AS UBEZLI/UBEZL3/UBCM4, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B., Cannata N., Zimbello R., Lanfranchi G., Valle G., "Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ardley H.C., Tan N.G.S., Rose S.A., Markham A.F., Robinson P.A., "Features of the parkin/ariadne-like ubiquitin ligase, HHARI, that regulate its interaction with the ubiquitin-conjugating enzyme,
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH UBEZLI, AND MUTAGENESIS OF GLN-187; ILE-188; CYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full Y., Takayama K., Ukai Y., Yoshimoto M.; "Molecular and biological characterization of a new ring finger protein, MOP-6 which is highly expressed in activated human
                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: MAINLY CYTOPLASMIC.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: CONTAINS 2 RING-TYPE ZINC FINGERS.
SIMILARITY: CONTAINS 1 IBR-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                   Trockenbacher A., Marksteiner R., Schneider R.,
(HHARI) (H7-AP2) (HUSSY-27) (MOP-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEN TRANSFERS IT TO SUBSTRATES. SUBUNIT: INTERACTS WITH UBEZLI.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 95-557 FROM N.A.
MEDLINE=20341325; PubMed=10880484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21276469; PubMed=11278816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 298-557 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 377-557 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       'Human ariadne homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast sequences.";
Yeast 18:69-80(2001).
                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Monocytes;
                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
PubMed=11124703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 AND TYR-258
                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol.
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EMBL; AJ243190; CAB45870.1; -.

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C->A,H: LOSS OF INTERACTION WITH UBEZLI.
Y->A: NO LOSS OF INTERACTION WITH UBEZLI.
UBEZLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouhin H., Braquart C., Charles J.-P., Quennedey B., Delachambre J.; "Nucleotide sequence of an adult-specific cuticular protein gene from the beetle Tenebrio molitor: effects of 20-hydroxyecdysone on mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bouhin H., Charles J.-P., Quennedey B., Delachambre J.; "Developmental profiles of epidermal mRNAs during the pupal-adult molt of Tenebrio molitor and isolation of a cDNA clone encoding an adult cuticular protein: effects of a juvenile hormone analogue."; Dev. Biol. 149:112-122(1992).
                                                                                                                                                                                                                                               QI->HV: NO LOSS OF INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                       H -> Q (IN REF. 2 AND 3).
D -> N (IN REF. 3).
F -> S (IN REF. 4).
ENWHOPWR -> AIGMILEQ (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insect Mol. Biol. 2:81-88(1993).
                                                                                                 SMART; SM00184; RING; 2.
PROSITE; PS00518; ZF_RING_1; FALSE_NBG.
PROSITE; PS50089; ZF_RING_2; 1.
Ubiquitin conjugation; Zinc-finger; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                       K -> T (IN REF. 4).
44BCA291863ABB6A CRC64;
                                                                                                                                                                                                                     COLLED COIL (POTENTIAL). INTERACTION WITH UBEZLI.
                                                                                                                                                        ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P26968: 027015, 007015, 001-406-1992 (Rel. 23, Created) 01-A0G-1992 (Rel. 23, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Adult-specific cuticular protein ACP-22 precursor.
                                                                                                                                                                                                                                                                                                                        -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                RING-TYPE 1.
                                                                                                                                                                                                         RING-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.5;
                                                                                                                                                                                                                                                                                                                          E -> D (IN
H -> Q (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGIEGPTLROWLAARAGGGGGGGGGIEGP 31
                                                                                                                                                                   GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                              IBR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GGGGSALGP-----GGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                           UBE2L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tenebrio molitor (Yellow mealworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=92097825; PubMed=1728581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97242547; PubMed=9087546;
AF072832; AAD28088.1; -. AJ130976; CAA10274.1; -. AJ009771; CAA08817.1; -. AB014774; BAB19786.1; -.
                                                           InterPro; IPR002867; IBR.
InterPro; IPR001841; Znf_ring.
Pfam; PF01485; IBR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   64126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%;
51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                       122
227
237
303
316
322
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317
389
                                                                                                                                                                                                                                                                                                                                                                                      322
557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7067;
                                                  605624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accumulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC22_TENMO
                                                                                                                                                                                       ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                       CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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δà
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30-MAY-2000 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) sex-lethal protein homolog (CCSXL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-binding; Repeat; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00961; HUDSXLRNA.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000504; RRM. PF00076; rrm; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19339; 1SXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                        NCBI_TaxID=7213;
                                                                                                                                                 STRAIN-BENAKIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
         DE DE DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Calcium-dependent protease, small subunit (Calpain regulatory subunit)
(Calcium-activated neutral proteinase) (CANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                    MEDLINE-20285452; PubMed-10825211;
Arthur J.S.C., Elce J.S., Hegadorn C., Williams K., Greer P.A.;
"Disruption of the murine calpain small subunit gene, Capn4: calpain
"sessential for embryonic development but not for cell growth and
                                                                                                                                                                                                                                                                                                                                                                                                              (regulatory) subunit.
--- SUBCELUIAR LOCATION: Cytoplasmic; Translocates to the plasma membrane membrane non Ca++ binding (By similarity).
--- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY-RICH (HYDROPHOBIC).
CALCIUM-BINDING.

EF-HAND 1 (POTENTIAL).

EF-HAND 2 (POTENTIAL).

ANCESTRAL CALCIUM SITE 3 (POTENTIAL).

ANCESTRAL CALCIUM SITE 4 (POTENTIAL).

CS78771942F157E9 CRC64;
                                                                                                                                                                                                                                                                                                                                          MOI. Cell. Biol. 20:4474-4481(2000).
-i- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
-i- SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.5; DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 AA.
                                                                                                       269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GGGGLGGGLGNVLGGLISGAAGGGGGGGG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGGIE---GPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                      11 GGGGGLGGGLGNVLGGLISGAAGGGGGGGG 40
                1 GGGGGIE---GPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                  PubMed=10825211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXL_CERCA STANDARD; 1061374; 30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF058298; AAC97194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AA; 28463 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:88266; Capn4.
InterPro: IPR002048; EF-hand.
Pfam; PF00035; efhand; 3.
PROSITE; PS00018; EF_HAND; 2.
PROILUM-binding; Repeat.
                                                                                                                                16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                         STANDARD;
                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1DKV
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                         CANS_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Best Local 5
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CA_BIND
CA_BIND
                                                                                                                                                                                                                                                                                                                                       division.
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                                                                                                                        088456
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                                                                                              CANS_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARILHUMAN STANDARD; PRT; 557 AA.

9814X5; Q9UP39; Q9UENO; O76026; Q9H376;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ariadne-1 protein homolog (ARI-1) (Ubiquitin-conjugating enzyme E2-binding protein 1) (UbcH7-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS
-!- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS; ADULT-SPECIFIC ISOFORMS
A1, A2, A3, A4, AND EMBRYO-SPECIFIC ISOFORMS E1, E2 AND E3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                         Saccone G., Peluso I., Artiaco D., Giordano E., Bopp D., Polito L.C.; "The Ceratitis capitata homologue of the Drosophila sex-determining gene Sex-lethal is structurally conserved, but not sex-specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels 11; Gaps
                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development 125:1495-1500(1998).
1- FUNCTION: UNKNOWN, APPARENTLY NOT INVOLVED IN SOMATIC SEX
DETERMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%; Score 74.5; DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Alternative splicing. GLY/ASN-RICH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CABA3DA5C2C8874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM A1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 GGGGGGGG------GGGGGGGGGMGGP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY - PRO
                                                                                                                                                                                                                                                                       MEDLINE=98171464; PubMed=9502730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF026145; AAC38968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 AA; 37188 MW;
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                                                                                                                                                                                                                                                                                                      "BETA3, a novel helix-loop-helix protein, can act as a negative regulator of BETA2 and MyoD-responsive genes.";
MO1. Cell. Biol. 16:656-633(1996).
-!-FUNCTION: INHIBITS DNA BINDING OF TCF3 (E47) HOMODIMERS AND TCF3 (E47) / NEURODI HETERODIMERS AND ACTS AS A STRONG REPRESSOR OF WITH CLASS A BASIC HELIX-LOOP-HELIX FACTORS. DESPTTE THE PRESENCE OF AN INTACT BASIC DOMAIN, DOES NOT BIND TO DNA.
-!-SUBGLIGHAR LOCATION: NUCLEAR (PACTOR).
-!-SUBGLIGHAR LOCATION: NUCLEAR (PACTOR).
-!-TISSUE SPECIFICITY: KINNEY, LUNG, BRAIN AND PANCREAS (INSULINOMA).
-!-SIMILARITY: BELONGS TO THE BASIC HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                       Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.5%; Score 75; DB 1; Length 367; 48.5%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Nuclear protein; Transcription regulation; Repressor.
                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                     367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 GGGGAGG------GGGGGGGGGGVSVPGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTL 33
                                                                                                                                     Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY - GLY
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96140430; PubMed=8552091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANS_RAT STANDARD; P
Q64537; P97572;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35905 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S80870; AAB50691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 48.5
Matches 16; Conservative
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 AA;
                                                                                                                                                                                                        NCBI_TaxID=10036;
                                                                                                                       BETA3 protein.
                                  BET3_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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RESULT 2
BET3_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protease, small subunit (Calpain regulatory subunit)
(Calcium-activated neutral proteinase) (CANP) (Fragment).
CAPN4 OR CSS1.
                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 94-266.

WEDLINE-97372890; PubMed=9228945;
Blanchard H., Grochulski P., Li Y., Arthur J.S.C., Davies P.L.,
Elce J.S., Cygler M.;
Structure of a calpain Ca(2+)-binding domain reveals a novel EF-hand and Ca(2+)-induced conformational changes.";
Nat. Struct. Biol. 4:532-538(1997).
-! FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited a proteolysis of substrates involved in Cytoskeletal remodelling and signal tranduction.
-! SUBNIT: Heterodimer of a large (catalytic) and a small
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                   MEDLINE=97107433; PubMed=8950173; Sorimachi H., Amano S., Ishiura S., Suzuki K.; Sorimachi H., Amano S., Ishiura S., Suzuki K.; Primary sequences of rat mu-calpain large and small subunits are, respectively, moderately and highly similar to those of human."; Biochim. Biophys. Acta 1309:37-41(1996).
                                                                                                                                                                                                                                                                                                                           Graham-Siegenthaler K., Gauthier S., Davies P.L., Elce J.S.; Arctive recombinant rat calpain II. Bacterially produced large and small subunits associate both in vivo and in vitro."; J. Biol. Chem. 269:30457-30460(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the plasma
membrane upon Ca++ binding (By similarity).
-!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF-HAND 2.
ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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7BF8E444576DD835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLY-RICH (HYDROPHOBIC).
                                                                                                                                                                                                                                                                                          SEQUENCE OF 83-266 FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=95074051; Pubmed=7982961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00036; efhand; 3.
PROSITE; PS00018; EF_HAND; 2.
Calcium-binding; Repeat; 3D-structure.
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28079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U53859; AAC53002.1; -. EEMBL; U10861; AAK64828.1; -. PDB; 1AJ5; 20-MAY-98. PDB; 1DVI; 27-MAY-98.
                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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1161
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266 AA;
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                                                                                                                                      NCBI_TaxID=10116;
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180
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Local Sim
16;
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DOMAIN
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 08:51:41; Search time 4.89696 Seconds

(without alignments)
324.181 Million cell updates/sec

Title: US-09-422-838C-34 Perfect score: 224

1 GGGGGIEGPTLRQWLAARAG......GGGGGGIEGPTLRQWLAARA 41

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Seguence:

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	-	mesocri	_	_						-					Q00179 aspergillus				-				Q9ng98 drosophila		_		_	-	0	σ.	~		053553 mycobacteri
	ID	JUND_CHICK	BET3_MESAU	CANS_RAT	CANS_MOUSE	SXL_CERCA	ARII_HUMAN	AC22_TENMO	CANS_BOVIN	CANS_PIG	CANS_RABIT	CANS_HUMAN	HXB3_MOUSE	OVO_DROME	CAZ_DROME	SR54_ASPNG	SUS_DROME	HXB3_HUMAN	SHX2_HUMAN	RB87_DROME	TMAF_AVIS4	ROA1_SCHAM	GRP1_PETHY	TP3A_DROME	MAF2_RAT	WASP_MOUSE	LAC1_NEUCR	LAC2_NEUCR	CIKF_HUMAN	TOP3_CAEEL	CIKF_MOUSE	M130_STRPU	CIKF_RAT	YZ08_MYCTU
	DB	-	-	-	_	Н	Т		٦	٦	-		Н	٦	Н	Н	٦	٦	_	П	-	Н	Н	-	-	٦	-		Н	٦	Н	Н	-	Н
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	Score	78	75	4	4		Α,	7	72	72	72	72	72	72	71.5	. ~	71	70.5	70	70	69.5	ູເດ	69	69	68.5	ω.	68.5				68.5	68.5		68.5
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> QY DP

P70390 mus musculu p1708 mus musculu Q01851 homo sapien P56959 mus musculu Q24119 drosophila P19289 thermoprote P16768 human cytom P57483 arabidopsis P53783 mus musculu Q43516 homo sapien P24029 aleutian mi P17151 human cytom
SHX2_MOUSE BR3A_MOUSE BR3A_HUMAN FUS_MOUSE TR4_DROME TR4_DROME TR4_DROME GRP_ARATH SOX1_MOUSE WATP_HUMAN CCAT_ADVG EP84_HCMVA
331 421 421 518 958 141 268 338 338 503
300. 44. 300. 44. 40. 10. 10. 10. 10. 10. 10. 10. 1
68 68 67 68 67 67 67 57 57 57 57
33 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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                                                                                                                                      Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00036; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
9
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=92019832; Pubmed=1923529;

Harl M., Hutchins J.T., Vogt P.K.;

Harl M., Hutchins J.T., Vogt P.K.;

"The chicken jund gene and its product.";

Oncogene 6:1620-1631(1991).

- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).

- SUBUNIT: BLOCATION: Nuclear.

- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.8%; Score 78; DB 1; Length 323; 57.6%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 AA; 33205 MW; A7F6D21A97DBB676 CRC64;
                                                                          01-AUG-1992 (Rel. 23, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Transcription factor jun-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY -GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X60063; CAA42665.1; -. PIR; S20099; S20099. HSSP; PO5412; IFOS. TRANSFAC; TO2196; -. InterPro; IPR002112; Leuzip_Jun. InterPro; IPR001811; bZIP.
                                                             01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0043; LEUZIPPRJUN. SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.89
Best Local Similarity 57.69
Matches 19; Conservative
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
166
266
298
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                                                                                                                                                                                                          NCBI_TaxID=9031;
                                  JUND_CHICK
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DOMAIN
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RESULT 1
JUND_CHICK
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Kajadicaan, M.A.; Rogers, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Squares, S.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Rosidues: 1-496 CCOL>
A;Residues: 1-496 CCOL>
A;Residues: 1-496 CCOL>
A;Residues: 1-496 CCOL>
A;Rosidues: 1-496 CCOL>
A;Rosidues: 1-496 CCOL>
A;Cross-references: GB:AL021926; GB:AL123456; NID:g3261520; PIDN:CAA17303.1; PID:g290957
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
31.7%; Score 71; DB 2; Length 496;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 14; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 9, 2002, 09:05:13 Job time : 10.2178 secs
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C;Accession: T09084
R;Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylino A;Reference number: 216411; MUID: 98281574
A;Accession: T09084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical glycine-rich protein Rv0109 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein FBL21.90 - Arabidopsis thaliana hypothetical protein FBL21.90 - Arabidopsis thaliana (mouse-ear cress)
(5.Species: Arabidopsis thaliana (mouse-ear cress)
(5.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-oct-1999
(5.Accession: T13021
R.Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; R.Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; R.Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; R.Berance number: 217587
A; Accession: T13021
A; Reference number: 217587
A; Residues: 1-371 CBEV>
A; Residues: 1-371 CBEV>
A; Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:FBL21.90
A; Cross-reference: cultivar Columbia; BAC clone FBL21
C; Genetics: A; Gene: ATSP:FBL21.90
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U97663; NID:g2109290; PIDN:AAC50018.1; PID:g2109291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                         .,
                                                                             DB 2; Length 1585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.2%; Pred. No. 3;
Matches 19; Conservative 3; Mismatches 17; Indels
A;Gene: CESP:Y50E8A.g
A;Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 GLGSGPLGP-----LLAAGGGGGGGGSSPGDGSTARWDEWL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGGIEGPTLRQW--LAARAGG-GGGGGGIEGPTLRQWLAAR 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                              31.9%; Score 71.5; DI
Best Local Similarity 50.0%; Pred. No. 9.8;
Matches 16; Conservative 2; Mismatches
                                                                                                                                                                                                                                      462 GGGGGAGG----GYAKPSGGGGGGGGGYAKPS 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 265/3; 331/3; 370/3; 455/1; 481/3
                                                                                                                                                                                                    1 GGGGGIEGPTLROWLAARAGGGGGGGGGIEGPT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: strain cw-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-490 <MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
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                                                                                                                                                                                                                          ŏ
                                                                                          A; Keslaues: 1-404 <5107
A; Cross-references: EMBL:L37083; NID:9567105; PIDN:AAC41563.1; PID:9567106
B; Stolow, D. T.; Haynes, S.R.
Nucleic Acids Res. 23, 835-843, 1995
A; Title: Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares homology A; Reference number: S54728; MUID:95223793
A; Accession: S54728
A; Mulcule type: DNA
A; Residues: 118-203,273-310 <5TW>A; Residues: 118-203,273-310 <5TW>A; Cross-references: EMBL:L37083
A; Cross-references: EMBL:L37083
A; Cross-references: FlyBase:FBgn0011571
A; Cross-references: FlyBase:FBgn0011571
C; Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein E; L20-195/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Steinhauer, W.R.; Sterling, J.F.; Graves, J.P. submitted to the EMBL Data Library, February 1995 A;Description: Comparison of suppressor of sable [su(s)] in two Drosphila species reveal A;Reference number: 214224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050.1; CESP:Y50E8A.9 A;Experimental source: clone Y50E8A C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y50EBA,g - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppressor of sable protein homolog - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
C;Accession: T13855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:U20660; NID:g671707; PID:g671708; PIDN:AAA62307.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.9%; Score 71.5; DB 2; Length 404; Best Local Similarity 59.3%; Pred. No. 2.9; Matches 16; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 GGGGGAGG------GGGGGGGGICG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 GGGGGGG --- RGFGGRRGGGGGGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: FlyBase:FBgn0013921
A;Introns: 112/1; 216/3; 702/2; 735/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21047
A; Accession: T31611
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A; Residues: 1-1473 <STE>
                                                                    A; Molecule type: DNA
A; Residues: 1-404 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T31611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T13855
                                        A; Accession: S54729
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Gaps 4;

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Ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Decies: 13-30an-1995 #sequence_revision 13-3an-1995 #text_change 16-Feb-1997
C;Accession: S16556
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A;Title: The ove gene of prosophila encodes a zinc finger protein required for female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T4979.
K;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Stolow, D.T.; Haynes, S.R. submitted to the EMBL Data Library, October 1994
A;Description: Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares A;Reference number: S54729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.Alternate names: caz protein
C:Species: Drosophila melanogaster
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 72; DB 2; Length 1213; Score 72; DB 2; Length 1213; Conservative 2; Mismatches 9: Tabals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 71.5; DB 2; Length 201; 43.2%; Pred. No. 1.5; tive 2; Mismatches 4; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A;Experimental source: BAC clone B9J10; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein B9J10.290 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GGGG-----RRGGGGGGGGVNG----RWSA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                    2 GGGGIEGPTLRQWLAARAGGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 GGGGASGP--GGGPSANSGGGGGGGGGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGGIEGPTLRQWLAARAGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S16356; MUID: 91293102
A; Accession: S16356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross.references: FlyBase:FBgn0003028
A;Introns: 931/3; 1152/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X59772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 43.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-1213 <MEV>
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-201 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: FlyBase:ovo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T49792
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                                                                                                                                                            RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                     δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rishan, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krumlau EMBO J. 11, 1825-1836, 1992.

A. Triller. Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with dif A; Accession: S20963; MuID:92258392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:X66177; GB:S35628; GB:S35738; NID:g312229; PIDN:CAA46951.1; PID:q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A56038
R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaste A;Reference number: A56038; MUID:95021209
A;Accession: A56038
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                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Mus musculus (house mouse)
C; Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C; Accession: S20963; D42694
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Sequence extracted from NCBI backbone (NCBIN:92310, NCBIP:92316)
Superfamily: homeotic protein Hox B3; homeobox homology
Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Residues: 1-1028 <GAR>
A;Cross-references: GB:U11383; NID:9520526; PIDN:AAB60216.1; PID:9520527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                       Score 72; DB 2; Length 405; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 32.1%; Score 72; DB 2; Length 1028; Best Local Similarity 55.2%; Pred. No. 5.9; Matches 16; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.1%; Score 72; DB 2; Length 433; Conservative 1; Mismatches 5. Todalic
                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
A;Introns: 88/1; 372/1
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Nazarali, A.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992
A.Titte: Hox-1.11 and Hox-4.9 homeobox genes.
A.Reference number: A42694; MUID:92212934
                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 GGGGSSG------GGGGGGGGGGDKSP 185
                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: .homeotic protein Hox 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGP 31
                                                                                                                                                                                                      373 GGGGIPG----QSMYMGAGGGGGAGG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Residues: 213-238 <NAZ>
Note: sequence extracted from NCBI backb
C:Superfamily: homeotic protein Hox B3; ho
C:Keywords: DNA binding; homeobox; nucleus
F:192-248/Domain: homeobox homology <HOX>
                                                                                                                                                                         1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: FlyBase:FBgn0003028
                                                                                  32.1%;
59.3%;
                                                               Ouery Match
Best Local Similarity 59.38
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                homeotic protein Hox B3 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary
A:Molecule type: DNA
A:Residues: 213-238 <NAZ>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-433 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary
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A; Status: prelimina
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C.Function:
A;Description: catalyzes the hydolysis of peptides
A;Description: catalyzes the hydolysis of peptides
A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and b
A;Note: cleaves preferentially after tyrosine, methionine, promoted to the profession of the profess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U64609; PIDN:AAB04598.1; GSPDB:GN00022; CESP:T28H11.5
A;Experimental source: strain Bristol N2; clone T28H11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:270284; PIDN:CAA94280.1; GSPDB:GN00022; CESP:K07F5.11
A;Experimental source: clone K07F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T28H11.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein KO7F5.11 - Caenorhabditis elegans
hypothes: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 21-Jan-2000
C;Accession: T23416
B:Hembry, C
Submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
A;Map position: 19pter-19qter
A;Introns: 70/2; 81/3; 111/3; 131/1; 152/3; 175/3; 202/1; 241/1; 260/3
C;Complex: heterodimer of L (large) and S (small) chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
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A;Introns: 89/1; 257/1
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Accession: T29167
R. Nelson, J.; Wohldmann, P. submitted to the EMBL Data Library, July 1996
A.Description: The sequence of C. elegans cosmid T28H11.
A. Reference number: Z20582
A. Accession: T29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%; Score 72;
55.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGGIEG--PTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GGGGLGGGLGNVLGGLISGAGGGGGGGG 44
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258 GGGGIPG----QSMYMGAGGGGAGG 280
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A;Accession: T23416
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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A; Residues: 1-268 <MIY>
A; Residues: 1-268 <MIY>
A; Cross-references: GB: M31502
R; Ohno, S.: Emort, Y.: Suzuki, K.
R; Ohno, S.: Emort, Y.: Suzuki, K.
R; Ohno, S.: Emort, Y.: Suzuki, K.
A; Title: Nuclectide sequence of a cDNA coding for the small subunit of human calcium-dep
A; Reference number: A93631; MUID: 86286563
A; Reference number: A93631; MUID: 86286563
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Nucletc Acids Res. 14, 8805-8817, 1986
A;Title: Gene organization of the small subunit of human calcium-activated neutral prote A;Reference number: A93648; MUID:87066759
A;Accession: A26107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Description: catalyzes the hydolysis of peptides
A, Description: catalyzes the hydolysis of peptides
A, Description: cleaves preferentially after tyrosine, methionine, or arginine residues and befo
C, Superfamily: calpain small chain; calmodulin repeat homology
C, Superfamily: calpain small chain; calmodulin repeat homology <EF1>
F; 154 Typomain: calmodulin repeat homology <EF2>
F; 170-199/Domain: calmodulin repeat homology <EF2>
F; 170-199/Domain: calmodulin repeat homology <EF2>
F; 170-199/Domain: calmodulin repeat homology <EF2>
F; 202-224/Domain: calmodulin repeat homology <EF5>
F; 205-266/Domain: calmodulin repeat homology <EF5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calpain (EC 3.4.22.17) small chain - rabbit calpain (CANP); calpain light chain; cal N.Alternate names: calcium-activated neutral proteinase (CANP); calpain light chain; cal S.Actionate names: calcium-activated neutral proteinase (CANP); calpain light chain; cal S.Secies: Oryctolagus cuniculus (domestic rabbit) c; species: Oryctolagus cuniculus (domestic rabbit) c; species: Oryctolagus cuniculus (domestic rabbit) c; baccession: A24816 (C; Accession: A24816 (C; Accession: A24816 (C; Accession: A24816 (C; A); Daid: Chem. 261, 9472-9476, 1986 (C) A; Daid: Chem. 261, 9472-9476, 1986 (C) A; Title: Isolation and sequence analysis of cona clones for the small subunit of rabbit A; Aritle: Organical A24816; MUID:86250903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calpain (EC 3.4.22.17) small chain - human Nichteniaes (CANP)
Nichternate names: calcium-activated neutral proteinase (CANP)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C.Accession: A26107; A23650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-26 < EMO>
A; Cross-references: GB:M13364; NID:g164875; PIDN:AAA81565.1; PID:g164876
C; Complex: heterodimer of L (large) and S (small) chains
C; Function:
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                                                                                                   32.1%; Score 72; DB 1; Length 266; 55.2%; Pred. No. 1.8;
                                                                                                                                                                                  8; Indels
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                                                                                                                                           pred. No. 1.8;
3; Mismatches
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A;Cross-references: GDB:119752; OMIM:114170
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55.2%; Pred. No.
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Dest Local Similarity 55.2%
Matches 16; Conservative
                                                                                                                                                                                                  Conservative
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A; Residues: 1-268 <OHN>
                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserva
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Matches
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Best Local Similarity
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                 Matches
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               Accession: 549194

GCR 17 protein - fruit fly (Drosophila melanogaster)

GCR 17 protein - fruit fly (Drosophila melanogaster)

GSPecies: Drosophila melanogaster

C; Species: Drosophila melanogaster

C; Accession: 549194

R; Parchment, C.; Hughes, D.M.; Lloyd, P.; Flavell, A.J.

A; Bescription: A variety of different glycine repeats in Drosophila genes.

A; Recession: 549194

A; Status: preliminary

A; Status: preliminary

A; Status: Preliminary

A; Rocession: 549194

A; Residues: 1-196 «PAR>

A; Cross-references: EMBL: X71974; NID: 9510501; PID: 9510502
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T
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C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acp-22 protein - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S12224
R;Bouhin, H.; Braquart, C.; Charles, J.P.; Delachambere, J.
submitted to the EMBL.nata Library, March 1993
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                   57 GLGGGLGG--LSGGLGGGGGGGGGGSSG 84
                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0003057
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Local Similarity 48.68;
es 17; Conservative 1
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Best Local Similarity 53.3%
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A; Accession: S32224
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A; Residues: 1-199 <BOU>
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       RESULT 12
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A; Accession: B2166
A; Molecule type: protein
C; Complex: heterodimer of L (large) and S (small) chains
C; Complex: heterodimer of L (large) and S (small) chains
A; Description: catalyzes the hydolysis of peptides
A; Note: cleaves preferentially after tyrosine, methonine, or arginine residues and b C; Keywords: acetylated amino end; calcium binding; cysteine proteinase; duplication;
E; Hopmain: calmodulin repeat homology <EF1>
F; Hopmain: calmodulin repeat homology <EF2>
F; Hodified site: acetylated amino end (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                         C.Species: Bos primigenius taurus (cattle)
C.Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 16-Jul-1999
C.Bacession: A34466
S.McClelland, P.: Lash, J.A.; Hathaway, D.R.
J. Biol. Chem. 264, 17428-17431, 1989
A:Title: Identification of major autolytic cleavage sites in the regulatory subunit o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross.references: GB:J05065; NID:g162780; PIDN:AAA30422.1; PID:g162781
C;Superfamily: calpain small chain; calmodulin repeat homology
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer;
E;1-51/Domain: g1ycine-rich cGLY>
F;91-122/Domain: calmodulin repeat homology <EF1>
F;134-166/Domain: calmodulin repeat homology <EF2>
F;167-196/Domain: calmodulin repeat homology <EF2>
F;189-231/Domain: calmodulin repeat homology <EF3>
F;292-231/Domain: calmodulin repeat homology <EF5>
F;232-263/Domain: calmodulin repeat homology <EF5>
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Proc. Natl. Acad. Sci. U.S.A. 82, 6075-6079, 1985
A;Title: A putative Ca2+-binding protein: structure of the light subunit of porcine c
A;Reference number: A25166; MUID:85298299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calpain (EC 3.4.22.17) small chain - pig
N.Alternate names: calcium-activated neutral proteinase (CANP); calpain light chain;
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-266 <SAK>
A;Cross-references: GB:M11778; NID:g164402; PIDN:AAA31010.1; PID:g164403; GB:M11779;
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                                                          Gaps
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&
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                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
1 Similarity 48.6%; Pred. No. 1.4;
17; Conservative 1; Mismatches
                                                                                          1 GGGGGIEGPTLRQW-----LAARAGGGGGGG 27
                                                                                                                                                             65 GGGGGGEGEREHELRGGGLELGGGGGGGGGGG 99
                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                              calpain (EC 3.4.22.17) light chain - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GGGGGLGGGLGNVLGGLISGAGGGGGGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGGIEG--PTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A34466; MUID:90008911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%;
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.28
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-263 <MCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffel, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; Koo, H.; Moffel, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter ears, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487 A;Accession: G84728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE002093; NID: 94263710; PIDN: AAD15396.1; GSPDB: GN00139
                                                              A; Cross-references: GB: AE005172; NID: 910092219; PIDN: AAG12635.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2932080 [imported] - Arabidopsis thaliana hypothetical protein At2932080 [imported] - Arabidopsis thaliana (mouse-ear cress) [c; Species: Arabidopsis thaliana (mouse-ear cress) [c; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 [c; Accession: G84728]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCR 101 protein - fruit fly (Drosophila melanogaster)
GCR 101 protein - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 24-Nov-1999
C; Accession: S49193
R; Parchment, C: Hughes, D.M.; Lloyd, P.; Flavell, A.J.
R; Parchment, C: Hughes, D.M.; Lloyd, P.; Flavell, A.J.
A; Description: A Variety of different glycine repeats in Drosophila genes.
A; Reference number: S49192
A; Reference number: S49192
A; Reference preliminary
A; Matures: preliminary
A; Matures: preliminary
A; Matures: Preliminary
A; Residues: PRNA
A; Re
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
33.0%; Score 74; DB 2; Length 239;
Best Local Similarity 55.6%; Pred. No. 1;
Matches 15; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                         Ouery Match 33.0%; Score 74; DB 2; Length 228; Best Local Similarity 45.7%; Pred. No. 0.97; Matches 21; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 GGGGGGGDT----GAGAGGGGYGGGGDTGAGGGVGSGQWCIAKA 153
                                                                                                                                                                                                                                                                                                                                                                                            1 GGGGGIEGPTLRQWLAARAGGGGGGGGIE-----GPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X71975; NID:9510508; PID:9510509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ajgene: FlyBase:anon-Pen101
Ajgenes: FlyBase:FBgn0011824
A;Cross-references: FlyBase:FBgn0011824
C;Superfamily: Phaseolus glycine-rich protein 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GGGGGAEGG-----RAVTGGGGGGGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 GGGGRGGGFRGGAGRNGGGGGGGG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
                                     A; Molecule type: DNA
A; Residues: 1-228 <STO>
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 2
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                                                                                                                                                                                            A; Map position: 1
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C;Genetics:
                                                                                                                                                               C;Genetics
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, C.A.; Li, Neoney, T.; Rowley, D.; Sakano, H.
Rizzo, K.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of circasonel of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Iwasaki, M.; Okumura, K.; Kondo, Y.; Tanaka, T.; Igarashi, H.
Nucleic Acids Res. 20, 4001-4007, 1992
A;Title: cDNA cloning of a novel heterogeneous nuclear ribonucleoprotein gene homologue
A;Reference number: 335500; MUID:92375684
A;Accession: S35500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF038613; PIDN:AAB92051.1; GSPDB:GN00022; CESP:F42A6.7
A;Experimental source: strain Bristol N2; clone F42A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
A; Introns: 9/3; 255/1
A; Introns: 9/3; 255/1
C; Superfamily: helix destabilizing protein; ribonucleoprotein repeat homology
F; 24-90/Domain: ribonucleoprotein repeat homology <RRM1>
F;115-181/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable beta-1,3 glucanase, 26636-27432 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterogeneous ribonuclear particle protein homolog - Caenorhabditis elegans N:Alternate names: heterogeneous nuclear ribonucleoprotein homolog C;Species: Caenorhabditis elegans C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999 C;Accession: S35500; T32620
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                                                                                                                                                                                                                                                           6; Indels 10; Gaps
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                                                                                                                                                                                        Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-346 < IWA>
A; Residues: EMBL: S43152
A; Cross references: EMBL: S43152
R; Du, Z.; Scheet, P.; Andrews, S.
B; Du, Z.; Scheet, P.; Andrews, December 1997
submitted to the EMBL Data Library, December 1997
A; Reference number: 221201
A; Accession: T32620
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43.6%; Pred. No. 1.2;
tive 3; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                DB 2;
                                                                                                                                                                                            Query Match
33.5%; Score 75; DB
Best Local Similarity 48.5%; Pred. No. 1.2;
Matches 16; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              83 GGGGAGG------GGGGGGGGGGVSVPGL 105
                                                                                                                                                                                                                                                                                                                                                       1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTL 33
                                                                                       A;Gene: beta3
C;Keywords: repressor; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 43.69
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-346 <DUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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D86416
                                                                           C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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NiAlternate names: protein Ar4922020
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C:Accession: T49109
R:Bevan, M:; Wedler, H.; Wambutt, R.; Bancroft, I:; Mewes, H.W.; Rudd, S.; Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Species: Cricetinae gen. Sp. (hamster)
C. Species: Cricetinae gen. Sp. (hamster)
C. Species: Cricetinae gen. Sp. (hamster)
C. Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C. Accession: JC6087
R. Peyton, M.; Stellrecht, C.M.M.; Naya, F.J.; Huang, H.P.; Samora, P.J.; Tsai, M.J.
Mol. Cell. Biol. 16, 626-633, 1996
A. Title: BETA3, a novel helix-loop-helix protein, can act as a negative regulator of A: Reference number: JC6087; MUID:96140430
A: Reference number: JC6087; MUID:96140430
A: Molecule type: mRNA
A: Residues: 1.367 < PEPx>
A: Residues: 1.367 < PEPx>
A: Cross-references: GB:S80870; NID:91911496; PIDN:AAB50691.1; PID:91911497
C; Comment: This factor belongs to the tissue-specific class B basic helix-loop-helix
                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T27609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 75.5; DB 2; Length 396; 53.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA A: Residues: 1.396 <BEV>
A: Residues: 1.396 <BEV>
A: Cross references: EMBL: AL022140; GSPDB:GN00062; ATSP:AT4922020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.4%; Score 77; DB 2; Length 307; 63.0%; Pred. No. 0.63; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                      A;Residues: 1-307 cDUZ>
A;Cross-references: EMBL:U40802; PIDN:AAA81510.1; CESP:2C477.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 32/1; 275/1
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: cultivar Columbia; BAC clone F1N20
                                                                                                                                                          A; Description: The sequence of C. elegans cosmid ZC477. A; Reference number: 220392 A; Accession: 727609 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JC6087
helix-loop-helix transcription factor, BETA3 - hamster
                                                                                                                                 Submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z25016
A; Accession: T49109
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-307 < DUZ>
                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: ZC477.1
A: Introns: 32/1; 275/1
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Xp. Parasitol. 68, 17-30, 1989
'Title: Schistosoma haematobium: analysis of eggshell protein genes and their expression Reference number: A44805; MUID:89137380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: EMBL:X60063; NID:962927; PIDN:CAA42665.1; PID:962928 C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology C:Keywords: DNA binding; nucleus; transcription regulation F:237-277/Domain: fos/jun DNA-binding domain homology <FyD>
                                                                                                                                                                                                                                                transforming protein junD - chicken
C:Species: Gallus gallus (chicken)
C:Decies: Gallus gallus (chicken)
C:Decies: Gallus gallus (chicken)
C:Accession: S20099
B:Hartl, M.; Hutchins, J.T.; Vogt, P.K.
Oncogene 6, 1623-1631, 1991
A:Title: The chicken junD gene and its product.
A:Reference number: S20099; MUID:92019832
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Schistosoma haematobium
C.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 05-May-2000
C.Accession: A44805; C44805
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                            5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule types: DNA
A.Residues: 1-70,96-140,142-220 <BO2>
A.Cross-references: GB:M27658; NID:9160979; PID:9160979
C;Superfamily: fluke eggshell protein
C;Keywords: egg shell
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-220/Product: eggshell protein #status predicted <AMT>
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hypothetical protein 2C477.1 - Caenorhabditis elegans
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57.6%; Pred. No. v.-.
... 0; Mismatches
     59.3%; Pred. No. 0.2; tive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTL 33
                                                                                                        354 GGGGIPGQSV--YMGAGGGGGGGGG 378
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                                                                             1 GGGGGIEGPTLRQWLAARAGGGGGGG 27
                              16; Conservative
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hes 19; Conservative
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Best Local Similarity
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A; Residues: 1-323 <HAR>
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Residues: 1-220 <BOB>
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A; Status: preliminary
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                October 9, 2002, 08:54:17; Search time 9.2178 Seconds (without alignments) 427.397 Million cell updates/sec
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224
1 GGGGGIEGPTLRQWLAARAG......GGGGGGIEGPTLRQWLAARA 41
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    283138 seqs, 96089334 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
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Description	hypothetical prote			himothetical prote	alwoine-rich prote	beliveloon-helix t	hotorogeneral ribo	necetogeneous rese	Production 101	L. L	nypormerica: proce	GCK I/ Process	acp-22 process	protei	(EC 3.4) (E)	(EC 3.4	\sim		hypothetical prote	homeotic protein H	DNA-binding profei		hynothetical prote	١.	KNA-DINGING PLOCES	Suppressor or same		hypothetical proce	phosphaciaying	
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Score	85	83	78	77	77	75.5	75	74.5	74	7.4	73	72	1 .	4 6		4 (7 (7/	2.5	7.7	72	72	71 5	71.5	71.5	71.5	71	7.1	
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37.1%; Score 83; DB 2; Length 388;

Query Match

hypothetical glyci signal recognition hypothetical glyci hypothetical prote hypothetical prote homeotic protein H hypothetical prote snRNP-associated p hypothetical glyci hypothetical glyci transforming prote hypothetical glyci glycine-rich cell glycine-rich cell glycine-rich prote hypothetical prote hypothetical prote phycine-rich cell glycine-rich prote	ENTS .tis elegans .oct-1999 #text_change 15-Oct-1999 t 1996	A.Reference number: 219331 A.Accession: T20961 A.Accession: T20961 A.Accession: T20961 A.Accession: T20961 A.Accession: T20961 A.Accession: T20961 A.Besidues: 1-500 CMIL> A.Besidues: 1-500 CMIL-> A.Besidues:	85; DB 2; Length 500; No. 0.16; smatches 9; Indels 0; Gaps 0; 30 451	T28H11.1 - Caenorhabditis elegans ditis elegans ditis elegans #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 ann, P. ID Data Library, July 1996 acquence of C. elegans cosmid T28H11. Z20582 Z20582 Y; translated from GB/EMBL/DDBJ NEL> EMBL:064609; PIDN:AAB04604.1; GSPDB:GN00022; CESP:T28H11.1 EMBL:0f4609; PIDN:AAB04604.1; GSPDB:GN00022; CESP:T28H11.1 es: strain Bristol N2; clone T28H11 colus glycine-rich cell wall protein 1.8
39 72 72 005 005 115 77 77 77 77 77 78 89 89 89 89 89 89 89 89 89 89 89 89 89	ALIGNMENTS Caenorhabditis ins evision 15-Oct eary, August 19	from GB/F TIDN:CABU:		or hon on or hon
H70839 JC4835 E70895 T727005 T1386 WJHU2G B84777 S22315 A70869 E95965 TV00799 T10799 T10799	S'- Caeno legans ce_revisi Library,	ted fro 3; PIDP 15B9 162/2;	5; .8c 4; 4; 3GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11.1 - Caenorh elegans ence_revision p. a Library, Ju ce of C. eleg 2 anslated from u64609; PIDN: rain Bristol
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496 534 767 1325 1325 1325 251 260 201 201 221 369 369 369		19531 ; translated L>: clone F15B :: clone F15B 3; 125/2; 162	vat LAJ : 'LSJ	protein T28H11.1 - Co enorhabditis elegans tt-1999 #sequence_rev: T29173 Wohldmann, P. the EMBL Data Librar; H. The sequence of C. H. The sequence of C. T29173 P. T29173 P. T29
31.7 31.7 31.7 31.7 31.7 31.2 31.2 31.2 31.2 30.8 30.8	al protein F15B9. Caenorhabditis e Oct-1999 #sequer nn: T20961 to the EMBL Data	nce number: Z19 ion: T20961 : preliminary: le type: DNA es: 1-500 (WIL> references: EME mental source: cs: CSP: F1589.5 sition: 5 sition: 5 sit 46/3; 63/3;	Similarity 6; Conser GIEGPTLROW ::	ical protein I S: Caenorhabdi 15-Oct-1999 #si ion: T29173 'J: Wohldmar d to the EMBL ption: T29173 : preliminary ion: T29173 : preliminary le type: DNA le type: DNA cle type: DNA cle type: DNA cle type: SNA in references: E mental source CESS: T28H11.1 CESS: T28H11.1 CESS: T28H11.1 FISHION: 4
717 717 717 717 70 70 70 70 70 69 69 69	RESULT 1 hypothetical protein C; Species: Caenorhak C; Date: 15-Oct-1999 C; Accession: T20961 R; Percy, C. submitted to the EMI	A.Reference number: A.Accession: T20961 A.Status: preliminar. A.Molecule type: DNA A.Residues: 1-500 <w a.cross-references:="" a.experimental="" a.gen<="" a.genetics:="" c.genetics:="" sourc="" td=""><td>Ma Loc 2 2 2</td><td>RESULT 2 hypothetical protein hypothetical protein c; Species: Caenorhat C; Date: 15-Oct-1999 C; Accession: T29173 RNalson, J; Wohldi submitted to the EM A; Description: The is A; Reference number: A; Reference number: A; Retarus: prelimina A; Molecule type: DN A; Residues: 1-388 A; Residues: 1-388 A; Cross-references: A; Experimental sour C; Genetics: A; Genetics: A; Map position: 4 A; Introns: 354/1 C; Superfamily: Phas</td></w>	Ma Loc 2 2 2	RESULT 2 hypothetical protein hypothetical protein c; Species: Caenorhat C; Date: 15-Oct-1999 C; Accession: T29173 RNalson, J; Wohldi submitted to the EM A; Description: The is A; Reference number: A; Reference number: A; Retarus: prelimina A; Molecule type: DN A; Residues: 1-388 A; Residues: 1-388 A; Cross-references: A; Experimental sour C; Genetics: A; Genetics: A; Map position: 4 A; Introns: 354/1 C; Superfamily: Phas
0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 T20961 hypothetical protein c; Species: Caenorhabó C; Date: 15-0ct-1999 C; Date: N. C. R. R. Percy, C. Submitted to the EMBI	A, Reference n A, Accession: A, Status: pre A, Molecule ty A, Residues: A, Cross-refea A, Experiment. C, Genetics: A, Gene: CESP A, Introns: A, Introns: A, Introns: A	Query Ma Best Loc Matches Qy 2 Db 423	RESULT 2 T29173 hypothetical protein T28H11.1 - Caenc Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispate: 15-0ct-1999 #sequence_revisit C; Accession: T29173 A. Bescription: The Sequence of C. els A. Reference number: 220582 A. Accession: T29173 A. Status: preliminary; translated fractions of the complex of

Job time : 6.81733 secs

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Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <u >Unknown></u>
32.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CIIY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /product= "Beta-ala' SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                           AppLICANT: Dower, William J.
AppLICANT: Dower, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36, 392
REGISTRATION NUMBER: 36, 392
REGERENCE/POCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                       ; Sequence 18, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                 32.6%
Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IEGPTLROWLAARA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                6 IEGPTLROWLAARA 19
                                                                                                                                    2 IEGPTLROWLAARA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-516-704-18
                                                                                                                                                                                                        RESULT 30
US-09-516-704-18
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                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                        32.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Barrett, Ronald W.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christlan
APPLICANT: Schatz, Peter J.
APPLICANT: Balssubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Pedduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 232, Application US/09244298A patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                          REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                      NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                              TYPE: amino acid
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                                 Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 32.6%; Score 73; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
ATTONNEY/ARGENT INFORMATION:
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITT: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: HINDIGG, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian APPLICANT: Schatz, Peter J. APPLICANT: Schatz, Peter J. APPLICANT: Balasubramanian, Palaniappan APPLICANT: Hendren, Richard W. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun TITLE OF INVENTION: RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-973-225-220
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                             NUMBER OF SEQUENCES: 232
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wel.
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0; Gaps
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 32.6%; Score 73; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
OTHER INFORMATION: /product= "Beta-ala"
US-09-244-298A-18
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                                                                                                           APPLICATION NUMBER: US/09/244,296A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W.
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                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HTUDICC, RODERT T.
REGISTRATION NUMBER: 36,39428
REFERENCE/DOCKET NUMBER: 98328
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEC ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                             : 16 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION
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1 IEGPTLROWLAARA 14
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Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATEMIT NELES #1.0, Version #1.30
SOFTWARE: PATEMIT NELES #1.0, Version #1.30
SOFTWARE: PATEMIT NELES #1.0, Version #1.30
SOFTWARE: PATEMIT NELES #1.30
ATTORNEY/AGENT INFORMATION:
NAME: HTUBLE ATTOR ROBERT #5,392
REFERENCE/DOCKET NUMBER: 95,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
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                                                                                                                                                                                                       Score 73; DB 2; Length 16;
Pred. No. 0.014;
0: Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                            32.6%; Scor.
100.0%; Pred. No. v.
... 0; Mismatches
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Haselden, Sherril S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattheakis, Larry C.
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GENERAL INFORMATION:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dower, William J.
Barrett, Ronald W.
Carirla, Steven E.
Duffin, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.6%
Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 14; Conservative
   TYPE: amino acid
STRANDEDNESS:
TOPOLGGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                              6 IEGPTLRQWLAARA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IEGPTLROWLAARA 15
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                                                                                                                                       ; MOLECULE TIPE
US-08-764-640-232
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                                                                                                                                                                                                                                 Query Match
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Gaps
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Wagstrom, Nicholas C.
Wrighton, Nicholas C.
Wrighton, PepTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-973-225-194
                                                                                                                                                                                                                                                                                                                                                                Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 220, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                     Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
Cwile, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 16 amino acids
                                                                                                                                       Gates, Christian
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 232
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Best Local Similarity
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RESULT 23
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                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwill, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Pedduturi, Surekha
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 15
OTHER INFORMATION: /product= "Beta-ala"
                                                                                                                                                       11-DEC-1996
                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
Research Triangle Park
                                                                                                                                                                                                                                                      NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REPERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yin, Oun
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0
                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
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FILING DATE: 11-DEC
CLASSIFICATION: 514
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APPLICANT: Dower,
                                    USA
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                                                      27709
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                                    COUNTRY:
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Balasubramanian, Palaniappan
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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11-DEC-1996
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; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
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STREET: Five Moore Drive, P.C
CITY: Research Triangle Park
                                                                                                                                                                              TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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IBM PC compatible
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REGIESTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 232;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR
                                                                                                                                                                                                                                      LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-764-640-194
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yin, Qun
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 linear
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APPLICANT:
APPLICANT:
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16 amino acids

LENGIH:

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ADDRESSEE:
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ. ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION WUMBER: 36,392
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Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: Bower, William J.
Cwirla, Steven E.
Gartes, Christian
                                                                                                                     Sequence 17, Application US/09516704; Patent No. 6251864; CENERAL INFORMATION: APPLICANT: Dower, William J. Barrett, Ronald W. Cwillia, Steven E. Gates, Christian
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 244
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6 IEGPTLRQWLAARA 19
                   2 IEGPTLRQWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
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                                                                                                        US-09-516-704-17
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Gaps
                                                                            Deprince, Randolph B. Podduturi, Surekha TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 STREET: Five Moore Drive, P.O. Box 13398
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Schatz, Peter J.
Balasubramanian, Palaniappan
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FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
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NAME: HULDLG., ROBERT, 39.
REGISTRATION NUMBER: 36,39.
REFERENCE/DOCKET NUMBER: PK3281
                                                  Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                            Research Triangle Park
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; Patent No. 5869451
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                   Hendren, Richard W.
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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STRANDEDNESS: <Unknown>
                                                                                                                                                             RECEPTOR
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                                                                                                                                                                                     NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO:
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US-09-244-298A-185
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: PK3065USW
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-248-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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HOLECLLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
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....eR: US/09/244,298A
N: 514
TW: 514
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.(CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                 LENGTH: 15 amino acids
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 185:
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 COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                        Length 15;
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                                                                                                                                                        32.6%; Score 73; DB 3; Le 100.0%; Pred. No. 0.013; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 185, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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INFORMATION FOR SEQ ID NO: 185:
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Best Local Similarity 100.1
Matches 14; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 14, Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-09-244-298A-185
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                                       TYPE: amino acid
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6 IEGPTLRQWLAARA 19
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ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                  ; Sequence 185, Application US/08764640; Patent No. 5869451; Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                     Deprince, Randolph B. Podduturi, Surekha
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research Triangle Park
                                                                                                                                                                         Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                          Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                              Glaxo Wellcome
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Best Local Similarity 100.
Matches 14; Conservative
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COMPUTER READABLE FORM:
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1 IEGPTLRQWLAARA 14
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                                                                                                                                        GENERAL INFORMATION:
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                                                   RESULT 14
US-08-764-640-185
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APPLICANT:
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APPLICANT:
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STATE:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPFRATING PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-973-225-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 185, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselden, Sherril S.
Mattheakis, Larry C.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatz, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                     NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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Matches 14; Conservative
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Gaps

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APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                               32.6%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                             100.0%; Preq. ...
                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08764640; Patent No. 5869451; Patent No. 5869451
                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/Mc-SOPERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,392
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glaxo Wellcome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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Matches 14; Conservative
TYPE: amino acid
                                                                                                                                                                          14; Conservative
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wel
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                                                                                                                                                                                                              6 IEGPTLRQWLAARA 19
                                                                                                                                                                                                                                      amino acid
                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                            ; TOPOI
; MOLECULE T
; SEQUENCE I
US-09-516-704-193
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                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-764-640-17
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                                                                                                                                       Query Match
                                                                                                                                                                            Matches
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                            32.6%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
CWAITA, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 IEGPTLRQWLAARA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-516-704-193
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                                       Gaps
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32.6%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
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us-09-422-838c-34.rai

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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Patent No. 6251864

GENERAL INFORMATION:

APPLICANT: Dower, William J.

CANIAL Steven E.

GARLE, Christian
Schatz, Peter J.

Balasubramanian, Palaniappan
Wagstrom, Christopher R.

Hendren, Richard W.

Dowert Steven E.

Hendren, Richard W.

Dowert Steven E.

Hendren Richard W.

Dowert Steven E.
                                                                                                        STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P. C
CITY: Research Triangle Park
                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
      TITLE OF INVENTION: PEPTIDES TITLE OF INVENTION: RECEPTOR
                                                                                         ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.6
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-244-298A-193
                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                         USA
                                                                                                                                                                                            27709
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US-09-516-704-13
                                                                                                                                                                         COUNTRY:
                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                     APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.6%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/09/244,298A FILLING DATE: 11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
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Barrett, Ronald W.
CWITA. Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                               Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                     Wagstrom, Christopher R
Hendren, Richard W.
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Sequence 13, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                              Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amiliary
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.C
CITY: Research Triangle Park
                                                           Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids IYPE: amino acid
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                   APPLICANT:
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APPLICANT:
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Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
PEPTIDES AND COMPOUNDS THAT BIND TO
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                  Score 73; DB 3; Length 14,
; Pred. No. 0.012;
.____hes 0; Indels
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                                                                                    32.6%; Scot.
100.0%; Pred. No. v.
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                         Sequence 193, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wrighton, Nicholas C
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Mattheakis, Larry C.
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ADDRESSEE: Glaxo Wellcome
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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LENGTH: 14 amino acids
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                                                                                                                          Best_Local Similarity 100.
Matches 14; Conservative
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ZIP: 27709
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Matches 14; Conserv
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US-08-973-225-13
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
RAME: Hubiec, Robert T.
REGISTRATION NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248 #1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
SOFTWARE: PatentIn Release #1.0, Version #1.30
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          11-DEC-1996
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Mattheakis, Larry C.
                                                                                                                                                             PK3281
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HEUDIGE, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-100.
INFORMATION FOR SEQ ID NO: 193:
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LENGTH: 14 amino acids
                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-193
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                                                        FILING DATE: 11 CLASSIFICATION:
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; Sequence 193, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
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NAME: HTUDIGG, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-100.
INFORMATION FOR SEQ ID NO: 13:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                            Research Triangle Park
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TITLE OF INVENTION: RECEPTOR
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                                                                                   Glaxo Wellcome
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                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 14; Conservative
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                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-08-764-640-193
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APPLICANT:
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                             CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY TO SAID POLYPEPTIDE
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     NOVEL POLYPEPTIDE GENE CDNA, VECTOR
                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 GGGGGAGALAAALAAAGAGGGLGGGGG--GGALAAALAA 487
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TIPE: DISSECTE, 3.30 INCH, 1.44 MB COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: Microsoft Windows 95 SCTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/864,038A FILING DATE: MAY 28, 1997
FILING DATE: MAY 28, 1997
FILING DATE: 15-UU1y-1996
ATTORNEY AGENT INFORMATION: NAME: C. Bruce Hamburg REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)96-2340
TELEFAX: (212)96-3773
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CONTAINED SECONTAINED SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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Patent No. 5869451
Patent No. 5869451 5837683
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                                                                                                                                                                                                           812-5 Hirano
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CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
     TITLE OF INVENTION:
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APPLICANT: Dower,
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                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-864-038A-3
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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Query Match
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                               Q
                                                                                                                                          9; Gaps
                                                                                            Query Match

34.2%; Score 76.5; DB 2; Length 25;
Best Local Similarity 40.6%; Pred. No. 0.0091;
Matches 13; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
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34.2%; Score 76.5; DB 3; Length 25;
Best Local Similarity 40.6%; Pred. No. 0.0091;
Matches 13; Conservative 8; Mismatches 2; Indels
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                                                                                                                                                                        7 EGPTLROWLAARAGGGGGGGGGIEGPTLROWLA 38
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: /product= "Ava" US-08-764-640-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: /product= "Ava" US-09-244-298A-231
                                                                                                                                                                                                                                                                                                              Sequence 231, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Podduturi, Surekha
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFRENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Mouse L. CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaxo Wellcome
NAME/KEY: Modified-site
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LENGTH: 25 amino acids
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MEDIUM TYPE: Floppy of
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yin, Qun
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                  LOCATION:
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APPLICANT:
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7 EGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLA 38

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Gaps
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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2 DGPTLREWISFXA------DGPTLREWIS 24
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OTHER INFORMATION: /product= "Av SEQUENCE DESCRIPTION: SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                   Sequence 231, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 244
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                                                                                                   US-09-516-704-231
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Sequence 185, App
Sequence 18, Appl
Sequence 194, App
Sequence 232, App
Sequence 18, Appl
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APP
APP
APP
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Sequence 185, App
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Sequence 193, App
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                                                                                  (without alignments)
146.898 Million cell updates/sec
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                                                                  October 9, 2002, 08:55:27; Search time 6.81733 Seconds
                                                                                                                                         1 GGGGGIEGPTLRQWLAARAG.......GGGGGGGIEGPTLRQWLAARA 41
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3 copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-464-038A-3

US-08-74-46-13

US-08-73-225-13

US-08-973-225-13

US-08-973-225-193

US-08-973-225-193

US-09-244-298A-13

US-09-516-704-13

US-08-764-640-17

US-08-764-640-185

US-08-764-640-185

US-08-764-640-185

US-09-244-298A-185

US-09-244-298A-185

US-09-26-40-185

US-09-16-704-185

US-09-16-704-185

US-08-764-640-184

US-08-973-225-184

US-08-973-225-184

US-08-973-225-184

US-08-973-225-184

US-08-973-225-184

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US-08-973-225-184

US-08-973-225-184
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                 OM protein . protein search, using sw model
                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                       US-09-422-838C-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match Length DB
                                                                                                                                                                        BLOSUM62
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7733
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                                                                                                                                      Perfect score:
                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                             Searched:
                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                               Run on:
                                                                                                                             Title:
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Sequence 194, App Sequence 232, App Sequence 194, App Sequence 192, App Sequence 232, App Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 195, App Sequence 195
6 3 US-09-244-298A-194 6 4 US-09-244-298A-232 6 4 US-09-516-704-18 6 4 US-09-516-704-18 6 4 US-09-516-704-194 2 US-08-516-704-194 6 4 US-09-516-704-232 2 US-08-317-401E-4 6 4 US-09-32-52-7 6 4 US-09-32-52-7 6 8 US-08-317-401E-2 1 US-08-157-349-9 1 US-09-157-349-9 1 US-09-157-349-9 1 US-09-157-349-9 1 US-09-157-349-9 1 US-09-157-349-9 1 US-09-157-349-9 1 US-09-053-003-40 1 US-09-053-003-40 1 US-08-053-003-40
73 32.6 16 73 32.6 16 73 32.6 16 73 32.6 16 73 32.6 16 72 32.1 268 72 32.1 268 72 32.1 268 72 32.1 268 72 31.7 31.7 70.5 31.5 201 70.5 31.5 201 69 30.8 14 69 30.8 14
200 200 332 332 332 344 444 444

ALIGNMENTS

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APPLICANT: SCHIZ, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: You' Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT IV.
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                              . Sequence 231, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                             MAPLICANT: DOWET, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Cates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                 US-08-764-640-231
                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
RESULT 1
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FEATURE

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6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
οy
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AAY96521 standard; peptide; 36 AA 04-SEP-2000 (first entry) AAY96521; RESULT 30 AAY96521

Cyclic or linear thrombopoietin mimetic peptide compound 2.

Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.

Synthetic.

_note= "optionally linked to an Fc molecule" Location/Qualifiers /note= "optional" /label= linker /label= TMP_1 23..36 /label= TMP_2 Disulfide-bond Modified-site Peptide Peptide

WO200024770-A2

04-MAY-2000.

99WO-US24834. 22-OCT-1999;

98US-0105348 23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Claim 16; Page 61; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], as new TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising %2.%_10, %2.%_11_1, %2.%_11_2, %2.%_11_2, %2.%_11_2, %2.%_11_2, %2.%_11_2, %2.%_11_3, %2.%_11_2, %2.%_11_2, %2.%_11_3, %2.%_11_4, %2.%_11_6, %2.%_11

36 AA; Sequence

ö Gaps 0; Length 36; Indels Score 168; DB 21; Pred. No. 6.7e-13; 1 IEGPTLRQCLAARAGGGGGGGGIEGPTLRQCLAARA 36 6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41 0; Mismatches 75.0%; 34; Conservative Best Local Similarity Query Match Matches δλ g

Search completed: October 9, 2002, 08:58:59 Job time : 19.4356 secs

9 10:30:18 2002

Wed Oct

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Gaps

.; 0

Indels

94.4%; Pred. No. 6.7e

34; Conservative

Best Local Similarity

Matches

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The present invention describes composition of matter (I) comprising an Fr domain, pharmacologically active peptides, and linkers. Where (I) is:

Every domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(L1)c-P1-(L2)d-P2.

(L3)d-P2.

(L3)d-P3.

(L3)d-P3.

(L3)d-P3-(L4)f-P4.

(L3)d-P3.

(L4)d-P2.

(L3)d-P3.

(L4)d-P3.

(L3)d-P3.

(L4)d-P3.

(L3)d-P3.

(L4)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L3)d-P4.

(L4)d-P4.

(L3)d-P4.

(L4)d-P4.

(L3)d-P4.

(L4)d-P4.

(L4
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
                                                                                              5;
    Length 34;
                                                                                                        Indels
ch 76.3%; Score 171; DB 21;
1 Similarity 94.4%; Pred. No. 2.8e-13;
34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                    6 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17298 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
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                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17298;
                   Query Match
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17298
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75.0%; Score 168; DB 21; Length 36;

36 AA;

Sequence

Query Match

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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d
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                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietlin; thrombopoietlh; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 168; DB 21; Length 36; 94.4%; Pred. No. 6.7e-13;
Live 0; Mismatches 2; Indels
6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                      TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                     AAB17299 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
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Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000.
                                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U,
                                                                                                                                                                                                                                       AAB17299;
                                                                                                                                         RESULT 29
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to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an (X1)a-P1-(X2)b, where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L3)e-P2, (L1)c-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2, (L3)e-P3, or -(L3)e-P3, or -(L3)e-P
                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour neorosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                     sequences used in the exemplification of the present invention.
                                                                                                                                                        DB 21; Length 35;
                                                                                                                                                                                                                Indels
                                                                                                                               Score 177.5; DB 21;
Pred. No. 5.2e-14;
                                                                                                                                                                                                                                                                                                6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17302 standard; Peptide; 40 AA
                                                                                                                                                     79.28;
                                                                                                                                                                                97.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2000 (first entry)
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                          35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17302;
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U,
                                                                                                                                                     Query Match
                                                                                                                                                                                Local
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 26
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Fe domain, pharmacologically active peptides, and linkers. Where FI an Fe domain, and M2 = are each independently selected from -(L)C-L). -(L1)C-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1 P2. P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and an b, s. The composition can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent invention.
                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive: EPO: TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                           Length 40;
                                                                                  Indels
                                         Score 174; DB 21;
Pred. No. 1.5e-13;
                                                                                                                   6 IEGPTLRQWLAARAGGGG----GGGGIEGPTLRQWLAARA 41
                                                                                                                                                          1 IEGPTLROWLAARAGGGKBRACGGGGIEGPTLROWLAARA 40
                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                             AAB17291 standard; Peptide; 34
                                    77.78;
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0428082.
                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                        Local Similarity
es 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04 - MAY - 2000.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                    AAB17291;
                                       Query Match
                                                                              Matches
                                                                                                                                                                                                                        RESULT 27
                                                                                                                                                          qq
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34 AA;

Sequence

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888888888

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                 thrombopotetin. The TMPS are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an
activate the c-Mpl receptor which mediates the activity of endogenous
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; exythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                 81.2%; Score 182; DB 21; Length 36; 94.4%; Pred. No. 1.6e-14; 1.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                 6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17296 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                               Local Similarity 94.4:
tes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                           36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17296;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P2-(L3)d-P3-(L3)d-P2-(L3)d-P3-(L3)d-P2-(L3)d-P3-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3
                                                                                                                                                                                                                                               ij
half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive, EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                  9:
                                                                                                                                                                                            DB 21; Length 42;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                    6 IEGPTLRQWLAARA-----GGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                  80.8%; Score 181; DB 21;
85.7%; Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17292 standard; Peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                              Best Local Similarity 85.74
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                        42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17292;
                                                                                                                                                             Seguence
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                     δλ
                         SSSSX
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FL-(X2)b, where: FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2.

(L1)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                        sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                      81.5%; Score 182.5; DB 21; Length 39; 92.3%; Pred. No. 1.5e-14; live 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                      6 IEGPTLRQWLAARAGG---GGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17306 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                               39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17306;
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 22
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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP.1-(L.1).nTMP.2], is new. TMP.1 and TMP.2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-X_{1,1,0}, X_2-X_{1,1,1}, X_2-X_{1,2}, X_2-X_{1,2,3}, X_2-X_{1,2,3}, X_2-X_{1,2,3}, X_2-X_{1,2,3}, X_2-X_{1,2,3}, X_1-X_{1,2,3}, X_1-X_{1,2,3}, and X_1-X_{1,2,3}, X_2-X_{1,2,3}, X_2-X_{1,2,3}, X_3-X_{1,2,3}, X_3-X_{1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    .
0
                                                                                                                                                                             Score 182; DB 21; Length 36;
Pred. No. 1.6e-14;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                           6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                  Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= linker
19.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19..32
/label= TMP_2
                                                                                                                                                                                81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                       94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000 (first entry)
                                                                                                                                                                                                  3est Local Similarity 94.4 datches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365108/31.
                                                                                                                               36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96526;
                                                                                                                               Sequence
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00000x0
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Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-F1-(X2)b, where FI = an Fc domain; XI and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a b, c, d, e, and f = are each independently linkers; and a b, c, d, e, and f = are each independently linkers; and a b, c, d, and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autolimune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                         81.7%; Score 183; DB 21; Length 38; 94.7%; Pred. No. 1.3e-14;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                 6 IEGPTLRQWLAARA--GGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17304 standard; Peptide; 39 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.7
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases -
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                                                                                                                                                                                                                                                         38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
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(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently laws extication and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; expthropoietin; thrombopoietin; interlenkin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                           .,
,
                                                                                                                                                                                                                               81.5%; Score 182.5; DB 21; Length 39; 92.3%; Pred. No. 1.5e-14; Live 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                   IEGPTLRQWLAARAGGG----GGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17305 standard; Peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                   39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U,
                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17305;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8×333355×8
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10 to 14 residues in length comprising X.2-X.1_0, X.2-X.1_1, X.2-X.1_2, X.2-X.1_3, X.2-X.1_4, X.1-X.1_0, X.1-X.1_1, X.1-X.1_2, X.1-X.1_3, and X.2-X.1_4, X.1_1 = 1, A, V, L, S or R; X.2 = E, D, K or V; X.3 = G or A; X.4 = P; X.5 = T or S; X.6 = L, I, V, A or F; X.7 = R or K; X.8 = Q, N, C or E; X.9 = W, Y or E; X.1_2 = A, I, V, L, F, R, G, S, or Q; X.1_3 = R, K, Y, N, Q or G; X.1_4 = A, I, V, L, F, T, R, E, Or G; L.1 = 1 inker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and thrombopoletin. The TWPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
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36 AA; Sequence

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.;
0
                                      0; Gaps
    82.6%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 7.2e-15; live 0; Mismatches 1; Indels
                                                                            6 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 41
Query Match
Best Local Similarity 97.29
Matches 35; Conservative
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AAB17294 standard; Peptide; 37 AA. 31-OCT-2000 (first entry) AAB17294; RESULT 18 AAB17294

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; TPO-mimetic peptide sequence SEQ ID NO:350.

autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vāscular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

Synthetic.

WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999;

98US-0105371 99US-0428082 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases

Example 1; Page 318; 608pp; English.

Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-Y1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)a-P2-(L3)a-P3, or -(L1)c-P1-(L2)d-P2-(L3)a-P3, or -(L1)c-P1-(L2)d-P2-(L3)a-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of ап The present invention describes composition of matter (I) comprising

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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 least 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer Thalf-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an F0 domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L3)e-F-3, or -(L1)c-P1-(L2)d-P2-(L3)e-F-3, or -(L1)c-F1-(L2)d-P2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L2)d-F2-(L3)e-F-3, or -(L1)c-F1-(L3)d-F2-(L3)e-F-3, or -(L1)c-F1-(L3)d-F2-(L3)e-F-3, or -(L1)c-F1-(L3)d-F2-(L3)e-F-3, or -(L3)e-F-3, or -(L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TFO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.9%; Score 183.5; DB 21; Length 37; 97.3%; Pred. No. 1.1e-14; 1.1ve 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | IEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 IEGPTLROWLAARA-GGGGGGGGGIEGPTLROWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17295 standard; Peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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8×8888888888×8

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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein Ab hinding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1 -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P-3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                    Score 185; DB 21;
Pred. No. 7.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                           6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17307 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                        82.6%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.23
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                               36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17307;
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
AAB17307
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      O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18032 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                   82.6%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 7.2e-15;
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGCGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                         6 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "optional"
15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                            AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2000 (first entry)
                                                                                                                                                                                                                                        Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                            36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96524;
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                             RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                              AAY96524
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O or 1, provided that at least 1 of a and b is 1. The composition can are expostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DMAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Feb domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAAB1803 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
      8888888888888
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36 AA; Seguence

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0
                                  Gaps
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0
83.0%; Score 186; DB 21; Length 36; 97.2%; Pred. No. 5.5e-15;
                              Indels
                                                                            1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                            6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                             0; Mismatches
                             35; Conservative
              Best Local Similarity
Query Match
                             Matches
                                                             à
                                                                                         a
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AAY96523 standard; peptide; 36 AA RESULT 14 AAY96523

04-SEP-2000 (first entry) AAY96523

Thrombopoietin mimetic peptide compound 4.

Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.

Synthetic

/note= "optionally modified by bromoacetyl or PEG" 'note= "optionally linked to an Fc molecule" Location/Qualifiers 15..22 /label= linker l..14 /label= TMP_1 Key Modified-site Modified-site Peptide Peptide Peptide

WO200024770-A2

/label= TMP_2

04-MAY-2000

99WO-US24834 98US-0105348 22-OCT-1999; 23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia

Claim 16; Page 62; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least

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0
10 to 14 residues in length comprising X_-2 \cdot X_{-1} = 0, X_-2 \cdot X_{-1} = 1, X_-2 \cdot X_{-1} = 2, X_-2 \cdot X_{-1} = 1, X_-1 \cdot X_{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic: VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 186; DB 21; Length 36; Pred. No. 5.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                           virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17303 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.0%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blanding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, b), and P4 = are each independently sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TRF; antiagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.6%; Score 194; DB 21; Length 60; 100.0%; Pred. No. 1.1e-15; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMP-TMP-Fc protein sequence SEQ ID NO:10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blaiding, protein half-life or incorporate function, and possibly placental transfer. AAA69443 to AAA69526 and AAB180915 to AAA69520 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoletin; interleukin 1; cytocoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.6%; Score 194; DB 21; Length 269; 100.0%; Pred. No. 5e-15; 1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17301 standard; Peptide; 36 AA.
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99US-0428082.
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nes 36; Conservative
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is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_{-1}, x_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J, Boone TC;
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99US-0428082
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Matches 36; Conservative
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AAB17282
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where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, astima, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Feb domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent uncleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; imunosoppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoieth; thrombopoieth; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385
                                                                                                                                                                                                                                                                                                                               Length 42;
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                                                                                                                                                                                                                                                                                                                               Score 194; DB 21;
Pred. No. 7.7e-16;
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                                                                                                                                                                                                                                                                                                                                                100.0%; Pr
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                                                                                                                                                                                                                                                                                        42 AA;
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where Pl, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA65256 and AAB16955 to AAA69303 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; NF; antagonist; MMP; inhibitor; erythoojetin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.6%; Score 194; DB 21; Length 36; 100.0%; Pred. No. 6.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17293 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.C
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17293
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independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                           86.6%; Score 194; DB 21; Length 36; 100.0%; Pred. No. 6.5e-16;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                            6 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin mimetic peptide compound 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAY96525 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-365108/31.
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                                                                                                                                                                                    36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
AAY96525
                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
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                                                                                                                                                    platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each
                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                            virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                    229 GGGGGIEGPTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAARA 269
                                                                                                                                                                                                                                              100.0%; Score 224; DB 21;
100.0%; Pred. No. 1.7e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                 AAB16959 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                       269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA69445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB16959:
                                                                                                                                                                                                                                                                                                                                                                                   AAB16959
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independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,

-(L1)c-P1-(L2)d P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

where P1, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; L1, L2, L3, and L4 = are each independently

independently linkers; and a, b, c, d, e, and f = are each independently

or I, provided that at least 1 of a and b 1s 1. The composition can

have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

activities. DNAs, vectors and host cells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer

half-life or incorporate functions such as Fc receptor binding, protein

A binding, complement fixation and possibly placental transfer. AAA69443

to AAA69526 and AAB16955 to AAB1803 represent nucleotide and amino acid

sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; mMMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                   98.2%; Score 220; DB 21; Length 268;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                          229 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                     1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 40
                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.9e-18;
                                                                                                                                                                                                                                                                                                                             100.0%; Preu. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16963 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                    3est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                  268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB16963;
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                      fatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                              The present invention describes composition of matter (1) comprising an Cr domain, pharmacologically active peptides, and linkers. Where (1) is:

(X1)a-F1-(X2)b. where: R1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
(MACPA) and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
conclusion of the composition can
activities. DNNs, vectors and host cells from the present invention can
activities. DNNs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
conseful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
containing, complement fixation, and possibly placental transfer. AAA69443
ct A binding, complement fixation, and possibly placental transfer. AAA69443
cc sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 224; DB 21; Length 42; 100.0%; Pred. No. 2.6e-19; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGGGIEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                        Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96530 standard; Protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Feige U, Cheetham J;
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Matches 41; Conservative
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        WPI; 2000-350702/30.
                                                                                     autoimmune diseases
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overlapping oligonucleotides were used to construct a synthetic gene encoding a thrombopoietin mimetic peptide (TMP), which was then fused in-frame to the Fc region of the human igdichain (see was then fused in-frame to the Fc region of the human igdichain (see AAY96529). A compound which binds to an mpl receptor comprising a TMP c dimer joined by a linker [TMP1-(L.1)_nTMP.2], is new. TMP1 and TMP2 c are amino acid sequences varying from at least 10 to 14 residues in c length comprising X.2-X.1.0, X.2-X.1.1, X.2-X.1.2, X.2-X.1.4, X.2-X.1, X.2-X.1.4, X.2-X.1.4, X.2-X.1.4, X.2-X.1.4, X.2-X.1.4, X.2-X.1, X.2-X.1, X.2-X.1, X.2-X.1, X.2-X.1, X.2-X.1, X.2-X.1, X.2-X.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; ant1-human immunodeficiency virus; ant1-HIV; ant1-anaemic; dermatological; immunosuppressive; ant1-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGIEGPTLRQWLAARAGGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGGGGIEGPTLRQWLAARAGGGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 224; DB 21;
100.0%; Pred. No. 2.6e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2A; Page 49-50; 91pp; English.
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Example 2A; Page 48; 91pp; English.
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Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA29229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                  A compound which binds to an mpl receptor comprising a thrombopoletin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_1 = 0, X_2 - X_1 = 0, X_2 - X_1 = 0, X_1 - X_1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                           production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 224; DB 21;
100.0%; Pred. No. 2.5e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17281 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                   Claim 16; Page 65; 91pp; English.
                                                          Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0
Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                  WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AA;
     (AMGE-) AMGEN INC
                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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Feige U, Liu C, Cheetham J, Boone TC;

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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an K10 armacologically active peptides, and linkers. Where (I) is:

(X10 -F1 - (X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1) C-P1 -(L1) C-P1 -(L2) d-P2, (L3) e-P3, or -(L1) C-P1 -(L3) e-P3, or -(L3) e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGGGGIEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 224; DB 21;
100.0%; Pred. No. 2.6e-19;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                               Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17308 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371.
99US-0428082.
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WPI; 2000-350702/30.
                                                                                                                                                       autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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1: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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3: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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6: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
7: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
8: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
10: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
12: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*
13: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
14: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
15: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
17: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
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18: /SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
                                                                                                                                                                                                                                                        October 9, 2002, 08:50:51; Search time 18.4356 Seconds (without alignments) 247.023 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGGIEGPTLRQWLAARAG........GGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_032802:*
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-422-838C-34
224
                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                 Run on:
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		Description	Thrombopoietin mim	TPO-mimetic peptid	Synthetic TMP-TMP	Thrombopoietin mim	Human IqG1 Fc TMP	Fc-TMP-TMP protein	TPO-mimetic peptid	TPO-mimetic peptid	Thrombopoietin mim	TPO-mimetic peptid	Synthetic TMP-TMP-
SUMMARIES		ID	AAY96528	AAB17281	AAB17308	AAY96530	AAY96531	AAB16959	AAB16963	AAB17293	AAY96525	AAB17282	AAB17311
		DB	21	21	21	21	21	21	21	21	21	21	21
	ø₽	Length	43	42	42	42	269	268	36	36	36	42	9
		Query Match Length DB	100.0	100.0	100.0	100.0	100.0	98.2	96.6	96.6	86.6	9.98	96.6
		Score	224	224	224	224	224	220	194	194	194	194	194
		Result No.		7	٣	4	S	9	7	8	σ	10	11

TMP-TMP-FC protein TPO-mimetic peptid Thrombopoietin mim TPO-mimetic peptid	megakaryocyte; production; anti-anemic; dermatological; an Fc molecule"
AAB16960 AAB17301 AAX96523 AAB17303 AAB17304 AAB17294 AAB17296 AAB17297 AAB17287 AAB16977	ide; 41 AA. ry) peptide compound 9. ; TMP; TPO; platelet; ency virus; anti-HIV; -inflammatory; linker n/Qualifiers "optionally linked to TMP_1 linker TMP_2 5348.
269 366 366 366 366 366 366 366 3	st entr metic p imetic; deficie ; anti- note= " note= " 027 label= 027 label= 027 label= 027 label= 027 label= 1027 label= 027 label= 027 label= 027
194 88 83 186 83 186 83 186 83 187 185 82 187 187 187 187 187 187 187 187 187 187	1 28 AY96528 s' 4-SEP-2000 nrombopoi nrombopoi nrithuman mmunosuppy rhthetic. sy adified-s aptide aptide aptide aptide 2200024770 2-OCT-1998
11111122222222222222222222222222222222	RESULT AAV9655 AAV9611 AAV9655 AAV9611 AAV9655

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                                                                                                 Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   former sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                               Ouery Match 28.9%; Score 55.5; DB 3; Length 690; Best Local Similarity 41.9%; Pred. No. 1.4e+02; Matches 13; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.6%; Score 55; DB 5; Length 103; Best Local Similarity 56.5%; Pred. No. 23; Matches 13; Conservative 1; Mismatches 5; Indels
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Hallsworth K.;
Hallsworth K.;
"The Sequence of C. elegans cosmid C18A3.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterice...
Waterston R.;
"Direct Submission.";
"Direct Submission.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U28944; AAK68193.1; -.
Hypothetical protein.
SEOGENCE 103 AA; 11420 MW; 6D3A1877857E5E64 CRC64;
EMBL; AY005477; AAG02575.1; -.
Hydrolase.
SEQUENCE 690 AA; 76226 MW; 6546BE2499D8D43C CRC64;
                                                                                                                                                                                                                                           0950V6 PRELIMINARY; PRT; 103 AA. 0950V6. 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 11.4 KDA PROTEIN. 018A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 9, 2002, 09:03:16 Job time : 14.9826 secs
                                                                                                                                1 IEGPTLROWLAARAGGGNGSGGIEGPTLROW 31
                                                                                                                                                   36 VKSPYLSTWLSAGTDGGNG-GYLAG----QW 61
                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 WLAARAGGGNGSGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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Q95QV6
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                             MEDLINE-99439764; PubMed-10508862; Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E., Kilimann M.W.;
                           0;
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0
29.2%; Score 56; DB 11; Length 4833; 50.0%; Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 11; Length 5038;
                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547600 MW; DADA460CF3B40888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Y19185; CAB60731.2; -.
HSSP; P04410; 1A25.
                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                PRT; 5038 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00168; C2; 2.

SMART; SM00295; PD2; 1.

SMART; SM00229; C2; 2.

SMART; SM00228; PD2; 1.

PROSITE; PS00049; C2_DOMAIN_1; UNKNOWN_1.

PROSITE; PS50004; C2_DOMAIN_2; 2.

PROSITE; PS50106; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGP 26
                                                                     1 IEGPTLRQWLAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                    Cell Biol. 147:151-162(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%;
50.0%;
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BLEEF MILES 134930; ACZ.
INTERPRO; IPR000008; C2.
InterPro; IPR001478; PDZ.
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                PRELIMINARY;
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P0436E04.1.
             Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kilimann M.;
                                                                                                                                                                                                                               ACZ OR ACZ.
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  Query Match
                                                                                                                                                                                                                 ACZONIN.
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Q9FTZ5;
                                                                                                                                                              090YX7;
                                                                                                                                                090YX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Q9FT25
                                                                                                                      RESULT 26
                                                                                                                                     090YX
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MEDLINE=20406523; PubMed=10952006;
Koibuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
"Molecular cloning and characterization of a gene encoding glutaminase
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                     Score 55.5; DB 10; Length 202; Pred. No. 40; 6; Mismatches 14; Indels 7
                                                                                   Sasaki T., Matsumotto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0436E04.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%; Score 55.5; DB 3; Length 690; 41.9%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002818; BAB16319.1; -SEQUENCE 202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thammarongtham C., Turner G., Moir A.J., Tanticharoen M. Cheevadhanarak S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A new class of glutaminase from Aspergillus oryzae."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Aspergillus oryzae.";
Appl. Microbiol. Biotechnol. 54:59-68(2000).
EMBL; AB02552; BA86934 li. -
SEQUENCE 690 AA, 76165 MW; E3DOB17841EEAOOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                          94 VVSPSCRRQTAGRHGGCGGGGRWMAAAGGRDGGGCRRWWAA 134
                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGNG-----SGGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                       690 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 VKSPYLSTWLSAGTDGGNG-GYLAG----QW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                       Query Match 28.9%;
Best Local Similarity 34.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, GLUTAMINASE (EC 3.5.1.2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                     SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae.
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             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUTAMINASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RIB40;
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RA Adams N.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., 10 PW. Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Baradon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakraroglu L., Beasley E.M.,
RA Borion R.C., Buszen D.B., Berman B.P., Bhandari D., Bolshakov S.F.,
RA Borkova D., Botchan M.R., Bounck J., Brockstein P., Brottler P.,
RA Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Gorkin R. Deubler C., Davenport L.B., Davies P.,
RA Gong F.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Jalai M., Alarvey D., Helman T.J., Hernandez J.R., Houston K.A.,
RA Jalai M., Ralush F., Karpen G.H., Ke Z., Kenison J.M., Ketchum K.A.,
RA Jalai M., Ralush F., Karpen G.H., Ke Z., Kenison J.M., Retchum R.A.,
RA Jalai M., Ralush F., Karpen G.H., Ke Z., Kenison J.M., Retchum R.A.,
RA Merkulov G., Milshina N.V., Morshy L., Muzny D.M., Nosheerin A.,
RA Melson D.M., Wurphy B., Murphy L., Muzny D.M., Nosheon D.L.,
RA Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.M., Murphy B., Murphy L., Muzny D.M., Nosheon D.L.,
RA Rasko P., Lei X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.M., Murphy B., Murphy L., Muzny D.M., Noshen D.L.,
RA Rainert R., Nelson K.A., Nixon K., Nusskern D.R., Pacle D.J.,
RA Rainert R., Remington K., Saunders R.D., Schoeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Strong M., Wang S., Sun E.,
RA Wang Z.-Y., Strong M.M., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RCBL_TaxID=7227;
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                         Score 56; DB 5; Length 3190;
Pred. No. 5.9e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                    E53526F78BC055A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
               InterPro; ITRO00433; ZnF_Zfinger.
InterPro; IPR000433; ZnF_ZZ.
Pfam; PF00493; Dromodomain; 1.
Pfam; PF02172; KIX; 1.
Pfam; PF02135; Zf-TAZ; 2.
Pfam; PF0259; ZZ; 1.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
PR051TE; PS00633; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN.
PROSITE; PS00631; BROMODOMAIN.
PROSITE; PS50014; BROMODOMAIN.
SEQUENCE 3190 AA; 331879 MW; E53526F78BC05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 3275 AA
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                               61.18;
                                                                                                                                                                                                                                                                                                                                                                      10 LAARAGGGNGSGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                             44 LTGGAGGGNGGGGASGVT 61
  InterPro; IPR003101; KIX.
                                                                                                                                                                                                                                                                                                                                 11; Conservative
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                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                         Query Match
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δ
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.",
Schence 287:2185-2195(2000).
BR EMBL, Abc03448; AaF46516.1; ...
BR EMBL, RE003448; AaF46516.1; ...
BR EMBL, RE003101; KIZ.
BR FIYBase; FEGNO015624; nel.
BR FIYBase; FEGNO0197; TAZ_finger.
BR FIYBASE; PRE00310; KIZ.
BR FIREPPO; IPRE0049; Dromodomain.
BR Fiam; PF00439; Dromodomain; 1.
BR Fam; PF00459; Bromodomain; 1.
BR Fam; PF00569; Zz; 1.
BR Pfam; PR00569; Zz; 1.
BR Pfam; PR00597; BROMODOMAIN.
BR SMART; SM00291; BROMODOMAIN.
BR SMART; SM00291; BROMODOMAIN.
BR SMART; SM00291; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
BR PROSITE; PS00631; BROMODOMAIN.
BR PROSITE; PS00631; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
BR PROSITE; PS00633; BROMODOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00499; C2 DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50106; PDZ; 1
SEQUENCE 4833 AA; 525056 WW; FF22EB3AAlaF9F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; Y19186; CAB60732.2; -. HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MX-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 5;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 4833 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99439764; PubMed=10508862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 147:151-162(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.28;
61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LAARAGGGNGSGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1349390; Acz.
InterPro; IPR000008; C2.
InterPro; IPR001478; FDZ.
Pfam; PF00168; C2; 1.
Ffam; PF00595; PDZ; 1.
SMART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kilimann M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR ACZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97263578; PubMed=9109493;
Akimaru H., Chen Y., Dai P. Hou D.X., Nonaka M., Smolik S.M.,
Akimaru H., Chen Y., Dai P. Hou D.X., Akimaru H.,
Armstrong S., Goodman R.H., Ishhi S.,
Armstrong S., Goodman R.H., Ishhi S.,
Prosophila CBP is a co-activator of cubitus interruptus in hedgehog
                                                                                                                                                                                                                                               "A novel 160-kDa phosphotyrosine protein in insulin-treated embryonic kidney cells is a new member of the insulin receptor substrate
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INSULIN RECEPTOR SUBSTRATE 4 (DA24A23.2) (INSULIN RECEPTOR SUBSTRATE
                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                        MEDLINE-97407931; PubMed-9261155;
Lavan B.E., Fantin V.R., Chang E.T., Lane W.S., Keller S.R.,
Lienhard G.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 56; DB 4; Length 125
71.4%; Pred. No. 2.3e+02;
Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1257 AA; 133766 MW; 4D512D65A7A80374 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF007567; AAC51738.1; -.
EMBL; AL033425; CAB90290.1; -.
HSSP; P935568; IIRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 3190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002404; Insulin_Recep_S-1.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                     Biol. Chem. 272:21403-21407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001487; Bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 386:735-738(1997).
EMBL: U88570; AAB53050.1; --
TRANSFAC; T03236; --
Flybase: F99700115624; nej.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREB-BINDING PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00628; INSULINRSI.
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.4 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 RAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02174; IRS; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro:
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Schulte U., Aign V., Mannhaupt G.; Nyakatura G., Mewes H.W., Mannhaupt G.; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                             Gaps
                                                        oryza sativa (Rice).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                              Match 29.2%; Score 56; DB 10; Length 584; Local Similarity 39.3%; Pred. No. 1e+02; Local Similarity 5; Mismatches 12; Indels les 11; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 56; DB 3; Length 776
50.0%; Pred. No. 1.4e+02;
. . . . . . . . . . . . . . . 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A4451109; CAC18624.2;
Hypothetical protein:
SEQUENCE 776 AA; 82771 MW; C9BEA870D94A37DE CRC64;
                                                                                                                                                                                                                                                                                        EMBL; AC025783; AAK20054.1; --
InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
SEQUENCE 584 AA; 64797 MW; 1A55160A532DCE83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1257 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 AA
                          PUTATIVE CYTOCHROME P450 MONOOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRQWLAARAGGGNGSGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 LRPPRSSGGGGGGGGGGGCDEPPITTSWVS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GGGNGSGGI---EG-PTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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nes 13; Conserva
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID=4530;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0679C08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 29.2%; Score 56; DB 10; Length 348; Local Similarity 37.9%; Pred. No. 61; les 11; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 9; Length 217;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                               Pfister P., Wasserfallen A., Stettler R., Leisinger T.; "Molecular analysis of Methanobacterium phage psiM2."; Mol. Microbiol. 30:233-244(1998).
EMBL. AF056412: AAC27071.1; --
Hypothetical protein.
SEQUENCE 217 AA; 24325 MW; 9F6B2BIBB5131468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002542; BAB19386.1; --
SEQUENCE 348 AA; 37176 MW; D4ABE5D80883E94C CRC64;
              83 EGAAAR-WRAARSPARGGQRGGHRRRGGGGGGGGRERPRRRR 123
                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 24.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                    217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 TIRAFLRSLSPPGSGSGDGGIPSPSVAAW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TLROWLAARA--GGGNGSGGIEGPTLROW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last seno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGNGSGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99009353; Pubmed=9791169;
                                                                                                                                                                                                  Methanobacterium phage psiMl.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLE P0679C08.26 PROTEIN. P0679C08.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
                                                                                                                                                                                                                                  NCBI_TaxID=78218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                    Viruses
                                                                                               080221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FPB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09AV27
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                                                             RESULT 18
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                                                                               080221
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches 10; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                   29.4%; Score 56.5; DB 16; Length 488; 40.0%; Pred. No. 75; tive 2; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0483F08."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 10; Length 125; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00019; AAA17274.1; -
SEQUENCE 518 AA; 56001 MW; 6641916CC84F374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002094; BAA96216.1; -.
Hypothetical protein.
SEQUENCE 125 AA; 13396 MW; C609DBDDB07BC505 CRC64;
488 AA; 52800 MW; 188918856F9774AA CRC64;
                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EGPTLRQWLAARA-------GGGNGSGGIEGPTLRQ 30
                                                                                                                                                                                                                           518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56.5;
Pred. No. 80;
                                                                                                                             189 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                  4 PTLRQW-----LAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PTLRQW-----LAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.2%;
38.1%;
                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 40.09
Matches 12; Conservative
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae.
                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robison K.;
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                      049843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9LWC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LWC8
                                                                      Matches
                                                                                                                                                                                                                                                                                                        HFLX.
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RAM REDLINES-10196006; PubMed=1071112;

RA Adams W.D. Cellikers S.E. Li P.W. Hoskins R.M. Gocayne J.D.,

RA Adams W.D. Cellikers S.E. Li P.W. Hoskins R.M. Galle R.F.,

RA Adams W.D. Cellikers S.E. Li P.W. Hoskins R.M. Galle R.F.,

Batch G.G. Worthan J. S.E. Richards S., Ashburner M., Henderson S.N.,

Sutcon G.G. Worthan J. R. Helt G., Nalson C.R., Miklos G.L.G.,

RA Bandon R.C., Roagers Y.-H.C., Blazel R.C., Champe N., Peiffers B.D.

RA Bandon R.C., Roagers Y.-H.C., Blazel R.C., Champe N., Peiffers B.D.

RA Ballew R.M., Basu A., Basendale J., Bayraktacoglu L., Beaslay E.M.,

RA Beeson K.J., Lewiss B.W., Bouck J. Brockstein P., Portler P.,

Bortcova D., Buctchan M.R., Bouck J., Brockstein P., Portler P.,

Bortcova D., Buctchan M.R., Bouck J., Brockstein P., Portler P.,

Bortcova D., Botchan M.R., Bouck J., Brockstein P., Portler P.,

Bortcova D., Botchar M., Burler H., Cadleu E., Center A., Chandra I.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. Deritz S.M.,

RA de Pablos B., Delcher A., Deng Z., Rays A.D., Dew I. Deritz S.M.,

RA Durbin K.J., Evangelista C.C., Ferriac C., Ferriac S., Fleischmann W.

RA Glodek A., Goog F., Gortell J.H., Gu Z., Galbart W.M. Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ingewam C.,

RA Alalil M., Kaltei B. Wolfneds T.G., Kravitz S., Kull D. Lei Z.,

RA Mattei B. Wolfneds T.C., Worded M.-B., Mosheefi A.,

RA Mattei B. Wolfneds T.C., Worded M.-B., Dusheefi R.,

RA Mand C.C., Siden-Kiamen G.S., Pans W., Phenson D.L.,

RA Mand C.C., Siden-Kiamen G.S., Scheeler F., Shen H.,

RA Mand C.C., Siden-Kiamen G.S., Scheeler F., Shen H.,

RA Mand C.C., Siden-Kiamen G.S., Scheeler F., Shen H.,

RA Mand C.C., Siden-Kiamen G.S., Shapeton M., Strong R., Shu B.,

RA Mand C.C., Siden-Kiamen G.S., Sanders R. D.C., Scheeler F., Shen H.,

RA Mand C.C., Siden-Kiamen G.S., Sanders R.D.C., Scheeler F., Shen H.,

RA Mand C.C., Siden-Kiamen G.S., Sanders R.D. C., Scheeler F., Shen H.,

RA Mand C.S., Woy M. Wurphy B.N., Worter E., Wang G., Shu S.,

RA Mand C.S., Spelled M., Pitt
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                              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 5; Length 867; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867 AA; 95938 MW; F4998152BB02D18C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09A535;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.7%; Sco. 63.6%; Pred. No. 1...
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SMART; SM00184; RING; 1.
SMORT; SM000355; ZNF_CAR1, 4.
PROSITE; PS000289; ZINC_FINGER_CAR2_1; 2.
DNA-binding; Metal-binding; Zinc_finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 GGGNG-GGVTGPTSSS-IAARA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GGGNGSGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 63.68
Matches 14; Conservative
                                                                                                                                   SECUENCE FROM N.A.
                                                                  Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                          STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE
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SIRAIN=AICL 19007 / UBI3;
MEDLINE-21173698; PubMod=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadden N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Egigmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Bavier R.M., Devlin K., Duthoy S., Feltwell T., Maclean J., Moule S., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56.5; DB 16; Length 249;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Complete proteome.
SEQUENCE 249 AA; 25448 MW; AD63BD04C1F77122 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ABC TRANSPORTER, ATP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; ALS83920; CAC31378.1; -.
Leproma; ML0997; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00005; ABC_tran; 1.
SMARY; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR003593; AAA.
InterPro: IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSSIBLE ATP/GTP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000765; GTP1_OBG. PRINTS; PR00326; GTP10BG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 42.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae.
                                                         Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=69394;
                                                                                                 Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IN;
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                                           CC2634
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Complete proteome.

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Rhabditidae; Peloderinae; Caenorhabditis.
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SEQUENCE
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                       Q9L8D4
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Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.; The composite genome of the legume symbiont Sinorhizobium meliloti."; Science 293:668-672(2001).

Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                      T5L23.27 OR AT4G03750.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                 Length 928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 200;
                                                                                                                             29.9%; Score 57.5; DB 16; Length 34.8%; Pred. No. 1.1e+02; tive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
"BAC T5L23 from chromosome IV, position 19 cM.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submirted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AC005142, AAD15331.1;
EMBL; AL161497; CAB77860.1;
                                                                                        11 protein; Complete proteome.
928 AA; 96335 MW; AE09A21B301C027E CRC64;
                                                                                                                                                                             2 EGPTLRQWLAARAGGG------NGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 200 AA; 21986 MW; 852942DF377C76C2 CRC64;
                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 22.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     200 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.7%; Score 57;
41.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 KGATLRKGFGGRAVAGNKEGGSDRPNLEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EGPTLROWLAARAGGGNGSGGIEGPTLRQ 30
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                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                          Query Match
Best Local Similarity 34.8%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 41.49 Matches 12; Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                               Q9SY53;
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                                                                                                                                                                                                                                                                 09SY53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             019476;
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                                                                                                                                                                                                                                        RESULT 10
Q9SY53
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    RA
RA
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DR
KW
KW
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MEDINE-20130945; PubMed=10662695; Melnamow M., Milnamow M., Molnar I., Schupp T., Ono M., Zirkle R.E., Milnamow M., Nowak-Thompson B., Engel N., Toupet C., Stratmann A., Cyr D.D., Gorlach J., Mayo J.M., Hu A., Goff S., Schmid J., Ligon J.M.; The biosynthetic gene cluster for the microtubule-stabilizing agents epothilones A and B from Sorangium cellulosum So ce90."; Chem. Biol. 7:97-109(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 VDGPALVRWLAAR-----GAPGPLREYEEERERARTAQEARRLWLAA 137
                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bactería; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.7%; Score 57; DB 2; Length 607; 32.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGNGSGGIEGP-------TLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                           Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                           53946 MW; 1416327086FE7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 AA; 66326 MW; F113CA299B25048E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 66.3 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            867 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 82;
3; Mismatches
                                                                                                                                                                                                                                           investigating biology,";
Science 282:2012-2018(1998).
SCHENC 278013; CAB01420.1: -
InterPro; IPR001254; Trypsin.
PROSITE; PS50240; TRYPSIN.DOM; Hydrolase; Scrine protease.
SEQUENCE 500 AA; 53946 MW; 1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                       MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 GSMLGRFLSNRGGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GPTLRQWLAARAGGGNGSGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                             29.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyangium cellulosum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                            SEQUENCE FROM N.A.
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les 16; Conserv
                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=6239;
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CG11414.
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                                                                 Percy C.M.;
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Hypothetical protein.
SEQUENCE 439 AA; 47297 MW; 533EEC240CEAlBA2 CRC64;
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                                           Best Local Similarity 30.03
Matches 15; Conservative
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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           SEQUENCE
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                                  Query Match
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                                                                                                                                                              Q9ZRB9
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL512667; CAC21636.2;
Interpro: IPR003838; DUF214.
SEQUENCE 496 AA; 49548 MW; 54EI10C4F86231A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SASAKI T., MATSUMOTO T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza satira nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0705501.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000492; BAA84610.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.7%; Score 59; DB 2; Length 496; 54.5%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                          Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9SDK6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                   496 AA.
                                PRT;
                  3 GPTLRQWLAARAGGGNGSGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 PTLQAQLGGGAGGGGGAGGSGG 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.58;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                   PRELIMINARY;
                                                                                                                                                                                  Streptomyces coelicolor.
                                                                                                                                                                                                                                                                   Seeger K.J., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                         STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                     09AD76
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                                                                               RESULT 6
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MEDLINE=21368334; PubMed=11474104; MEDLINE=21368334; PubMed=11474104; MEDLINE=21368334; PubMer F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P., Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gowie A., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missioni meliloti (Sinorhizobium meliloti).
Raizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57.5; DB 10; Length 392;
Pred. No. 46;
DB 10; Length 439;
                                                                                                             1 IEGPTLRQWLAARAGGGNGSGG------IEGPTLRQWLAARA 36
                                                                                                                                                 2, Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=SP+,93-137;
Parnis A., Lifschitz E.;
"The Tomato Homeobox 1 gene.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 AA; 43306 MW; C18916A988063DA8 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           Volume (Trembline). 10, Created) 01-MAY-1999 (Trembline). 10, Last sequence update) 01-MAY-1999 (Trembline). 10, Last sequence update) 01-PRC-2001 (Trembline). 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC02633.
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                                                                                                                                                                                                                                                                                                                       392 AA.
                              45;
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   Score 58;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX 1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.9%;
         30.2%;
30.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 OWLSPTAAAGGGGNGGGG 75
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Matches 12; Conservative
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Wed Oct

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P0039A07.6 PROTEIN. P0039A07.6.
                                                                                                                                                                                                              Treponema pallidum.
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
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                                                                                         083436;
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                                                                    083436
                           RESULT 4
083436
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                                                                                         Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
Kim H., Rambo T., Henry D., Simmons J.;
Rice Genomic Sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC078891; AAK52534.1;
Nucleocapsid; Ribonucleoprotein.
SEQUENCE 491 AA; 58271 MW; EDEEB988DBOAA3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%; Score 61.5; DB 13; Length 431; 38.1%; Pred. No. 17; 7; Indels 17; rative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 491;
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                                                                                                                                                                                                                        PROSITE; FSJULY: PROSITE; PSURVATE; PROMOTE; PROSITE; PSURVATE; PSURVATE; PROBLE; Unclear protein.

DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
pUTATIVE 01 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA.
                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POU-DEX PROTEIN BRAIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 QWIAALSHGGPGGGGGGGGGGGGGGGGGEAP----WAAAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QWLAARA------GGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.4%; Pred. NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.2%; Score 60; 42.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001356; Homeobox.
Interpro; IPR000327; POU.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00028; POUDOMAIN. ProDom; PD000583; POU; 1. SMART; SM00389; HOX; 1. SMART; SM00352; POU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 38.1%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q94LP1
  Q9PVG9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki T., Matsumoto T., Yamamoto K.; sasaki T., Matsumoto T., Yamamoto K.; oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0039A07.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.7%; Score 59; DB 10; Length 253; 48.1%; Pred. No. 20; tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 683; 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003235; BAB64100.1; -
SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 AA; 74518 MW; F91407FA7094AAD1 CRC64;
                                                                                                                                                                                                 Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBL_TaxID-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                 Last annotation update)
                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 PLILEWL----GNAYYRSGIEGAALHOWGAAR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%; Score 60; 43.8%; Pred. No.
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PRT;
                                                                                                                                                                                                                                                                                                                         STRAIN-NICHOLS;
MEDLINE=98332770; PubMed=9665876;
                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Las CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001220; AAC65409.1; -. IIGR; TP0421; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 281:375-388(1998).
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001258; NHL.
InterPro; IPR001440; TPR.
Pfam; PF01436; NHL; 4.
Pfam; PF00515; TPR; 1.
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Matches 14; Conservative
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  PRELIMINARY;
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Oppuge coturnix co
0941pl oryza sativ
084346 treponema p
084346 oryza sativ
09436 oryza sativ
09ad76 streptomyce
092kb oryza sativ
092kb rizobium m
092kb rizobium m
092kb rizobium m
09476 caenorhabdi
0918d4 polyangium
09476 caenorhabdi
0918d4 polyangium
09476 caenorhabdi
0918d4 morosphila
09436 aralobacter
090500 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91qc9 oryza sativ
                                                     October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without allgoments) 482.803 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                562222
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                            562222 seqs, 172994929 residues
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                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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094LP1
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092XB3
092XB3
092XB3
095Y53
091446
091446
091449
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mnc:*
sp_organale:*
sp_nage:*
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sp_unclassified:*
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sp_bacteriap:*
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: sp_archea:*
: sp_bacteria:*
                                                                                           US-09-422-838C-32
192
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Maximum DB seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
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17 56 29.2 125 10 091MCB 091MCB 091MCB 0772 118 56 29.2 217 9 091021 091022 091021 0	Q91wcB oryza sativ O80221 methanobact O9fpbB oryza sativ O9ar27 oryza sativ O9ar27 oryza sativ O9bad neurosporar O14654 homo sapien O01586 drosophila Q94y27 mus musculu Q9qx7 mus musculu Q9qx7 mus musculu Q9qx7 mus musculu Q9qx7 mus musculu Q9dx7 mus musculu Q9dx7 mus musculu Q9dx7 mus musculu Q9dx7 mus musculu Q9dx0 caenorhabdi Q9aru5 oryza sativ Q9aru5 oryza sativ Q9aru5 drosophila Q9ary1 caulobacter O9x60 drosophila Q9ary2 drosophila Q9ary2 drosophila Q9yd0 petromyzon Q9se5 streptomyce Q9se5 streptomyce Q9se5 oryza sativ Q9px10 homo sapien	PAA. DaA. Euupdate) Lion update) Embryophyta; Tracheophyta; Poales; Poaceae; A, chromosome 1, PAC (/DDBJ databases. EIC77B2 CRC64; DB 10; Length 360; 33; 11; Indels 0; Gaps 0;	AA.
17 56 18 56 19 56 20 56 21 56 22 56 22 56 23 56 24 56 25 56 26 27 28 56 28 28 56 28 28 56 29 55:5 39 55:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 39 54:5 30 0916C9 00 0000000000000000000000000000000000	2 1125 10 2 217 9 2 217 9 3 48 10 2 2 17 9 3 1257 4 4 2 3 1257 4 4 4 8 3 11 5 6 6 9 0 6 104 1 6 1134 10 6 1134 10 6 1134 10 6 1134 10 6 1134 10 6 124 10 7 4 4 9 9 10 7 4 8 8 9 9 10 8 6 9 0 0 8 7 8 8 10 9 8 9 0 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PRELIMINARY; PRT; 360 A/ (TEMBLE-1.15, Last sequence u. (TEMBLE-1.18, Last annotation C FINGER PROTEIN. (Rice) iridiplantae; Streptophyta; Embandiplantae; Streptophyta; Embandiolophyta; Liliopsida; Esionyzeae; Oryza. oryzeae; Oryza. A N.A. IPPONBARE; atsumoto T., Yamamoto K.; atsumoto T., Yamamoto K.; atsumoto T., Yamamoto K.; by Oryzeae; Oryza. a nipponbare(GA3) genomic DNA, by 1000571; Zf-CCCH. 2; Zf-CCCH. 2; Zf-CCCH. 2; Zf-CCCH. 32.3%; Score 62; DB Larity 48.0%; Pred. No. 13; Conservative 2; Mismatches NULAGGGGGGGGGGG 50 MIANTAGGGGGGGGGG 50	
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us-09-422-838c-32.rsp

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                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

V -> L (IN REF. 2).

E -> D (IN REF. 2).

MISSING (IN REF. 2).

L -> I (IN REF. 2).

L -> I (IN REF. 2).

G -> D (IN REF. 2).

H -> Q (IN REF. 2).

H -> D (IN REF. 2).

H -> H (IN REF. 2).

MISSING (IN REF. 2).

H -> H (IN REF. 2).

V -> A (IN REF. 2).
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"Dual start motif in two lambdoid S genes unrelated to lambda S.";

"Dual start motif in two lambdoid S genes unrelated to lambda S.";

"Dual start motif in two lambdoid S genes unrelated to lambda S.";

"Dual start motif in two lambdoid S genes unrelated to lambda S.";

"EDNATION: ESSENTIAL FOR LYSIS OF BACTERIAL CELL WALL, BY SHOWING CELL WALL HYDROLYZING ACTIVITY. ACTS AS A TRANSGLYCOSYLASE.

"CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between Nacetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.

"INTERNATIVE BELONGS TO FAMILY 24 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage P21 (Bacteriophage 21).
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysozyme (EC 3.2.1.17) (Lysis protein) (Muramidase) (Endolysin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                        Phosphorylation, ATP-binding; Serine/threonine-protein kinase. DOMAIN 12 278 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100792 MW; FFE88E3F5D2035BE CRC64;
                                                                                                                SH3 domain; Membrane; Calmodulin-binding; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50.5; DB 1;
Pred. No. 1.8e+02;
                                                                                                                                                                                                  CALMODULIN-BINDING.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
                           PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; FALSE_NEG.
                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA.
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Pfam; PF00959; Phage_lysozyme; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 625 WWQARLGTVGGSAGLIPSPELQEWRIA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 WLAARAGGGNGSGG-IEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91210180; PubMed=2019562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M65239; AAA32350.1; -. PIR; S22906; LZBP21.
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Best Local Similarity 44.49
Matches 12; Conservative
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568
650
897
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719 7
739 7
897 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambda phage group.
NCBI_TaxID=10711;
                                                                              PS50002;
                                                      PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYCV_BPP21
                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                     NP_BIND
BINDING
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                              PROSITE;
                                                                                       PROSITE;
                                                         PROSITE;
                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DECOLINE FROM N.A. Marcotte W.R. Jr., Schnaitman C.A.;
Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;
Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;
Blasband A.J., Marcotte W.R. Jr., Schnaitman C.A.;
Blambdoid bacteriophage.";
J. Biol. Chem. 261:12723-12732(1986).
J. Biol. Chem. 261:12723-12732(1986).
J. FUNCTION: ESSENTIALE FOR LYSIS OF BACTERIAL CELL WALL, BY SHOWING CELL WALL HYDROLYZING ACTIVITY. ACTS AS A TRANSGLYCOSYLASE.
J. CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between nacetyl-belglucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.
J. SIMILARITY: BELONGS TO FAMILY 24 OF GLYCOSYL HYDROLASES.
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Lysozyme (EC 3.2.1.17) (Lysis protein) (Muramidase) (Endolysin).
                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Late protein; Hydrolase; Glycholase; Bacteriolytic enzyme. ACT_SITE 35 35 PROTON DOMOR ARE SITE.
Late protein; Hydrolase; Glycosidase; Bacteriolytic enzyme.
ACT_SITE 35 35 PROTON DONOR (BY SIMILARITY).
ACT_SITE 44 44 NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 165;
                                                                                                Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                         4; Indels
                                                            14ECECD883232D3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2DA65CCF1EA9329B CRC64;
                                                                                                  26.0%; Score 50; DB 1;
                                                                                                                                                                                                                                                                                                                               165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%; Score 50; DB 35.3%; Pred. No. 43; iive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PTLRQWLAARAGGG-----NGSGGIEG 25
                                                                                                                     Pred. No. 43;
6; Mismatches
                                                                                                                                                                                 4 PTLRQWLAARAGGG-----NGSGGIEG 25
                                                                                                                                                                                                                          3 PSLRKAVAAAIGGGAIAIASVLITGPSGNDGLEG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||: :|| |||
3 PSLRKAVAAAIGGGAIAIASVLITGPSGNDGLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October 9, 2002, 09:00:20 Job time: 5.3831 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR002196; Phage_lysozyme.
Pfam; PF00959; Phage_lysozyme; 1.
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA; 17998 MW;
                                                            165 AA; 17996 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J02580; AAA32300.1; -.
                                                                                                                        35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 35.3
Matches 12; Conservative
                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C25647; WMBPP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage PA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBL_TaxID=10738;
                                                                                                                                                                                                                                                                                                                             LYCV_BPPA2
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SEQUENCE
                   ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                             Matches
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
A manatides P.G., Scherer S.E., Holt R.A., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bardkaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Perryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%; Score 50.5; DB 1; Length 620; 50.0%; Pred. No. 1.3e+02; ive 2; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dimitratos S.D., Woods D.F., Bryant P.J.; Camquk, Lin-2, and CASK: novel membrane-associated guanylate kinase homologs that also contain CaM kinase domains."; Mech. Dev. 63:127-130(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin J.-R., Ollo R.; "A new Drosophila Ca2+/calmodulin-dependent protein kinase (Caki) is localized in the central nervous system and implicated in walking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAKI_DROME STANDARD;
024210; 024272; 03VD77; 03VD79;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2nd (Rel. 40, Last annotation update)
Carlcium/Calmodulin-dependent protein kinase (EC 2.7.1.123) (CAKI)
CAKI OR CMG OR CG13412 OR CG6703.
Pfam; PF00037; fer4; 3.
Pfam; PF0107; NIR_SIR; 1.
PRINTS; PR01039; SIROHAEM.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS0055; NIR_SIR; 1.
Hypothetical protein; Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S; Complete proteome.
                                                                                                                                                                                                                                                                        IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) AND SIROHEME
                                                                                                                                                                                                                                            IRON-SULFUR (4FE-4S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
9D71D2580D7D0BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 EGPLVRATLAC-PGGGNCSSGLVDTT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EGPTLRQWLAARAGGGNGSGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97321552; PubMed-9178262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96203108; PubMed=8617233;
                                                                                                                                                                                                                                                                                                                                                                                                                620 AA; 69793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 15:1865-1876(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.0 Matches 13; Conservative
                                                                                                                                                                                                                                        428
434
468
472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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468
472
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                                                                                                                                                                                                                                               428
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAKI_DROME
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PROSITE; PS00856; GUANYIATE_KINASE_1; 1. PROSITE; PS50052; GUANYIATE_KINASE_2; 1. PROSITE; PS50106; PDZ; 1.

S_TKC; 1.

SMART; SM00072; GUKC; I SMART; SM00228; PDZ; I. SMART; SM00326; SH3; I. SMART; SM00220; S_TKC; Pfam; PF00018; SH3; 1

InterPro; IPR002290; Ser_thr_pkinase. Pfam; PF00625; Guanylate_kin; 1.

Pfam; PF00595; PDZ; 1. Pfam; PF00069; pkinase; 1.

Pfam; PF02828;

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harrey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Mount S.M., Muy M., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Resee M.G., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., RA Sheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O., Ra Globs R.A., Myers E.W., Rubin G.M., Venter B., Zhao G., Zhao Q., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Chan M., Science 287:2185-2195(2000). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). FRAMESHIFTS AND REF.3 SEQUENCE DIFFERS DUE TO ONE FRAMESHIFT. -!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO EMBL; U53190; AAC80169.1; -... EMBL; X94264, CAA63940.1; ALT_FRAME. EMBL; AE003736; AAF55520.1; ALT_SEC. EMBL; AE003736; AAF5522.1; ALT_SEQ. FlyBase; FBgn0013759; Caki. InterPro; IPR000719; Euk_pkinase. InterPro; IPR000619; Guanylate_kin. InterPro; IPR004172; L27. CALMODULIN, OR NUCLEOTIDES. IPR001478; PDZ InterPro; IPR001452; SH3 HSSP; 014936; 1KWA. InterPro;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson B., Pearse R.V. II, Schlegel P.N., Cichon Z., Schonemann M.D., Bardin C.W., Rosenfeld M.G.; "Sperm 1: a POU-domain gene transiently expressed immediately before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melosis I in the male germ cell.";
Proc. Natl. Acad. Sci. US.A. 90:11084-11088(1993).
-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO THE OCTAMER MOTIF ('ATGTTAAT'). MAY EXERT A REGULATORY FUNCTION IN MEIOTIC EVENTS THAT ARE REQUIRED FOR TERMINAL DIFFERENTIATION OF
               R MIM; 6028by;
R InterPro; IPR003874; SAP.
R InterPro; IPR003877; SPRY.
R InterPro; IPR003877; SPRY.
R InterPro; IPR003878; SPRY.
DR Pfam; PF00527; SAP; 1.
DR SMART; SM00613; SAP; 1.
DR SMART; SM00449; SPRY; 1.
RW Nuclear protein; Ribonucleoprotein; RNA-binding; DNA-binding; MW Phosphorylation; ATP-binding; Alternative splicing.

I 160 ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: HIGHLY RESTRICTED TO ADULT TESTIS.
-!- DEVELOPMENTAL STAGE: EXPRESSED TRANSIENTLY IMMEDIATELY PRIOR TO MEIOSIS I DURING SPERMATOGENESIS IN THE MALE GERM CELL.
-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                          Length 824;
                                                                                                                                                                                                                                                                      POLY-GLY.
MISSING (IN SHORT ISOFORM).
F7D04BEA481C8FEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                            RNA-BINDING (RGG-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sperm 1 POU-domain transcription factor (SPRM-1).
                                                                                                                                                                                                                                                                                                                                 26.6%; Score 51; DB 1; I
71.4%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 AA.
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                              GLY-RICH.
                                                                                                                                                                                                                             POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L23864; -; NOT_ANNOTATED_CDS. HSSP; P20263; 10CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94068549; PubMed=7902581;
                                                                                                                                                                                                                                                                                                    90479 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                           13 RAGGGNGSGGIEGP 26
 PIR; S22765; S22765.
MIM; 602869; -.
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713
739
213
824 AA;
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                                                                                                                                                                                                                                                                                  VARSPLIC
SEQUENCE
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NP_BIND
DOMAIN
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P56225:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIL-JAL J DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
Bult C.J., White O. Olsen G.J. Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A. Gocayne J.D.,
Verlavage A.R., Doughnerty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Klenk H.-P., Roberts K.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                           Homeobox; DNA-binding; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 273:1058-1073(1996).
-!- SIMILARITY: TO COENZYME F420 HYDROGENASE BETA SUBUNIT.
-!- SIMILARITY: TO M.JANNASCHII MJ1349, MJ0725 AND MJ0551.
-!- SIMILARITY: TEM C.TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                 ς,
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                                                                                                                                                                                                                                                                                                                                  26.3%; Score 50.5; DB 1; Length 335; 40.0%; Pred. No. 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                      335 AA; 37159 MW; 820B9AC12D6B10D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 72;
5; Mismatches
                                                                                                                              PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR000660; Nir_Sir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      17 GNGSGGIEGPTLRQ-----WLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                               || || ||:::|
14 GNSGGLEGPVPMRVDTPTWLSSQA 38
                  Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; PoU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein MJ0870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67531; AAB98876.1; -.
                                                                                                                                                                                                                                Spermatogenesis; Meiosis.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                             SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MJ0870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y870_METJA
                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              058280;
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y870_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
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SEQUENCE
                                                                                                               Query Match
REPEAT
                    REPEAT
                                           REPEAT
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                           RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Azawa K., Zawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R.,
RA Kuchi P., Lawi S., Matsuo Y., Nikaido I., Rochiwa H.,
RA Schiml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schiml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Hume D.A., Kamiya M., Lee N.H.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wushawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mitochondrial precursor proteins import receptor (Translocase of outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nacure 409:003-039/(2014).

-!- FUNCTION: RECEPTOR THAT ACCELERATES THE IMPORT OF ALL
-!- FUNCTION: RECEPTOR PROTEINS (BY SIMILARITY).

MITOCHONDRIAL PRECORESOR PROTEINS (BY SIMILARITY).

-!- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
LEAST B DIFFERENT PROTEINS (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
-!- SIMILARITY: CONTAINS 10 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOS. NOTE TO THE OFFICE OF THE OFFICE OFFICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                         611 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPR 3.
TPR 4.
TPR 5.
TPR 6.
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-EmbryO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK012084; BAB28018.1; ~.
MGD; MGI:106295; D16Wsu109e.
                      Db . 453 GPPPRGGMAQKLGSGRGTGQMEG 475
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                          membrane TOM70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                     OM70_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fackelmayer F.O., Richter A.; Packelmayer F.O., Richter A.; Packelmayer F.O., Richter A.; Purification of two isoforms of hnRNP-U and characterization of their nucleic acid binding activity. ; Packelman acid binding activity. ; Packelman acid binding activity as: 104.104.224[1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SICOLOGIAZIONI BINDS TO PRE-MRNA. HAS HIGH AFFINITI FOR SCRIDED DIA PUNCTION: PENELON (SAR) DNA. BIND TO DOUBLE-AND SINGLE-STRANDED DNA ATTACHED REGION (SAR) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Nuclear; component of ribonucleosomes.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- PTM: Extensively phosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fackelmayer F.O.; also known a variant of human scaffold attachment factor A (SAF-A), also known as haterogeneous nuclear ribonucleoprotein U (hnRNP-U)."; submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (SHORT FORM).
MEDLINE=94154006; PubMed=7509195;
Packelmayer F.O., Richter A.;
"hnRNP-U/SAP-A is encoded by two differentially polyadenylated mRNAs in human cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAS HIGH AFFINITY FOR SCAFFOLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kiledjian M., Dreyfuss G.;
"Primary structure and binding activity of the hnRNP U protein:
                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heterogenous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAP-A).
HNRPU OR SAFA OR U21.1.
                                                                                                                                Score 51; DB 1; Length 611;
                                                                                                                                                                1.1e+02;
ohea 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (SHORT FORM), AND RNA-BINDING DOMAIN. MEDLINE-92331618; PubMed-1628625;
         479 512 TPR 8.
514 547 TPR 19.
548 581 TPR 10.
611 AA: 67521 MW; 486FB79FC4CE5B4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROU HUMAN
000839, 0075507;
0108393 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1217:232-234(1994).
                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                             11 AARAGGGN---GSGGIEGP----TLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                    14 AAAPGSGNGVGGGGTAGPGSGAGTLPRWHVALA 47
                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
TPR 8.
TPR 9.
TPR 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94347778; PubMed=8068679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X65488; CAA46472.1; -.
EMBL; AF068846; AAC19382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding RNA through RGG box.";
EMBO J. 11:2655-2664(1992).
                                                                                                                                                      26.6%;
44.1%;
                                                                                                                                                                                       Local Similarity 44.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROU_HUMAN
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                    1;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                       01-MXY-1992 (Rel. 22, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
19pothetical 20.2 kba protein in RNA2.
Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G3B2_HUMAN STANDARD; PRT; 482 AA.
G9UN86, 075149, 060606;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2010 (Rel. 40, Last annotation update)
16-0CT-2011 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                    ï
               DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.6%; Score 51; DB 1; Length 201; 53.8%; Pred. No. 40;
                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91311402; PubMed-1856689;
Rott M.E., Tremaine J.H., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9038506E18D7B450 CRC64;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
             26.8%; Score 51.5; 1 50.0%; Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS A AND B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY
                                                                                                                                                                                                                      PRT;
                                                                                     7 ROWLAARAGGGNGSGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 RAGGGGGGKEVFKAGRTLLKVLKA 38
                                                                                                                   39 RQDSQAERYGGGGGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 RAGGGNGSGGIE----GPTLRQWLAA 34
                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AA; 20194 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D12477; BAA02044.1; -. PIR; JQ1094, JQ1094. HSSP; P04002; IWFA. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kennedy D., Mattick J.S.;
                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                      STANDARD;
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66
148
                                 Similarity
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                                                                                                                                                                                                                                                       01-MAY-1992 (
01-MAY-1992 (
16-OCT-2001 (
                                                                                                                                                                                                                      YR21_TRSVR
P25245;
                                                                                                                                                                                                                                                                                                                                                                             Nepovirus
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               Query Match
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                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH IKAPPABALPHA.

MEDLINE=20549669; PubMed=10969074;
Prigent M., Barlat I., Langen H., Dargemont C.;
IkappaBalpha and IkappaBalpha /NF-kappa B complexes are retained in the cytoplasm through interaction with a novel partner, RasGAP SH3-binding protein 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
"Characterisation and chromosomal location of G3BP-1 and G3BP-2a/b, members of a novel SH3 domain-binding and RNA-binding protein family implicated in signal transduction."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 275:36441-36449(2000).
-!- FUNCTION: PROBABLE SCAFFOLD PROTEIN THAT MAY BE INVOLVED IN MRNA TRANSPORT (POTENTIAL).
                                                                                                                                                                                                                                                        Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNT: BINDS TO THE N-TERMINAL DOMAIN OF IKAPPABALPHA.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 NTF2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2545C6A3F1AAE218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM B).
S -> P (IN REF. 2).
E -> V (IN REF. 3).
M -> I (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9:
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GLU-RICH.
GLY-RICH.
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PROSITE; PS50177; NTF2_DOMAIN; I.
PROSITE; PS50102; REM; I.
PROSITE; PS00030; REM; II.
PROSITE; PS00030; REM_RNP_I; FALSE_NEG.
DOMAIN

1133
NTF2.
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4; Mismatches
                                                                                                                                                                                                                          MEDLINE=98403880; PubMed=9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF145284; AAD51932.1; --
EMBL, AB014560; BAA31635.1; --
EMBL, AF051311; AAC15705.1; --
HSSP, P09651; 14A1.
InterPro; IPR002075; NTF2.
InterPro; IPR00504; RRM.
PFam; PF02136; NTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GPTLRQWLAARAGGGNGSGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54111 MW;
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Matches 10; Conservative
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460
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                                                                                                                                                                                                       rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guitard E.;
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                                                                                                                                             -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
Germann U.A., Lerch K.; "Isolation and partial nucleotide sequence of the laccase gene from Neurospora crassa: amino acid sequence homology of the protein to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                             -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION. Secreted (Potential).
-!- SIMILARITY: BELOWGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TYPE 3) (PROBABLE)
(TYPE 3) (PROBABLE)
(TYPE 1) (PROBABLE)
(TYPE 2) (PROBABLE)
(TYPE 3) (PROBABLE)
(TYPE 3) (PROBABLE)
(TYPE 3) (PROBABLE)
(TYPE 1) (PROBABLE)
(TYPE 1) (PROBABLE)
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COPPER (TYPE 3) (PROBABLE)
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PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A28523; KSNCLO.
PIR; A29762; A29762.
InterPro; IPR00117; Cu-oxidase.
InterPro; IPR00135; MultiCu_oxidse2.
Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
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                                                                                       human ceruloplasmin.";
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619 AA;
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1;
    DB 1; Length 619;
              Pred. No. 99;
0; Mismatches 12; Indels
 26.8%; Score 51.5;
                                                         7 ROWLAARAGGGNGSGGIEGPTLRQ-W 31
                50.0%;
                           13; Conservative
Query Match
Best Local Similarity
                             Matches
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39 RODSQAERYGGGGGGGCCNSPINRQCW 64 RESULT 21 d

LAC2_NEUCR

OBB6CCDE18841145 CRC64;

68120 MW;

SEQUENCE

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                                                                                                                                                                                                                                                                                               Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-896(1988).
--- FUNCTION. LIGNIN DECRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
---- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                             Germann U.A., Mueller G., Hunziker P.E., Lerch K.; "Characterization of two allelic forms of Neurospora crassa laccase.
                            01-JUL-1989 (Rel. 11, Created)
01-FBE-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 110.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                               -:- CORACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-:- SUBCELLULAR LOCATION. Secreted (Potential).
-:- SIMILARITY: BELOWGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LACCASE
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88087214; Pubmed=2961749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M18334; AAA33592.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Repeat.
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619 AA;
                                                                                                                                           Neurospora crassa.
                                                                                                                                                                                        NCBI_TaxID=5141;
LAC2_NEUCR
P10574;
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MEDLINE=87067412; PubMed=2947240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAC1_NEUCR
P06811;
                                                                                                                                   ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAC1_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria: CFB group; Flavobacteria; Flavobacteriaceae; Flavobacterium.
NCBI_TaxID=261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-84066129; PubMed=6646204;
MEDLINE-84066129; PubMed=6646204;
Okada H., Negoro S., Kimura H., Nakamura S.;
"Evolutionary adaptation of plasmid-encoded enzymes for degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-UDL-1999 (Rel. 38, Last annotation update)
6-aminohexanoate-dimer hydrolase (EC 3.5.1.46) (Nylon oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                     S (IN REF. 2).
PPHRGPAGNWGPP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7e+02;
.7e+02;
... 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32DDF16B9B52420A CRC64;
                                                                                                                                                                                                                                                                                                                       3 X 50 AA TYPE C REPEATS. 3-1.
                                                                                                                                                                                                       POLY-PRO.
4 X 57 AA TYPE A REPEATS.
                                                                                                                                                                                                                                                                                    2 X TYPE B REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                      R -> A (IN REF. 2

P -> PPHRGPAGNWOFF.

D -> K (IN REF. 2

C -> K (IN REF. 2

E -> D (IN REF. 2

L -> R (IN REF. 3

C -> A (IN REF. 3

G -> A (IN REF. 3

D -> R (IN REF. 3

G -> A (IN REF. 3

D -> R (IN 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 GPSLRPQNSTTW---RDGGGRGPDELEGP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLR-----QWLAARAGGGNGSGGIEGP 26
                                                                                                                                                POLY-PRO.
POLY-GLY.
POLY-GLY.
                                                                                                                                      POLY - PRO
                                                                                                                                                                                          POLY - PRO.
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                                                                                                                       POLY-PRO
                                                                                                        GLN-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavobacterium sp. (strain K172).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227840 MW;
        EMBL; M33512; AAA35586.1; JOINED.
EMBL; Z15025; CAA7874.1; -.
PIR; B35098; B35098.
PIR; S36152; S36152.
MIM; 142580; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 306:203-206(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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1285
1400
1611
1729
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1948
2014
2089
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                                                                                                                                                                                             1442
1991
1795
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1400 140
1611 161
1729 172
2142 AA;
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035
068
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P07061;
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CONFLICT
CONFLICT
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SEQUENCE 88087214; PubMed=2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;

"Characterization of two allelic forms of Neurospora crassa laccase."

Amino- and carboxyl-terminal processing of a precursor.";

J. Biol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- PATHWAY: SECOND STEP IN THE DEGRADATION OF 6-AMINOHEXANOIC ACID CYCLIC DIMER, A BY-PRODUCT OF NYLON MANUFACTURE.
--- MISCELLANEOUS: THE BII ENZYME IS 100 TIMES MORE ACTIVE TOWARD THE SUBSTRATE THAN THE BII' ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 185:521-524(1989).
-!- CATALYTIC ACTIVITY: N-(6-aminohexanoyl)-6-aminohexanoate + H(2)0
2 6-aminohexanoate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Ullishiol oxidase) (Laccase allele OR).
                                                                                                       Ranzaki N., Okada H.;
Ranzaki N., Okada H.;
Ronstruction of hybrid genes of 6-aminohexanoic acid-oligomer
hydrolase and its analogous enzyme. Estimation of the intramolecular
regions important for the enzyme evolution.";
J. Blol. Chem. 259:13648-13651(1984).
                                                                                                                                                                                                                                                                                                                                           MEDLINE 90076168; PubMed=2512123; Nebric 20, Okada H.; Negoro S., Mitamura T., Oka K., Kanagawa K., Okada H.; Negoro S., Mitamura T., Oka K., Kanagawa K., Okada H.; Nepermination of the active-site serine of 6-aminohexanoate-dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 26.8%; Score 51.5; DB 1; Length 392; Local Similarity 45.7%; Pred. No. 65; es 16; Conservative 0; Mismatches 16; Indels
[2]
SEQUENCE FROM N.A.
SEQUENCE-85054785; PubMed-6389532;
NEGORO S., Nakamura S., Kimura H., Fujiyama K., Zhang Y.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 AA; 42693 MW; 9CF34C393C3E53D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 EGSYTROWWCTGNERGNVSGIGIHGONL--WLDPR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EGPTLRQWLAARAGGGNGSG-GIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nylon degradation; Hydrolase; Plasmid. ACT_SITE 112 112 SEQUENCE 392 AA; 42693 MW; 9CF34C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X00046; CAA24927.1; -. EMBL; D26094; BAA05087.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A22644; A22644.
PIR; A29516; A29516.
PIR; S06849; S06849.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D2 (Forkhead-related protein FKHL17) (Forkhead-
FOXD2 OR FKHL17 OR FREAC9.
                                                                                                                                                                                                                                           SMART; SM00432; MADS; 1.
PROSITE: PS00350; MADS_BOX_1; 1.
PROSITE: PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98066765; PubMed=9403061;
Enstasson S., Betz R., Lagercrantz S., Larsson C., Ericksson S., Cederberg A., Carlisson Enerbacek S.;
"Cloning and characterization of freez-9 (FKHL17), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 1; Length 448;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enerbaeck S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                  B3CDCA7E0D97C23B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
-!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      MADS
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                                                                                                                                                                              TRANSFAC; T00763; ...
InterPro; IPR002100; MADS-box.
Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                46115 MW;
                                                                                                                                   EMBL; X56451; CAA39832.1; -.
                                                                                                                                                                                                                            PRINTS; PRO0404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                 27.18;
64.78;
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                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LARRAGNGAGCPGIRGP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                   S15018; S15018.
                                                                                                                                                                HSSP; P11831; 1SRS.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE 448 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FXD2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Q63245; 2HFH.

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                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banerii J., Sands J., Strominger. J.L., Spies T.;
"A gene pair from the human major histocompatibility complex encodes large proline rich proteins with multiple repeated motifs and a single ubiquitin-like domain.";
Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Large proline-rich protein BAT2 (HLA-B-associated transcript 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Dense Alu clustering and a potential new member of the NF kappa family within a 90 kilobase HLA class III segment.";
                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i TISSUE SPECIFICITY: LIMITED TO CELL-LINES OF LEUKEMIC ORIGIN.
                                                                                                                                                                                                                                                                                               27.1%; Score 52; DB 1; Length 497; 61.9%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                       Transcription regulation.
                                                                                                                                                                                                                                                                49007 MW; EAAF498D216BE019 CRC64;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                  FORK-HEAD.
                                                                                                                                                                                                                           POLY-GLY.
POLY-GLY.
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                                                                                                                                                                                                             POLY-ALA.
                                                                                                                                                                                                                                                          POLY-ALA
                       InterPro; IPR001766; Fork_head.
Pfam: PF00250; Fork_head; 1.
PRINTS: PR00053; FORKHEAD.
SMART: SM00339; FH; 1.
PROSITE: PS00657; FORK_HEAD_1; 1.
PROSITE: PS50039; FORK_HEAD_2; 1.
DNA-Dinding; Nuclear protein; Transc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=T-cell;
MEDLINE=90192810; PubMed=2156268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93272029; PubMed=8499947;
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                                                                                                                                                                                                                                                                                                                                                      4 PT--LRQWLAARAGGGNGSGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M33509; AAA35585.1; -. EMBL; M33518; AAA35586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-1860 FROM N.A
                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
T02485; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: UNKNOWN
                                                                                                                                                                                                                                                                497 AA;
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                              101
126
247
296
398
421
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               MIM; 602211;
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P48634;
 TRANSFAC;
                                                                                                                                                                            DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                             DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DISEASE: DEFECTS IN SIX3 ARE THE CAUSE OF HOLOPROSENCEPHALY TYPE 2 (HPE2); A COMMON, SEVERE MALFORMATION OF THE BRAIN THAT INVOLVES SEPARATION OF THE CENTRAL NERVOUS SYSTEM INTO LEFT AND RIGHT
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SIX/SINE OCULIS FAMILY OF HOMEODOMAIN
25 80

81 210 NEUROTROPHIN-5.

97 170

141 199

158 201 N-LINKED (GLCNAC. ..) (POTENTIAL).

76 76 N. LINKED (GLCNAC. ..) (POTENTIAL).

210 AA; 22426 MW; DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallis D.E., Roessler E., Hehr U., Nanni L., Wiltshire T., Richieri-Costa A., Gillessen-Kaesbach G., Zackai E.H., Rommens J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99107815; PubMed=9889003; Granadino B., Gallardo M.E., Lopez-Rios J., Sanz R., Ramos C., Ayuso C., Bovolenta P., Rodríguez de Cordoba S.; "Genomic cloning, structure, expression pattern, and chromosomal location of the human SIX3 gene."; Genomics 55:100-105(1999).
                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "SIX3, a member of the Sine oculis/Six family of transcription factors, is expressed in the developing and adult human eye."; Submitted (NOV-1938) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark B.J., Hanson I.M., Brown A.G., Ferrier R.K., Prosser J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: MAY BE INVOLVED IN VISUAL SYSTEM DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutations in the homeodomain of the human SIX3 gene cause
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Homeobox protein SIX3 (Sine oculis homeobox homolog 3).
                                                                                                                                                                                                                                 129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                                                                                                                                                   3 GPTLRQWL-----AARAGGGNGSGGIEGPTLRQWLA 33
                                                                                                                                                         Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS HPE2 VAL-226; ALA-250 AND PRO-257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99377859; PubMed=10454822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99295940; PubMed=10369266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ophthalmic Genet. 20:1-15(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     holoprosencephaly.";
Nat. Genet. 22:196-198(1999).
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                   SIX3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: PHOSPHORYLATED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91184140; PubMed=2009862; Mohun T.J., Chambers A.E., Towers N., Taylor M.V.; Mohun T.J., Chambers A.E., Towers N., Taylor M.V.; Expression of genes encoding the transcription factor SRF during early development of Kenopus laevis: identification of a CArG box-binding activity as SRF."; EMBO J. 10:933-940(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          257 257 R -> P (IN HPE),
/FTIG=VAR_003773,
332 AA; 35486 MW; 21EA07F6A2DD978F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: BINDS DNA AS A MULTIMER, PROBABLY A DIMER.
                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
L -> V (IN HPE2).
/FTIG=VAR_003771.
V -> A (IN HPE2).
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01-NoV-1991 (Rel. 20, Last sequence update)
01-CT-1994 (Rel. 30, Last annotation update)
Serum response factor (SRF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                         PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                      POLY-GLY.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52;
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                                                                                                                                                                                                                                                                                                                      Disease mutation; Holoprosencephaly
                                                                                                                                                                                               InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
Pfam; PP00046; homeobox: IPR01157; PR00031; HTHREPRESSR.
                                                                                         EMBL, AF092047; AAD11939.1; --
EMBL, AF0404339; AAD1573.1; --
EMBL, AF083891; AAD51091.1; --
EMBL, AJ012611; CAB42539.1; --
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NCBI_TaxID=8355;
                                                                                                                                                    P40424; 1B72.
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                                                                                                                                                                                                                                                                                                                                                                                                               250
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226
                                                                                                                                                                    MIM; 603714;
                                                                                                                                                                                   MIM; 157170;
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P23790;
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NT5_HUMAN
                                        RESULT 14
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Testis;
MEDLINE-2027481; PubMed-10819330;
MEDLINE-2027481; PubMed-10819330;
Sakai T., Toyoda A., Hashimoto K., Maeda H.;
Sakai T., Toyoda A., Hashimoto K., Maeda H.;
sakai T., Toyoda A., Hashimoto M., Maeda H.;
and mapping to the human chromosome 14q11 region.";
DNA Res. 7:137-41(2000)
                                                                                                                               Gaps
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PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 6.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 79;
                                                                           Query Match

27.6%; Score 53; DB 1; Length 631;
Best Local Similarity 37.0%; Pred. No. 69;
Matches 10; Conservative 4; Mismatches 13; Indels
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PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 631 AA; 69199 MW; 01ACA20600C9322F CRC64;
                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   722 AA
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C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
                                                                                                                                                                                                                      603 PIISKLYQGGPGGGGGGGASGGPTIEE 629
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                             4 PTLRQWLAARAGGGNGSGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000822; Znf-C2H2. Pfam; PF00096; zf-C2H2; 9. SMART; SM00355; ZnF_C2H2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB015427; BAA90526.1; -.
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                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein 219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                     Z219_HUMAN
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SEQUENCE
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Prostate;
MEDLINE=92212967; PubMed=1313578;
MEDLINE=92212967; PubMed=1313578;
IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., Le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEĞLINE-92075279; PubMed-1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-ZAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
MEDLINE=20095835; PubMed=10631974;
Robinson R.C., Radziejewski C., Spraggon G., Greenwald J.,
Rostura M.R., Burtnick L.D., Stuart D.I., Choe S., Jones B.Y.;
The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-binding site.";
Protein Sci. 8:2589-2597(1999).
--- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY
                                                                                                                                                    Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4) (NT-4) (Neutrophic factor 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYMPATHETIC NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribution, and receptor specificity."; proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00248; NGF_1; 1.
PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal; 3D-structure.
1 24
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M86528; AAA60154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1. PRINTS; PR00268; NGF. ProDom; PD002052; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00140; NGF; 1.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuron 7:857-866(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 188M; 09-FEB-99.
PDB; 1898; 26-FEB-99.
MIM; 162662; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JH0503; JH0503.
PIR; A42687; A42687.
                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      NTF5 OR NTF4.
       NT5_HUMAN
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POTENTIAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type specific expression in developing limbs and gonads.";
EMBO J. 8:1507-1515(1989).
-i- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-89335622; PubMed-2569970;
Dolle P., Duboule D.;
"Two gene members of the murine HOX-5 complex show regional and cell-
                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renucci A.G.P., Zappavigna V., Zakany J., Izpisua-Belmonte J.-C.,
Buerki K., Douboule D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLUTAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LIMB BUDS.
-!- SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comparison of mouse and human HOX-4 complexes defines conserved sequences involved in the regulation of HOX-4.4.";
                                                                                                                                                                                                                                                                                                                                                         27.9%; Score 53.5; DB 1; Length 112; 35.9%; Pred. No. 12; tive 5; Mismatches 7; Indels 13
                                                                                                                                                                                                                                                                                                             SEQUENCE 112 AA; 12164 MW; B4CD4D7C0D9F00A1 CRC64;
                                                                                                                                                                                                                                                          Antigen; Immune response; Signal; Complete proteome. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRQWLAA--RAGG-----GNGSGGI---EGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 LROWVSAGRRVGGRRRGRSNSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HOMEOBOX protein Hox-D9 (HOX-4.4) (HOX-5.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 339 AA
                                                                                                                                                                                                                                                                                                       LSR2 PROTEIN.
                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92224884; PubMed=1348690;
                                                                                                                                                                             EMBL: ALS83917; CAC29742.1; --
EMBL: X53487; CAA37572.1; --
PIR: S14407; S14407.
Leproma; ML0234; --
                                                                                                                                                           EMBL; M67510; AAA25351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 272-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62669; CAA44542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X14714; CAB57813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 11:1459-1468(1992).
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S09398; S09398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HXD9_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sednences
                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENOMICS 14:803-808(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
                                                                                                                                                                                                                                                                                                                                                           8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                  Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grosz M.D., Womack J.E., Skow L.C.;
"Syntenic conservation of HSP70 genes in cattle and humans.";
                                                                                                                                                                                                                                                                                                                    27.6%; Score 53; DB 1; Length 339; 37.5%; Pred. No. 39; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                     370DC47C6929F7E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           631 AA.
                                                                                                                                                                                                                                       POLY-GLY.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                    101 GRYVRSWMEPLPGFPGGAGGGGGGGGGGG 132
                                                                                                                                                                                                                                                                                                                                                                                  3 GPTLRQWL-----AARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                       GLY-RICH.
                                                                                                                                                                                                                                                                         HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93122795; PubMed=1478667;
                                                                                                                                                                                                                                  119 131 POI
163 176 SEF
272 331 HON
339 AA; 34992 MW;
                                                              MGD; MGI:96210; Hoxd9.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat shock 70 kDa protein 3.
                                                                                                                PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L10428; AAA30569.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                Local Similarity 37.5 ies 12; Conservative
                                                                                                Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 14:863-868(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                PIR; S20880; S20880.
                              HSSP; P02834; 1B8I.
TRANSFAC; T01755; -.
 PIR; S09569; S09569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS73_BOVIN
                                                                                                                                                                                                                                                                  DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIRALMSHANCE AND AMEDIANE STRAINS STRAINSHANCE OF STANDER STRAINSHANCE OF STANDER STAN
                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                             Mizrahi V., Huberts P., Dawes S.S., Dudding L.R.; A PCR method for the sequence analysis of the gyrA, polA and rnhA gene segments from mycobacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: SINGLE-CHAIN MONOMER WITH MULTIPLE FUNCTIONS.
-i- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                               01-07T-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA POLYMETSE I (EC 27.7.7) (POL I).
POLA OR RV1629 OR WI1665 OR MTCY01B2.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR002562; 3_5_exonuclease.
Interpro; IPR002411; 5_3_exonuclease.
Interpro; IPR0024919; DNA_pol_I.
Interpro; IPR001099; DNA_pol_A.
Interpro; IPR001099; Exo_N_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01367; 5_3_exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                MEDLINE=94124016; PubMed=8294019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE007030; AAK45935.1; -. P19821; 1BGX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295554; CAB08882.1;
                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuberculist; Rv1629; -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 136:287-290(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003584;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + (DNA)(N).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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MEDLINE=21128732; PubMed=11234002;

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mundall K., Basham D., Brown D., Chillingworth T., Connor R., Mundall K., Davlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murthy L., Oliver K., Quall M.A., Rajandream M.A., Ratherford K.M., Rutter S., Seeger K., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
pfam; pF02739; 5_3_exonuc_N; 1.

Pfam; pF00476; DNA_pol_A; 1.

PRINTS; PR00868; DNAPOLI.

SNART; SM00474; 35EXOC: 1.

SNART; SM00475; HH1; 1.

SNART; SM00278; HH1; 1.

SNART; SM00278; HH1; 1.

SNART; SM00278; HORI; 1.

PROSITE; PS00447; DNA_POLXMERASE_A; 1.

PROSITE; PS00447; DNA_DIACECTED DNA POLYMERASE_A; 1.

PROSITE; PS00447; DNA_DIACECTED DNA POLYMERASE_A; 1.

Hydrolase; Exonuclease; DNA_DIACECTED DNA_DIAGING; COMPLETE PROCECOME.

SEQUENCE 904 AA; 98471 MW; 1C8E560FESF74323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92040086; PubMed=1840579; sela S., Thole J.E., Ottenhoff T.H., Clark-Curtiss J.E.; in Thole J.E., Ottenhoff T.H., Clark-Curtiss J.E.; independent of Mycobacterium leprae antigens from a cosmid library: characterization of a 15-kilodalton antigen that is recognized by both the humoral and cellular immune systems in leprosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 88:1054-1058(1991).
-!- FUNCTION: DOMINANT T-CELL ANTIGEN AND STIMULATES
-LYMPHOPROLIFERATION.
-!- DISBASE: MOST PROBABLY CAUSES THE LYMPHOPROLIFERATIVE RESPONSES
OCCURRING IN LEPROSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91126054; PubMed=1992456;
Laal S., Sharma Y.D., Prasad H.K., Murtaza A., Singh S., Tangri S.,
Misra R.S., Nath I.;
"Recombinant fusion protein identified by lepromatous sera mimics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   native Mycobacterium leprae in T-cell responses across the leprosy
                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                    Score 54; DB 1; Length 904; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
Bacteria, Firmicutes; Actinobacteria, Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1LSRZ protein precursor (15 kba antigen) (A15)
LSRZ OR ML0234.
                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect. Immun. 59:4117-4124(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 24-115 FROM N.A.
                                                                                                                                                                                                                                                                                28.1%;
                                                                                                                                                                                                                                                                                                    58.88;
                                                                                                                                                                                                                                                                                                                                                                                                       325 TVROWLAEHAGDGRRAG 341
                                                                                                                                                                                                                                                                                                                                                                5 TLRQWLAARAGGGNGSG 21
                                                                                                                                                                                                                                                                                                      Best Local Similarity 58.8 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSR2_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-TN;
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                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSR2_MYCLE
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                                                           MEDLINE=92212967; PubMed=1313578; IP N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H., Yancopoulos G.D.;
                                                                                                                                                                                            MEDLINE-92075279; PubMed=1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
 Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                         Rosenthal A.;
"Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                               -i- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR SENSORY AND SYMPATHETIC NEURONS.
-i- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADULT
                                                                                                                  "Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribution, and receptor specificity."; Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
R -> P (IN REF. 2).
DF5112C05C5D5B85 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 GSPLRQYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLRQWL-----AARAGGGNGSGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEX2_HUMAN STANDARD; PRT; 702 AA. 013207; 016424; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROTROPHIN-5.
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BY SIMILARITY.
BY SIMILARITY.
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M86742; AAA41728.1; EMBL; S69323; AAB20548.1; -. PIR; JH0504; JH0504. PIR; B42687; B42687; B42897; B42897; B42897; DILEMPTO; IPR002072; NGF. Pfam; PF00043; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22332 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                  Neuron 7:857-866(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00140; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor; Signal
                                             SEQUENCE FROM N.A.
                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                              TISSUE-Fetal kidney;
MEDLINE-96015055; PubMed-8530034;
Campbell C., Goodrich K., Casey G., Beatty B.;
Cloning and mapping of a human gene (TBX2) sharing a highly conserved protein motif with the Drosophila omb gene.";
                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Nuclear (Potential).
-:- TISSUE SPECIFICITY: EXPRESSED PRIMARTLY IN ADULT IN KIDNEY, LUNG, AND PLACENTA. WEAK EXPRESSION IN HEART AND OVARY.
-:- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF GENES REQUIRED FOR MESODERM DIFFERENTIATION. PROBABLY PLAYS A ROLE IN LIMB PATTERN FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             Law D.J., Gebuhr T., Garvey N., Agulnik S.I., Silver L.M., "Identification, characterization, and localization to chromosome 17921-22 of the human TBX2 homolog, member of a conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 1; Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01283; TB0X.1; 1.
PROSITE; PS01264; TB0X.2; 1.
PROSITE; PS0252; TB0X.3; 1.
Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGKA -> TDKT (IN KEF. 2).
C6477134C69D7C2C CRC64;
T-box transcription factor TBX2 (T-box protein 2).
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L; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA
                                                                                                                                                                                                                                               MEDLINE=96169568; PubMed=8597636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                 SEQUENCE OF 152-245 FROM N.A.
                                                                                                                                                                                                                                                                                                         developmental gene family.";
Mamm. Genome 6:793-797(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74194 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U28049; AAA73861.1; -
EMBL; S81264; AAB36216.1; -
HSSP; P24781; IXBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001699; T-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 LASVAGGGNGGGG--GP 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00907; T-box; 1. PRINTS; PR00937; TBOX. SMART: SM00425; TBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein.
                                                                                                                                                                                                                                 TISSUE=Fetal kidney;
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 1
702 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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DOMAIN
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                                                                                                           REP PROCESSING.

RAY MEDLINE-980(0849; PubMed-9738469;

RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Mori K.,

RA Nagahama M., Taniguchi T., Hashimoto E., Imamaki A., Matsuda Y.;

RA Sayithetic processing and quaternary interactions of proprotein

RT convertaes SPC4 (PACE4).";

RT CONVERTED TO REPRESENT AN ENDOPROPRESE ACTIVITY WITHIN THE

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE REGALORY FOR THEIR

CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RANG OR LYS.

WHERE XAA CAN BE ANY AAINO ACID AND YAA IS ARG OR LYS.

WHERE XAA CAN BE ANY AAINO ACID AND YAA IS ARGOONER, SUGGESTING THAT

WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT

WHEREAS MATURE PACE4A-I EXISTS ONLY AS A MONOMER NOR CLEAVAGE REFECTS ITS TERTIARY OR QUATERRARY STRUCTURE

CONTOUR SECRETED AND REMAIN PROBEBLY IN ZYMOGEN FORM

AND PACE4CS ARE NOT SECRETED AND REMAIN PROBEBLY IN ZYMOGEN FORM

AND PACE4CS ARE NOT SECRETED AND REMAIN PROBEBLY IN ZYMOGEN FORM

AND PACE4CA HIGHT BE SECRETED

CONTOUR SACRATORY PACE4A-I AND PACE4-I AND PACE4-I AND PACE4-I AND PACE4CS, PACE4D, PACE4B-I AND PACE4CS, PACE4D, PACE4B-I AND PACE4CS, PACE4D, PACE4B-I AND PACE4CS, PACE4D, PACE4B-I AND PACE4CS, PACE4CS, PACEACS, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- TISSUE SPECTEICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN, RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BUN, SKELETAL MUSCLE, KIDNEY, PANCRARA-II IS AT LEAST COMPARATIVELY HIGHER LEVELS. IN THE LIVER. PACE4A-II IS AT LEAST EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE EXPRESSED IN PLACENTA. PACE4B-II IS EXPRESSED IN CEREBELLUM, PACE4B-II IS AT LEAST PRESENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEREBELLUM.

--- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSIGNING THE POLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACE4D LACKS THE PROPEPTIDE DOMAIN.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
"Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; piochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED
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AB001905;
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EMBL;
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EMBL;
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EMBL;
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophic factor 4).
NTF 4) (Neutrophic factor 4).
NTF 5 OR NTF4 OR NT4.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                             29.4%; Score 56.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AARAGGGNGSGGIEGPTLR-----OWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AAGAGGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB001907; BAA21625.1; JOINED.
EMBL; AB001908; BAA21625.1; JOINED.
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BAA21623.1
                                                                                                                                                  AB001904; BAA21623.1
AB001905; BAA21623.1
                                                                                                                    BAA21623.1
                                                                                                                           BAA21623.1
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     AB001900;
                                                                                                                                                                                                  AB001914;
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                                                                                                                                                            AB001905;
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AB001906;
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P34131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001412; tRNN-synt_I.
Interpro; IPR002904; tRNA-synt_I.spfan; PF01921; tRNA-synt_I.spfan; PF01921; tRNA-synt_I.spfan; PF01921; TRNA-synt_I.spfan; PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                            17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + L-1ysyl-trna(Lys).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                         10-UCIT-2001 (Rel. 40, Last sequence update)
16-CCIT-2001 (Rel. 40, Last annotation update)
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS).
LYSS OR APBOIGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; Q15099; Q15100; Q9UEJ1; Q9UEJ2; Q9UEJ7; Q9UEJ9; Q9UEG7; Q9VEG9; Q9Y4H1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
    30.5%; Score 58.5; DB 1; Length 266; 35.4%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 29.9%; Score 57.5; DB 1; Length 562; Il Similarity 42.9%; Pred. No. 20; 12; Conservative 4; Mismatches 9; Indels :
                         Pred. No. 7.9;
2; Mismatches 12; Indels
                                                                                                     6 LRQWLAARAGGG--NGSGGIEGPTLR--------QWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 AA; 65114 MW; 753664E2937FBF27 CRC64;
                                                                                                                                                                                                                           562 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 QWLAARAGGGN---GSGGIEGPTLRQWL 32
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP000058; BAA79072.1; -
                                     17; Conservative
                                                                                                                                                                                                                         STANDARD;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                Aeropyrum pernix
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                                        Matches
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PAC4_HUMAN
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MEDIINE=97335942; PubMed=9192737; Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.; "A novel human PACE4 isoform, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus."; J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.; "Genomic organization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease.",
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Paired basic anno acid cleaving enzyme 4 precursor (EC 3.4.21.-)
(Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                       "Identification of a second human subtilisin-like protease gene in the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                               Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
MEDLINE=98021085; PubMed=9378725;
                                                                                                                                                                                                                                               TISSUE=Hepatoma, and Kidney;
MEDLINE-92075167; PubMed-1741956;
Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97064242; PubMed-8906881; Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Functional analysis of human PACE4-A and PACE4-C isoforms: identification of a new PACE4-CS isoform."; FEBS Lett. 396:31-36(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W., Moehring T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 200:943-950(1994)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING (ISOFORM PACE4CS).
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=94235049; PubMed=8179631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=99233559; Pubmed=10215603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. 122:438-452(1997).
                                                                                                   convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cerebellum;
                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PACE4 isoforms.
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2;

Gaps

Indels

7;

6; Mismatches

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6 LRQWLAA-----RAGGGNGSGGI---EGPTLRQW 31
13; Conservative
    Matches
                                                                                                 RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CDC 1531 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                 Sinching-B9295987; PubbWed-9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekata F., Badcock K., Basham D., Ehollingworth T., Connor R., Badcock K., Basham D., Ehoullingworth T., Connor R., Davies R., Devilin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rotter S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.5%; Score 58.5; DB 1; Length 112; 33.3%; Pred. No. 3.6;
                                             Query Match 30.5%; Score 58.5; DB 1; Length 105; Best Local Similarity 50.0%; Pred. No. 3.3;
                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DOMINANT T-CELL ANTIGEN AND STIMULATES
LYMPHOPROLIFERATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A4B32E478CBAC3E4 CRC64;
           90 95
105 AA; 11235 MW; 8B27C7FB9922BC7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; Immune response; Signal; Complete proteome.
                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                  112 AA.
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                                                                          3; Mismatches
                                                                                                                                                                                                                                                                   LSR2 protein precursor.
LSR2 OR RV3597C OR MT3704 OR MTCX07H7B.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                    PRT;
                                                                                                       1 IEGPTLRQWLAARAGGGNGSGGIEGP 26
                                                                                                                      AE007170; AAK48061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 112 AA; 12098 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 295557; CAB08947.1; -.
                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; MT3704; -.
TubercuList; Rv3597c; -.
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
                                                                                                                                                                                                    LSR2_MYCTU
006285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                         SEQUENCE
            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                        LSR2_MYCTU
                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- TISSUE SPECIFICITY: UBUIDDITIONS.
-:- DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE
CARDIOENCEPLACOMYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS
CHARACTERIZED BY HYPETROPHIC CARDIOMYOPATHY. LACTIC ACIDOSIS, AND
GLIOSIS: HERRY AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX
ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEDLINE-20014747; PUDMEd=1054592;
PAPAGODOULOU L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I., Sapadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I., Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Van Coster K., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S., De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.; Fratal infantile cardioencephalomyopathy with COX deficiency and mutations in SCO2, a COX assembly gene.";
Nat. Genet. 23:333-337(1999).
Nat. Genet. 23:333-337(1999).
TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR003782; SCO1_SenC.
Pfam: PF02630; SCO1-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation; Polymorphism.
MITOCHONDRION (POTENTIAL).

MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R -> P (IN DBSNP:140523).

/FTIG=VAR_011738.
E -> K (IN FIC).
/FTIG=VAR_00894.
S -> F (IN FIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smink L.J., Burton J.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_008875.
BC2F40E057329BF3 CRC64;
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48 LKQWVAAGRRVGGRRRGRSGSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                                                                                                       SCO2_HUMAN STANDARD; PRT; 266 AA. 043819; 090K87; 30-MaY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                 SCO2 protein homolog, mitochondrial precursor
                                                                                                                                                                    266 AA.
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Monocytes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Wed Oct

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                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).
MEDLINE=97285914; PubMed=9141131;
Brange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L.;
"A model of insulin fibrils derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin).";
Proteins 27:507-516(1997)
                                                                                                                                                                                                                                                 -:- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
                                                                                                                                                                                                                                                                                               CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal; 3D-structure.
                                                                    X-RAY CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
Reynolds C.D.;
                                                                                                                                                                                                                                                                                                                                         -:- SÜBCELLÜLAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-:- DATABASE: NAME-Protein Spotlight;
NOTE-ISSUE 9 Of APTIL 2001;
WWW-*http://www.expasy.org/spotlight/articles/sptlt009.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 105;
AMIDES, SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AA; 11393 MW; 75307CF78E61C06A CRC64;
                                                                                                                "The structure of des-Phe bl bovine insulin."; Acta Crystallogr. B 38:3028-3032(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN B CHAIN.
              Ryle A.P., Sanger F., Smith L.F., Kitai R.;
"The disulphide bonds of insulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58.5; DF
Pred. No. 3.3;
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50.0%;
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                                        Biochem. J. 60:541-556(1955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART; SM00078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00049; Insulin; 1.
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PDB; 1CPH; 31-OCT-93.
PDB; 1DPH; 31-OCT-93.
PDB; 1PID; 07-DEC-96.
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1APH; 31-OCT-93.
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A40909; A40909.
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Best Local Similarity
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STRAND
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TURN
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Gaps

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Indels

Mismatches

3;

Conservative

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Matches

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                                                                                                                                                                                                                                                                                                                                        MEDLINE-94280618; PubMed-8011164; Ohlsen S.M., Lugenbeel K.A., Wong E.A.; "Characterization of the linked ovine insulin and insulin-like growth factor-II genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-72258016; PubMed-4626369; Peterson JD., Nehrlich S., Oyer P.E., Steiner D.F.; Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                        Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procedure.";
J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AN FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULTINE DOWN.
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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INSULIN A CHAIN.
INTERCHAIN.
                                                                                                                                                        01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                            105 AA
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"The structure of pig and sheep insulins.";
Biochem. J. 60:556-565(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; 1.
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26
                DNA Cell Biol. 13:377-388(1994).
1 IEGPTLRQWLAARAGGGNGSGGIEGP
                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 25-54 AND 85-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00262; INSULIN; 1.
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                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                          Bovidae; Caprinae; Ovis.
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HSSP; P01315; 9INS.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 57-82.
                                                                                                                                                                                            Insulin precursor.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
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                                                                                                            INS_SHEEP
P01318;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 08:51:41 ; Search time 4.29977 Seconds
(without alignments)
324.181 Million cell updates/sec

Title: US-09-422-838C-32 Perfect score: 192 Sequence: 1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES I DB ID Description	1 INS_BOVIN P01317 bos taurus	1 INS SHEEP	1 LSR2_MYCTU	1 SCO2_HUMAN 043819	1 SYK_AERPE Q9yft9	1 PAC4_HUMAN P29122	1 NT5_RAT P34131	1 TBX2_HUMAN Q13207	1 DPO1_MYCTU	1 LSR2_MYCLE	1 HXD9_MOUSE	1 HS73_BOVIN P34933 bos t	1 z219_HUMAN Q9p2y4 homo	1 NT5_HUMAN P34130 homo	1 SIX3_HUMAN 095343 homo sap	1 SRF_XENLA P23790 xenop	1 FXD2_HUMAN 060548 homo	1 BAT2_HUMAN P48634 homo	1 NYLB_FLASK P07061 flavo	1 LAC1_NEUCR	1 LAC2_NEUCR P10574	1 YR21_TRSVR P25245 tomat	1 G3B2_HUMAN Q9un86	1 OM70_MOUSE Q9czw5 mus m	1 ROU_HUMAN Q00839	1 SPM1_RAT P56225	1 Y870_METJA Q58280	1 CAKI_DROME Q24210	1 LYCV_BPP21 P27359	1 LYCV_BPPA2 P10439	1 LYCV_ECOLI P78285	TACTOR OF THE PROPERTY OF THE
% Query Match Length	105	105	112	366	562	696	209	702	904	112	339	631	722	210	332	448	497	2142	392	619	619	201	482	611	824	335	620	897	165	165	165	000
	30.5				29.9			28.1	28.1	27.9				27.3	27.1				26.8							26.3			26.0			
Score					57.5			54	54	53.5	53	53	53	52.5	52	52	52	52		51.5		51	51	51	51	50.5	50.5	50.5	20	20	20	
Result No.	1	7	m	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	•

066408 aquifex aeo	Q9tt91 macropus eu	P36021 homo sapien	Q9h461 homo sapien	P52027 deinococcus	P11675 pseudorabie	Q9uug0 s fatty aci	P25545 xanthobacte	P47937 mus musculu	Q63003 rattus norv	P98161 homo sapien	P37455 bacillus su
YZ17_AQUAE	MKR1_MACEU	MOT8_HUMAN	FZD8_HUMAN	DPO1_DEIRA	IE18_PRVIF	FAS1_SCHPO	CBBR_XANFL	NK3R_MOUSE	5E5_RAT	PKD1_HUMAN	SSB_BACSU
-	~	Н		, ,	٦	Н	-	٦	Н	Н	Н
348	478	613	694	926	1461	2073	333	385	825	4303	172
26.0	26.0	26.0	26.0	26.0	26.0	26.0	25.8	25.8	25.8	25.8	25.5
20	20	20	20	20	20	20	49.5	.49.5	49.5	49.5	49
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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The
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanger F., Tuppy H.; "The amino-acid sequence in the phenylalanyl chain of insulin. 2. investigation of peptides from enzymic hydrolysates."; Biochem. J. 49:481-490(1951).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salokangas A., Smyth D.G., Markussen J., Sundby F.;
"Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanger F., Thompson E.O.P.; The glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates."; Blochem. J. 53:366-374(1953).
                                                                                                                                                                                                                                                       D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                                                                                                                                                                                   "Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid for bovine preproinsulin."; Mol. Endocrinol. 1:327-331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=71116409; PubMed=5545080;
Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D.,
Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=71166442; PubMed=4928892;
Nolan C., Margoliash E., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
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                                                      21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                             105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreas.";
J. Biol. Chem. 246:1365-1374(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71257721; PubMed=5105368;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88288209; PubMed=2456452;
                             STANDARD;
                                                                                                                                     taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-105.
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SEQUENCE OF 57-82.
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                                                                                                        Insulin precursor.
                                                                                                                                                                                             NCBI_TaxID=9913;
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                            INS_BOVIN
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RESULT 1 INS_BOVIN
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Gaps

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Length 452; Indels

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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 06-Oct-2000
                  R;James, K.D.; Parkhill, J; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: 222967
A;Accession: T4548
A;Accession: T4548
A;Molecule type: DNA
A;Residues: 1-452 <JAM>A;Residues: 1-452 <JAM>A;Experimental source: Cosmid L373
C;Genetics: C;
                                                                                                                                                                                                                                                                                                         A;Note: MLCB373.28
C;Keywords: hydrolase; serine proteinase
F;182,224,305/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 2;
Pred. No. 96;
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.y 52.9%; Pred. No. 90,
... 2; Mismatches
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Best Local Similarity 52.97
Conservative
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Job time: 10.0937 secs
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                                                                                                    R.Duboule, D.; Dolle, P.
EMBO J. 8, 1497-1505, 1989
A.Title: The structural and functional organization of the murine HOX gene family resemt
A.Reference number: S09569; MUID:89356621
A.Accession: S09569
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Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                     R;Dolle, P.; Duboule, D. EMBO J. 8, 1507-1515, 1989
A;Title: Two gene members of the murine HOX-5 complex show regional and cell-type specif A;Reference number: S09398; MUID:89356622
A;Accession: S09398
A;Molecule type: DNA
A;Residues: 272-331 < DOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:X14714; GB:M21040; NID:g51427; PIDN:CAB57813.1; PID:g6015583 C;Genetics:
                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 272-331 < DUB>
A;Cross-references: EMBL:X14714; NID:951427; PIDN:CAB57813.1; PID:96015583
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
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A;Residues: 1-382 <STO>
A;Cross-references: GB:AL450380; NID:g13092536; PIDN:CAC29684.1; GSPDB:GN00147
C;Genetics:
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                                                                           A; Cross-references: EMBL: X62669; NID: 951414; PIDN: CAA44542.1; PID: 951416
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;273-329/Domain: homeobox homology <HOX>
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Pred. No. 82;
2; Mismatches 6; Indels
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C,Superfamily: Escherichia coli trypsin-like proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLRQWL-----AARAGGGNGSGGIEGP 26
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Pred. No. 7
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52.9%;
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Local Similarity 37.5%;
Les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9
Matches 9; Conservative
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                             A; Molecule type: DNA
A; Residues: 1-339 <REN>
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  A; Accession: S20880
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A;Cross-references: GB:M67510; NID:g149915; PIDN:AAA25351.1; PID:g149917
R;Laal, S.; Sharma, Y.D.; Prasad, H.K.; Murtaza, A.; Singh, S.; Tangri, S.; Misra, R. Proc. Natl. Acad. Sci. U.S.A. 88, 1054-1058, 1991
A;Title: Recombinant fusion protein identified by lepromatous sera mimics native Myco A;Reference number: S14407; MUID:91126054
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C; Species: Mus musculus (house mouse)
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
C; Accession: $20889; $09569; $09398
R; Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboul EMBO 7. 11, 1459-1468, 1992
A; Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences in A; Reference number: $20879; MUID: 92224884
              R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Teference number: A70500; MUID:98295987
A;Accession: C70559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternate names: 15K antigen
C; Species: Mycobacterium leprae
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 20-Jun-2000
C; Accession: B43601; 314407
R; Sela, S.; Thole, J.E.R.; Ottenhoff, T.H.M.; Clark-Curtiss, J.E.
Infect. Immun. 59, 4117-4124, 1991
A; Title: Identification of Mycobacterium leprae antigens from a cosmid library: chara
                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: 295554; GB: AL123456; NID: 93261771; PIDN: CAB08882.1; PID: 921139
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K;Residues: 24-112 <LAA>
A;Cross-references: EMBL:X53487; NID:944410; PIDN:CAA37572.1; PID:91333780
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Pred. No. 1.4e+02;
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain H37Rv
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Matches 14; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-904 <COL>
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A; Residues: 1-112 <SEL>
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C; Accession: C70559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Chlamydomonas reinhardtii
C; Species: Chlamydomonas reinhardtii
C; Species: Chlamydomonas reinhardtii
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C; Accession: T08179
R; Gloeckner, G; Beck, C.F.
Submitted to the EMBL Data Library, October 1996
A; Description: Molecular characterization of a gene (LRG5) involved in blue light signal A; Reference number: Z16399
A; Accession: T08179
A; Accession: T08179
A; Molecular type: mRNA
A; Residues: 1-640 < GLO>
A; Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>..</u>
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: G01840
R;Campbell, C.E.
submitted to the EMBL Data Library, May 1995
A;Reference number: G08602
A;Reference number: G08602
A;Accession: G01840
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-702 <CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U28049; NID:g924927; PIDN:AAA73861.1; PID:g924928
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 2; Length 702;
Pred. No. 1.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 2; Length 640;
Pred. No. 1e+02;
                                                                         28.1%; Score 54; DB 2; Length 296; 59.1%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 17421-17422
C; Superfamily: mouse transcription factor tbx2; T-box homology
F;104-285/Domain: T-box homology <TBX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11, Indels
                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AARAGGGNGSGGIEGPTLRQWLAA 34
                                                                                                                                                                                                                   4 PTLRQWLAARAGG-----GNG 19
                                                                                                                                                                                                                                                                                         66 PTLRQWAAASAIGILLLAIGNG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%;
50.0%;
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70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LAARAGGGNGSGGIEGP 26
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                                                                                                                                              13; Conservative
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nes 12; Conserv
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                                                                                Query Match
Best Local Similarity
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          A; Gene: YPO1203
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T08179
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riccle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajanfram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Riference number: A70500; MUID:98295987
A; Accession: D70505
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C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Species: Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AG0147
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
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C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005673; NID:913424605; PIDN:AAK24935.1; GSPDB:GN00148 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable HflX - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 31;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 ENPAILQYLADLAPERGLAPPAGGLERVRLQEWLA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.5; DE
Pred. No. 71;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%;
40.0%;
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Best Local Similarity 40.09
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                         A; Residues: 1-209 <STO>
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A; Residues: 1-296 <KUR>
                                                                                                                                                                                                                           A;Status: preliminary
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F;8-72/Domain: ribonucleoprotein repeat homology <RRM1>
F;120-183/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoglucomutase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20.Apr-2001 #text_change 20.Apr-2001
C;Accession: D87259
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: ribonucleoprotein
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
C; Accession: S71185
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C87617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                              3,
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                DB 2; Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 545;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:M98340; NID:g166843; PID:g166844
                                                                                                                                                                                                                                                                                                                                                                                                splicing factor SF-2 homolog - Arabidopsis thaliana
C: Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 LAGEAITDILTAAPGNGEAIGGLKVCTQNAWFAAR 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted to the EMBL Data Library, October 1992
A;Reference number: S71185
A;Accession: S71185
                                                                                                       rred. No. 57;
1; Mismatches
                                                             Score 55.5; 1
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 RGGGRGBGGSRGPSRRSEFRVLVTWLASSA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 RAGG-GNGSGGIEGPTLRQ-----WLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 28.6%; Score 55; Local Similarity 34.3%; Pred. No. (es 12; Conservative 4; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55;
                                                                                                                                                                              11 AARAGGGNG---SGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                     23 AARAGRGSGRGADGGREGRTGRASLVAR 50
                                                             28.9%;
57.1%;
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 43.89
Matches 14; Conservative
                                                                                    Local Similarity
hes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                    Matches
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C;Species: Homo sapiens (man)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 16-Feb-1997
C;Accession: A33558
R;Carr, C.S.; Sharp, P.A.
Mol. Cell. Biol. 10, 4384-4388, 1990
A;Title: A helix-loop-helix protein related to the immunoglobulin E box-binding prote
A;Reference number: A35558; MUID:90318407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-176, P7, 178-209 <BER1>
A; Cross-references: GB:S69323; NID:g240025; PIDN:AAB20548.1; PID:g240026
C; Comment: This protein is a targed-derived, diffusible neurotrophic factor.
C; Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro
C; Superfamily: nerve growth factor beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M86742; NID:g205775; PIDN:AAA41728.1; PID:g205776
R;Berkemeier, L.R.: Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenth
Neuron 7, 857-866, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotrophin-4 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Datession: B42687; JH6504; JH6604; JH66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB. A;Reference number: JH0503; MUID:92075279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
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                                                                                                                                                                                    Score 56; DB 2; Length 3190;
Pred. No. 2.9e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-79/Domain: propeptide #status predicted <PRO>
F:80-209/Product: neurotrophin-5 #status predicted <NEU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQWL-----AARAGGGNGSGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 55.5; 35.0%; Pred. No. 24
                                                                             c; Superfamily: bromodomain homology F;1723-1780/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor TFEB - human (fragment)
A;Cross-references: FlyBase:FBgn0015624
                                                                                                                                                                                                    29.2%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                10 LAARAGGGNGSGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                      44 LTGGAGGGNGGGGASGVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 35.03
Matches 14; Conservative
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A; Residues: 1-514 <CAR>
A; Cross-references: GB:M33782
                                                                                                                                                                                                                                         Best_Local Similarity 61.1'
Matches 11; Conservative
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A; Residues: 1-209 <BER>
A; Accession: JH0505
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A; Residues: 1-209 <IPA>
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A; Status: preliminary
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                                                     A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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C;Species: Drosophila melanogaster
C;Species: 20.56p-1999 #sequence_revision 20.56p-1999 #text_change 17-Nov-2000
C;Date: 20.56p-1999 #sequence_revision 20.56p-1999 #text_change 17-Nov-2000
C;Accession: T1382 #sequence_revision D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; GC
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; GC
Nature 386, 735-738, 1997
Nature 386, 735-738, 1997
Nature 2000 #sequence contivator of cubitus interruptus in hedgehog signalling.
A;Reference number: 217785; MUID:97263578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Moorl, K.; Kli, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; Na
J. Biochem. 121, 941-948, 1997
A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease containing
A;Reference number: UC5570; MUID:97335942
A;Reference number: GC570
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: brain cerebellum C; Comment: This enzyme is a processing protease and responsible for processing of variouch it is retained intracellularly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subtillsin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C; Superfamily: subtilisin-like proteinase PACE4; subtilisin homology C; Reywords: alternative splicing; glycoprotein; hydrolase; serine proteinase F; 1-62/Domain: signal sequence #status predicted <PRO> F; 196-434/Domain: propeptide #status predicted <PRO> F; 196-434/Domain: subtilisin homology <PRO> F; 205-2068/Domain: hydrophobic cluster #status predicted <HCL> F; 205, 246, 347, 420/Active site: Asp, His, Asn, Ser #status predicted F; 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:D87993; NID:92330548; PIDN:BAA21791.1; PID:92330549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                         7;
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Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                   29.4%; Score 56.5; DB 1; Length 969;
44.8%; Pred. No. 81;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
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A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                            A; Cross-references; GDB:131390; OMIM:167405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AARAGGGNGSGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-975 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PACE4
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
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Gaps

7;

7; Indels

Length

DB 1;

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A;Cross-references: GDB:131390; OMIM:167405
A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Reywords: alternative splicing; hydrolase; serine proteinase
F;196-444/Domain: subtilisin homology <SBT>
F;205,246,420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                Score 56.5; DE
Pred. No. 55;
2; Mismatches
                                                                                                                                                                                                                                                                                                              11 AARAGGGNGSGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                                                                                                                   24 AAGAGGAGGAGGPGFRPLAPRRWL 52
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                                                                                                                                                                                                   Query Match 29.4%;
Best Local Similarity 44.8%;
Matches 13; Conservative
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-962 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-969 <KIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: JC5571
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                                                                                                                                                                                                                                                                                                                                                                   q
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                                                                                                                                                                                                                                                                                                                    δλ
                       R;Cole, S.T.; Eigimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subtilisin-like proprotein convertase (EC 3.4.21..) PACE4 precursor, splice form C - hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: JC2191
K:Tsuji, A.; Higashine, K.; Hine, C.; Mori, K.; Tamai, Y.; Nagamune, H.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 200, 943-950, 1994
A;Title: Identification of novel cDNAs encoding human kexin-like protease, PACE4 isoform
A;Reference number: JC2191; MUID: 94235049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment: This protein consists of a signal peptide, a propeptide, a substilisin-like Comment: This protein cleaves precursor proteins at dibasic amino acid residues.
                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: ML0997
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: GTP-binding protein hflx; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>,</del>;
                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: GB:AL450380; NID:g13093026; PIDN:CAC31378.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hflX protein - Mycobacterium leprae
N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar.1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72938
R;Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993 A;Description: Mycobacterium leprae cosmid B2235. A;Reference number: $72587 A;Accession: $72938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.5;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names: kexin-like protease isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 PRLKGWGESMSRQVGGRAGGSGGGVGLRGP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PTLROW-----LAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PTLRQW-----LAARAGGGNGSGGIEGP 26
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40.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 12; Conserv
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A; Residues: 1-652 <TSU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-518 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
     C; Accession: G87033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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N;Alternate names: kexin homolog
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C;Accession: A33490
R;Kiefer, M.C.; Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
DNA Cell Biol. 10, 757-769, 1991
A;Title: Identification of a second human subtilisin-like protease gene in the fes/fp
A;Reference number: A39490; MUID:92075167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: brain cerebellum C; Comment: This enzyme is a processing protease and responsible for processing of var ch it is retained intracellularly.
                                                                                                                                                                   R;Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.;
J. Biochem. 121, 941-948, 1997
                                                                                                                                                                                                                                                   A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain A;Reference number: JC5570; MUID:97335942
subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form E-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: DDBJ:D87994; NID:q2330550; PIDN:BAA21792.1; PID:q2330551
                      C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily: subtliisin-like proteinase PACE4; subtliisin homology C; Keywords: glycoprotein; hydrolase; serine proteinase F;1-62/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;205,246,347,420/Antive site: Asp, His, Asn, Ser #status predicted F;259/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;63.149/Domain: propeptide #status predicted <PRO>F;196-434/Domain: subtilisin homology <SBT>F;938-954/Domain: hydrophobic cluster #status predicted <HCL>
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Pred. No. 80;
2; Mismatches
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A;Cross-references: GDB:131390; OMIM:167405
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3 GPTLRQWLAARAGGGNGSGGIEG 25
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A; Residues: 1-249 <STO>
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                                                                                                                                                                                      RESULT 8
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                                        δ
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID: 99310339
A;Reference number: A72450; MUID: 99310339
A;Accession: F72771
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 < KAM>
A;Residues: 1-56 < KAM>
A;Experimental source: strain Kl
C;Genetics
A;Gene: APE0161
C;Superfamily: Lyme disease spirochete lysine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aypothetical protein F1589.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T20961
R.Percy, C.
submitted to the EMBL Data Library, August 1996
A.Reference number: 213351
A.Accession: T20961
A.Scatus: preliminary, translated from GB/EMBL/DDBJ
A.Scatus: preliminary, translated from GB/EMBL/DDBJ
A.Scatus: 1-500 cWIL>
A.Residues: 1-500 cWIL>
A.Residues: 1-500 cWIL>
A.Status: 1-500 cWIL>
A.Status: 1-500 cWIL>
A.Scatus: 1-500 cWIL>
A.Status: 1-500 cWIL>
A.Statu
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.7%; Score 57; DB 2; Length 200; 41.4%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                               Score 57.5; D
Pred. No. 37;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EGPTLRQWLAARAGGGNGSGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QWLAARAGGGN --- GSGGIEGPTLRQWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
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Matches 11; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: AT4g03750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
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E85047
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Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A; Residues: 1-487 <KIE>
A; Note: the lack of a domain necessary for correct folding and activity of other seri
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form N;Alternate names: subtilisin homolog precursor, short splice form
                                                                                                                                                                                                                                       ABC transporter, ATP-binding protein CC2634 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005673; NID:g13424211; PIDN:AAK24601.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                             C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87575
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C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 31-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
C;Keywords: alternative splicing; hydrolase; serine proteinase
F:196-434/Domain: subtilisin homology <SBT>
F:205,246,420/Active site: Asp, His, Ser #status predicted
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44.8%; Pred. No. 42;
tive 2; Mismatches 7; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 29.4%; Score 56.5; Local Similarity 42.9%; Pred. No. 22; hes 15; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:131390; OMIM:167405
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probable Isr2 protein - Mycobacterium tuberculosis (strain H37RV)

probable Isr2 protein - Mycobacterium tuberculosis
(;Species: Mycobacterium tuberculosis
(;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
(;Accession: F70954
R;Cole, S.T.; Brosch, R.; Parkhi, L.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Pavlin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Attles Sagares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295887
A;Accession: F70954
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
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A;Cross-references: GB:295557; GB:AL123456; NID:93242276; PIDN:CAB08947.1; PID:921139
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                 R.Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W. FEBS Lett. 349, 205-209, 1994 Afrittle: Existence of a molecular ruler in proteasomes suggested by analysis of degra A; Reference number: S46258; MUID:94326921
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A;Molecule type: DNA
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.5%; Score 58.5; DB 1; Length 105; 50.0%; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circy Avords: hormone; pancreas circy Avords: hormone; pancreas F;1-24/Domain: signal sequence #status predicted <SIG>F;2-5-54/Domain: signal sequence #status experimental <BCH>F;25-54/B5-105/Product: insulin #status experimental <AMTP-F;25-54/B5-105/Promain: connecting peptide #status experimental <CPEP>F;57-85-105/Domain: insulin chain A #status experimental <ACH>F;31-91,43-104,90-95/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
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3; Mismatches
                             A, Molecule type: protein
A, Residues: 25-30, X', 32-42, XX', 44-54 <CH2>
R; Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai, R.
Biochem. J. 60, 541-556, 1955
A, Title: The disulphide bonds of insulin.
                                                                                                                                                                                                                            A. Reference number: A90343
A. Contents: annotation; amides; disulfides
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Best Local Similarity 33.3%
watches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.09
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 25-54 <WEN>
C; Superfamily: insulin
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A;Status: preliminary
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A; Residues: 57-82 <SALD
R; Sanger, F.; Thompson, E.O.P.
Bjochem. J. 53, 356-374, 1953
A; Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of A; Reference number: A90342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 85-105 <SAN>
R;Sanger, F.; Tuppy, H.
Biochem. J. 49, 481-490, 1951
A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigat
A;Reference number: A90341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C; Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C; Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C; Date: 24-Apr-1984 #sequence_revision 540341; S48184; S48185; S46258; AOI
R; Date: 24-Apr-1984 #sequence_revision 54034; S4034; S4034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. Blochem. 20, 183-189, 1971
A;Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancreas.
A;Reference number: A91185; MUID:71257721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Site-specific oxidation of histidine residues in glycated insulin mediated by A; Reference number: $48184; MUID:9433378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 25-105 <NOL>
R; Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
J. Biol. Chem. 246, 1355-1374, 1971
A; Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A; Reference number: A92074; MUID:71116409
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M54979; NID:9163578; PIDN:AAA30722.1; PID:9163579
                                                                                                                                                                                                                                                              Length 77;
            F;1-30/Domain: insulin chain B #status experimental <BCH>F;1-30,57-77/Product: insulin #status experimental <MAT>F;31-56/Domain: connecting peptide #status experimental <CPEP>F;31-77/Domain: insulin chain A #status experimental <ACH>F;7-77/Domain: insulin chain A #status experimental <ACH>F;7-63,19-76,62-67/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: fetal pancreas R.Nolan, C.; Margoliash, E.; Peterson, J.D.; Steiner, D.F. J. Biol. Chem. 246, 2780-2795, 191. Biol. Chem. 246, 2780-2795, 191. A; Reference number: A92080; MUID:71166442 A; Accession: A92080
                                                                                                                                                                                                                                                          Score 58.5; DB 1;
Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGNGSGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%;
50.0%;
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A; Residues: 25-54 <SA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-105 <DAA>
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                   Query Match
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2002, 08:54:17; Search time 8.09368 Seconds October Run on:

(without alignments)
427.397 Million cell updates/sec

US-09-422-838C-32

192 1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Conserved hypothet	insulin programor	recurrent discrete	ייים לאטן	7357	➣		APC transcal proce	Abc cidisporter, A		Piopanie AIP/GIP-D	⋝:				Subcilisin-like pr	ckes-binding prote	neurotrophin-4 pre	ption ta	Splicing ractor SF	phosphoglucomutase	grutathlone S-tran	Propapie HILA - My	ro.	LRG5 protein - Chl	()		LSR2 T-Call pution	homeotic protein a	
SUMMARIES		B71325	INSH	IPBO	F70954	F72771	E85047	120961	E87575	839490	687033	62,038	10101	105571	A30400	105570	713828	B42687	435658	S71185	787259	707617	D20505	20000	AGO14 /	6/T80.L	G01840	C70559	B43601	S20880	Н86930
DB	:	7	Н	-	7	٠,	٠,	2	~	· ~	N	0	۰,	10	-	10	۱,	٠,	۱,	۰,		۱,	۰,	, ,	4 (7	~	N	~	~	7
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probable serine pr conserved hypothet	"Ifocuerical ploce neurotrophin-4 pre hypothetical prote	hypothetical prote	hypothetical prote	transcription fact cell death suppres	hypothetical prote pre-pro-legumin -	probable immediate	MHC class III hist	MHC class III hist
T45448 B95325 T25893	A42687 T31193	T49792	T26808	AC2068	T06021 T10519	T03166	836152	B35098
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27.6 27.6 27.6	27.3	27.1	27.1	27.1	27.1	27.1	27.1	27.1
53 53	52.5 52	52 52	52	250	22	52 52	25	25
30 31 32	33 4	35 36	37	900	4 4	4 4 2 3	44	45

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A) Status: preliminary; nucleic acid sequence not shown; translation not shown A) Molecule type: DNA A) Mesidues: 1-683 <COL>
A) Cross-references: 08:AE001220; GB:AE000520; NID:93322705; PIDN:AAC65409.1; PID:9332 A) Experimental source: strain Nichols A) Genetical F00421
A) Genetical F00421
                                                                                                                                 RiFraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Ison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998 Science 281, 375-388, 1998 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770
conserved hypothetical protein TP0421 - syphilis spirochete C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999 C; Accession: B71325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.2%; Score 60; DB 2; Length 683; 43.8%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
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insulin precursor - sheep

RESULT 2

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: S16430, S16431
B. C. Accession: S16430
A. Title: The structure of pig and sheep insulins.
A. Ariticle: The structure of pig and sheep insulins.
A. Arcession: S16430
A. Accession: S16430
A. Accession: S16430
A. Reterance number: Agold4
A. Reterance number: Agold4
A. Reterance number: Agold4
A. Reterance number: Agold4
A. Title: Determination of the anino acid sequence of the monkey, sheep, and dog proin

A; Accession: S16431

A,Molecule type: protein A,Residues: 31-56 <PET> C,Superfamily: insulin C,Reywords: hormone; pancreas

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us-09-422-838c-32.rai

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Gaps
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                          Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.0%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.0063; tive 0; Mismatches 0; Indels
                                        38.0%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.0063; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.O. Box 13398
                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J.
Barrett, Ronald W.
CWilla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-516-704-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: October 9, 2002, 09:06:34
Job time : 5.98595 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.C
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                     Sequence 194, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEOUENCES: 244
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COMPUTER READABLE FORM:
                                                                                     Conservative
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                   1 IEGPTLROWLAARA 14
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                                            Query Match
Best Local Similarity
Matches 14; Conserva
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US-09-516-704-194
    US-09-516-704-18
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                             38.0%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0063; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glavo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Beta-ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE, DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPROME: 912-48-1000
INFORMATION FOR SEQ. ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /product= "1 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J. Barrett, Ronald W. Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 16 amino acids
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                                      TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: PK TELECOMMUNICATION INFORMATION:
                                                                                         LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                      Matches 14; Conservative
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                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                       US-09-244-298A-232
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US-09-516-704-18
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                    APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

38.0%; Score 73; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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STREET: Five Moore Drive, P.O. Box 13398
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OTHER INFORMATION: /product- "Beta-ala"
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING BATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 194, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
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Podduturi, Surekha
                                                                                                                                                      Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
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                                                                                                                                                                        STATE:
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.0%; Score 73; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 0.0063; Matches 14; Conservative 0; Mismatches 0; Indels
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 ·
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CITY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanlan, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                    APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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SOFTWARE: Patent...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
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; Patent No. 6121238
; GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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APPLICANT:
COUNTRY:
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                                                                                                            38.0%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER EACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                              SEQUENCE DESCRIPTION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THROMBOPOIETIN RECEPTOR
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-08-973-225-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                            Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselden, Sherril S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattheakis, Larry C. Schatz, Peter J.
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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NAME: Hrubiec, Robert T.
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NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 232
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                                                                                                                  Query Match 38.09
Best Local Similarity 100.0
Matches 14; Conservative
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Best Local Similarity
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                      LOCATION:
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                                                                            US-08-973-225-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: HILDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248 1000
INFORMATION FOR SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
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SEQUENCE DESCRIPTION: SEQ ID NO: 220:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                         Wagstrom, Christopher R.
Wrighton, Nicholas C.
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GENERAL INFORMATION: APPLICANT: Dower, William J.
              Sequence 220, Application US/08973225A; Patent No. 6083913
GENERAL INFORMATION:
                                                                                                                                                                           Haselden, Sherril S.
Mattheakis, Larry C.
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                                                                          APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 27709
COMPUTER READABLE FORM:
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Best Local Similarity 100.0
watches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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APPLICANT:
APPLICANT:
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APPLICANT:
US-08-973-225-220
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CORRESPONDENCE ADDRESS:

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Query Match
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
MINDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.0%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.0063; ative 0; Mismatches 0; Indels
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
          : Five Moore Drive, P.O. Box 13398
Research Triangle Park
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CITY: Research Triangle Park
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNELYAGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE: CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
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Patent No. 5869451
Patent No. 5869451 5837683
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Glaxo Wellcome
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                                                                                                        COMPUTER READABLE FORM:
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; MOLECULE TYPE: peptide
US-08-764-640-194
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
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APPLICANT: Dower
                                                                                      27709
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STATE:
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0; Gaps
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.0063; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA: US/08/973,225A
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
APPLICATION NUMBER: US/08/764,640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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                                                                                                             REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                         NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                         11-DEC-1996
N: 514
                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                       16 amino acids
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100.

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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-232
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                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
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                     FILING DATE:
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.0%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.0063; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPENATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COTHER INFORMATION: /product= "Beta-ala"; OTHER INFORMATION: /product= "Beta-ala"
                                                                                                                                                                                                                    STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
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Hendren, Richard W.
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; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 anino acids
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: CWITIA, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                          Glaxo Wellcome
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Best Local Similarity 100.C
Matches 14; Conservative
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APPLICANT:
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Schatz, Peter J.
Schatz, Peter J.
Balasubramanian, Palaniappan
Magstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.0%; Score 73; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0058; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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Patent No. 5869451
Patent No. 5869451 5837683
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                     Sequence 185, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
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Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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APPLICANT: DOWER,
APPLICANT: BATTECT
APPLICANT: GATES,
APPLICANT: GATES,
APPLICANT: Schafz,
                                                     1 IEGPTLROWLAARA 14
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US-08-764-640-18
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US-09-516-704-185
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1 IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENY APPLICATION DATE:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.0%; Score 73; DB 3; I Best Local Similarity 100.0%; Pred. No. 0.0058; Matches 14; Conservative 0; Mismatches 0;
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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11-DEC-1996
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                                                                                                                                                                                                              PK3281
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                                                                                                                                                              NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27709
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APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                         38.0%; Score 73; DB 3; 1
100.0%; Pred. No. 0.0058;
tive 0; Mismatches 0
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: CURNOWN>
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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ADDRESSEE: Glaxo Wellcome
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; Patent No. 6251864
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
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Best Local Similarity 100.00
Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                            Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                               ; MOLECULE TYPE: peptide US-09-244-298A-185
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                                         amino acid
                                                                                linear
                                                     STRANDEDNESS:
                                                                              TOPOLOGY:
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                                                                                                                                                           Query Match
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NUMBER OF SEQUENCES: 232
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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Matches 14; Conservative
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ADDRESSEE: Glaxo Wel
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                                                                                                                       COUNTRY: US
ZIP: 27709
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                                                                                                        STATE: NC
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APPLICANT:
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                                                                                                                                                                                                                   Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.0%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.0058; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ_ID NO: 17:
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
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TOPOLOGY: linear
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MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-973-225-17
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Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
CWITIA, Steven E.
Duffin, David J.
Haselden, Sherril S.
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                               Haselden, Sherril S.
Mattheakis, Larry C.
             Sequence 17, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                   APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwila, Steven E.
Duffin, David J.
Gates, Christian
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15 amino acids
                                                                                                                                                                                                      Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27709
COMPUTER READABLE FORM:
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Matches 14; Conservative
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US-08-973-225-185
US-08-973-225-17
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Gaps
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Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRING APPLICATION DATA:
APPLICATION DATE: U4-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET WUMBER: 98,050SWW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                                                                                    THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
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APPLICANT: Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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LENGTH: 15 amino acids
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Barrett, Ronald W.
Cwirla, Steven E.
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                                                                                                                                  38.0%; Score 73; DB 2; Length i5; 100.0%; Pred. No. 0.0058; tive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
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CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ; Sequence 185, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                            Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PR:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaxo Wellcome
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                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 1
                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 15 amino acids amino acid
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                                                                                                                                                                                                          1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                           1 IEGPTLROWLAARA 14
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-764-640-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yin, Qun
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                                                                                                                                                  Best_Local Similarity
                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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Matches 14; Conserv
                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                  ch 38.0%; Score 73; DB 4; Length 14; 1 Similarity 100.0%; Pred. No. 0.0054; 14; Conservative 0; Mismatches 0; Indels
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                                               ATTORNEY/AGENT INFORMATION

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 193:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 aming acids
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <UNKnown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schatz, Peter J. APPLICANT: Balasubramanian, Palaniappan
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FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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APPLICANT:
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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                                    ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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NUMBER OF SEQUENCES: 244
                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
                     CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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ZIP: 27709
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                                                                                                STATE: NC
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEFPIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                           APPLICANT: Deprince, Randolph B.
APPLICANT: Poduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0054; ative 0; Mismatches 0; Indels
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Balasubramanian, Palaniappan
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                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6251864
GENERAL INFORMATION:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Research Triangle Park
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TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
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INFORMATION FOR SEQ ID NO: 193:
                                                                           Barrett, Ronald W. Cwirla, Steven E. Gates, Christian
                                            GENERAL INFORMATION:
APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                             Glaxo Wellcome
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 244 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy of
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                           Patent No. 6121238
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STATE:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                             38.0%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0; Indels
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STREET: Five Moore Drive, P.O. Box 13398
               ATTORNEY/AGENT INFORMATION:
NAME: HUDDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELEOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
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TECHPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
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SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWILLA, Steven E.
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Mattheakis, Larry C.
Schatz, Peter J.
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duffin, David J. Gates, Christian
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LENGTH: 14 amino acids
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Best Local Similarity 100.(
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLROWLAARA 14
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
         Length 14;
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0; Indels
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 38.0%; Score 73; DB 3; I 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
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11-DEC-1996
                                                                                                                                                                                               Sequence 13, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 193, Application US/09244298A
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Podduturi, Surekha
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,3
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INFORMATION FOR SEQ ID NO: 1
Query Match 38.0 Best Local Similarity 100. Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
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les 14; Conservative
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MOLECULE TYPE: peptide
                                                                        1 IEGPTLRQWLAARA 14
                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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APPLICANT:
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APPLICANT:
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Matches
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APPLICATION NUMBER: US/08/973,225A
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                USA
                                                                                                                               27709
                                      ADDRESSEE:
                                                                                                                  COUNTRY:
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                                                                                                                                                                                                       TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

38.0%; Score 73; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 CLASSIFICATION: 514 NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                      Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                         Wagstrom, Christopher R. Hendren, Richard W.
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Patent No. 5869451
Patent No. 5869451 5837683
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                                                                                                                                                           Deprince, Randolph B. Podduturi, Surekha
          Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PK.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 919-246-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: __inear
; MOLECULE TYPE: peptide
US-08-764-640-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA 14
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Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO A THEMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.0%; Score 73; DB 2; Length 14; 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                  Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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Mattheakis, Larry C.
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Sequence 13, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
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                                       Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PK:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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COMPUTER READABLE FORM:
Glaxo Wellcome
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-193
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CORRESPONDENCE ADDRESS:
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39.8%; Score 76.5; DB 3; Length 25;
Best Local Similarity 40.6%; Pred. No. 0.0039;
Matches 13; Conservative 8; Mismatches 2; Indels
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APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                                                                 2 EGPTLRQWLAARAGGGNGSGGIEGPTLRQWLA 33
                                                                                                                                                                                                       LOCATION: 13
OTHER INFORMATION: /product= "Ava"
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
Yin, Qun
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                                                                                                                                                                                                                                                                                                                          Sequence 231, Application US/09244298A Patent No. 6121238
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NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-100:
INFORMATION FOR SEQ ID NO: 231:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Glaxo Wellcome
Five Moore Drive,
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NAME/KEY: Modified-site
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                                                                                              Query Match 39.8%
Best Local Similarity 40.6%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                  RESULT 2
US-09-244-298A-231
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                                                         US-08-764-640-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 13
OTHER INFORMATION: /product= "Ava"
SEQUENCE DESCRIPTION: SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
:||||||:|:: | :||||||:|:: | 2 DGPTLREWISFXA-----DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EGPTLRQWLAARAGGGNGSGGIEGPTLRQWLA 33
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                                                                                                                                                                                                   APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 231:
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                                                                                                                                                                                                                                                                                               Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Sequence 197. Appl
Sequence 17. Appl
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Sequence 17. Appl
Sequence 17. Appl
Sequence 185. Appl
Sequence 185. Appl
Sequence 186. Appl
Sequence 187. Appl
Sequence 188. Appl
Sequence 188. Appl
Sequence 198. Appl
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Sequence 231, App
Sequence 231, App
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                                                                                             (without alignments)
146.898 Million cell updates/sec
                                                                                October 9, 2002, 08:55:27; Search time 5.98595 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.3
Copyright.(c) 1993 - 2002 Compugen Ltd.
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1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
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US-08-764-640-133
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US-08-764-640-173
US-08-764-640-174
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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	1-76 - 640-2 1-76 - 640-2 14-640-2 15-76 - 6
27888333333355 38333333333333333333333333	SSULT 1 Sequence 23 Sequence 23 Sequence 24 Sequence 24 Sequence 25 Sequence 26 Sequence 2
	M I M A A A A A A A A A A A A A A A A A

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; amunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF: antagonist; MMP: inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
1 IEGPTLRQWLAARAGG----GGIEGPTLRQWLAARA 32
                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
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                                                                                                                                                                    AAB17298 standard; Peptide; 36 AA
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                                                                                                                                                                                                                                                                                31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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22-OCT-1999;
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                                                                                                                                                                                                                          AAB17298;
                                                                                                           RESULT 30
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q The present invention describes composition of matter (I) comprising an (X) The present invention describes composition of matter (I) comprising an (X) The TPI-(X2D, where: FI = an Fc domain, I and X2 = are each idependently selected from -(II)-C-PI-(II)-C-PI-(I2)d-P2.

(LI)-C-PI-(LZ)d-P2-(L3)e-P-3, or -(L1)-C-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4 (M) and P4 = are each independently sequences of paramacologically active peptides: LI, LZ, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombois, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer control in composition and provide and incition and possibly placental transfer. AAA69443

(C) AAA69526 and AAB16995 to AAB18003 represent invention. 1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36 Query Match Best Local Similarity '

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0; Gaps

Indels

81.2%; Score 156; DB 21; Length 36; ilarity 88.9%; Pred. No. 2.9e-12; Conservative 0; Mismatches 4; Indels

Sequence

1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36

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| I IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36
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9, 2002, 08:58:58 Search completed: October Job time: 16.1874 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an Kr domain, pharmacologically active peptides, and linkers. Where (I) is: (X1a-Fr-(X2)b, where FI = an Fc domain, X1 and X2 = are each independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2, -(L1)C-P1-(L2)d-P2, -(L3)e-P3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptides; L1, L2, and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, and f = are each independently independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; eythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                              5;
            85.9%; Score 165; DB 21; Length 34; 91.7%; Pred. No. 2.2e-13; ive 0; Mismatches 1; Indels
                                                                                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGG -- GGGGIEGPTLROWLAARA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17290 standard; Peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
Query Match
Best Local Similarity 91.79
Watches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17290;
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
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85.7%; Score 164.5; DB 21; Length 33;

Query Match

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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P2, -(L2)d-P2, (L1)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4, where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or provided that at least 1 of a and b 1s 1. The composition can activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNP; antagonist; mmy; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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88.9%; Pred. No. 1.5e-12;
tive 0; Mismatches 0; Indels
                                     Indels
Pred. No. 2.5e-13;
                                                                                                                  1 IEGPTLRQWLAARAGGG---GGIEGPTLRQWLAARA 33
                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:345.
                                     0; Mismatches
                                                                            1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA
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                                                                                                                                                                                                                     AAB17289 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J,
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                    91.78;
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                                       33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases -
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Best Local Similarity
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                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                             AAB17289;
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                                         Matches
                                                                                                                                                                                  RESULT 29
                                                                                                                                                                                                       AAB17289
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to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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is:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autolimune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin i; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                        Score 170; DB 21; Length 40;
Pred. No. 6.5e-14;
0; Mismatches 2; Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGN----GSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                 TPO-mimetic peptide sequence SEQ ID NO:352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17296 standard; Peptide; 42 AA.
                                                                                                                                                     88.5%;
85.0%;
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99US-0428082
                                                                                                                                         Query Match
Best Local Similarity 85.09
Matches 34; Conservative
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                                                                                           40 AA;
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                                                                                              Seguence
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      8.236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes composition of matter (I) comprising an K10a-r1-(X2)b, where F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L3)e-P2, (L3)e-P2, (L3)e-P2, (L3)e-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2, (L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, c, d, e, and f = are each independently novided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autolmunne disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vyctocxaic Techl Lymphocyte antigen 4; tumour necrosis factor; vascular endochbilal growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                               9
                                                  88.0%; Score 169; DB 21; Length 42; 81.0%; Pred. No. 9.1e-14; 1.1ve 0; Mismatches 2; Indels
                                                                                                                           1 IEGPTLRQWLAARA-----GGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                        AAB17291 standard; Peptide; 34 AA
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                                                                                          34; Conservative
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                                                                      Local Similarity
                   42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000
                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                               AAB17291;
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                          Matches
                                                                                                                                                                                                                     RESULT 27
                                                                                                                                                                                                                                         AAB1729.
XX
So
                                                                                                                             δ
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34 AA;

Seguence

q δ

8\$\$\$\$\$\$\$\$\$\$

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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-FI-(X2)b, where: FI = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-PI-(L2)d-P2,

-(L1)c-PI-(L2)d-P2-(L3)e-P^3, or -(L1)c-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4,

where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69256 and AAB16955 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antiagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i; cytocoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                       Score 170.5; DB 21; Length 39;
Pred. No. 5.5e-14;
0; Mismatches 2; Indels 3
                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGG---NGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGKPEGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17305 standard; Peptide; 39 AA
                                                                                                                                                                                                                88.8%;
87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0105371
99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                             34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                      39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17305;
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17305
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The present invention describes composition of matter (I) comprising an Fe domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3
                                                                                                                                                                                                                              ij
                     AAA69443
                     A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69226 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
half-life or incorporate functions such as Fc receptor binding, protein a binding complement fixation, and possibly placental transfer. AAA694
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin icytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                 3;
                                                                                                                                                                                DB 21; Length 39;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                        5e-14;
2;
                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGG---NGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                              Pred. No. 5.5e
0; Mismatches
                                                                                                                                                                                     88.8%; Score 170.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17302 standard; Peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105371.
99US-0428082.
                                                                                                                                                                                                                   87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                       39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17302;
                                                                                                                                          Sequence
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 X G G G G
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O or 1, provided that at least 1 of a and b is 1. The composition can activities. ONRs. vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fr domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fr receptor binding, protein to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, mimetic; IL.11 TNF; antagonist; inhibitor; erythropoietin; thrombopoietin; interleukin 1; veytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vescular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                     2; Indels 1;
                                                                                                                                                                                        89.3%; Score 171.5; DB 21; Length 37; 91.9%; Pred. No. 4e-14;
                                                                                                                                                                                                                                            1 IEGPTLRQWLAARA-GGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGGGGGGGGGGGGTEGPTLROWLAARA 37
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                            AAB17295 standard; Peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0105371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                                                                                                                                                                  34; Conservative
                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                           37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000.
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         AAB17295:
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                      Local
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                  RESULT 22
                                                                                                                                                                                                                                                                                                                                AAB17295
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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc domain, pharmacologically active peptides, and linkers. Where (I) is: independently selected from -(Li)c-Pi -(Li)c-Pi -(Li)d-P2, (Li)d-P2, (Li)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antiqen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                 Length 38;
                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                    89.1%; Score 171; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARA--GGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17304 standard; Peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                             l Similarity 89.58;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases -
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                      38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17304
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q
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cc vhcre Pl. P2, P3, and P4 = are each independently sequences of where Pl. P2, P3, and P4 = are each independently sequences of paramacologically active peptides; Ll, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently of or l, provided that at least l of a and b is l. The composition can of or l, provided that at least l of a and b is l. The composition can activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can activities. DNAs, vectors and host cells from the present invention can serial for treating pharmaceutical compositions. The compositions are composited for the use of an FC domain (rather than a Fab domain) can provide a longer the use of an incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 because used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L3)c-P1-(L2)d-P2, -(L3)d-P2, -(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; CTLA4; minetic; IL-1; TNF; antagonist; man; inhibitor; erythropoietin; thrombopoietin; interleukin is cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 21; Length 268;
Pred. No. 5.1e-14;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17292 standard; Peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.7%;
milarity 94.3%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
hes 33; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17292:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 20
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The present invention describes composition of matter (1) comprising an Fr domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2
pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, thrombolytic and immunosuppressive have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNBA, vectors and host cells from the present invention can activities. DNBA, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autolimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer The use of an Fc domain (rather than a Fab domain) can provide a longer thalf-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoiethi; thrombopoletin; interleukin 1; vyctocxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothedial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.3%; Score 171.5; DB 2. 94.4%; Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17294 standard; Peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Il Similarity 94.4%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18095 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note'= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                  Length 36
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                               93.2%; Score 179; DB 21; 94.4%; Pred. No. 4.7e-15;
                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24834.
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                                                                                                                                                                                                                                Best_Local Similarity 94.49
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC.
                                                                                                                                                                                  36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024770-A2
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96524;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                               RESULT 18
                                                                                                                                                                                                                                                                                                                                                                              AAY96524
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10 to 14 residues in length comprising X_{-2} \times X_{-1} = 0, X_{-2} \times X_{-1} = 1, X_{-2} \times X_{-1} = 1, X_{-1} \times X_{-1} = 1, X_{-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: \langle XI \rangle a - FI - \langle XI \rangle b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; finuncosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 179; DB 21; Length 36; Pred. No. 4.7e-15; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB16959 standard; Protein; 268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA69445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
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thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically, active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                   virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                        Score 182; DB 21;
Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                          234 IEGPTLROWLAARAGGGGGGGGGIEGPTLROWLAARA 269
                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                              AAB17303 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Cheetham J,
                                                                                                                                                                                                                                          94.8%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.4<sup>1</sup>
Matches 34; Conservative
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                                                                                                                                                                                                                269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17303;
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
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pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blaiding, protein half-life or incorporate functions such as Fc receptor blaiding, protein A binding, complement fixation, and possibly placental transfer. AAA6944 to AAA69526 and AAB18091S to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 179; DB 21; Length 36; 94.4%; Pred. No. 4.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGCGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17307 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.27
Best Local Similarity 94.44
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17307;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17307
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L3)d-P2, (L3)d-P3, (L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can cartivities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (tather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, torbeln the activities or incorporate functions such as Fc receptor binding, complement fixation, and possibly placental transfer. AAAA6943 to AAAA69526 and AABI6955 to AABI8003 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4: mimetic; IL-1; TRF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.8%; Score 182; DB 21; Length 60; 94.4%; Pred. No. 3.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
                   Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB16960 standard; Protein; 269 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0105371.
99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AA;
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autoimmune diseases -

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The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X3)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-F1-(L2)d-F2.

(L1)c-F1-(L2)d-F2-(L3)e-P^3, or -(L1)C-F1-(L2)d-F2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently linkers; and as b, 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, promplement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB180303 represent uncleotide and amino acid considered and the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; IgGl; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new, TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment c diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 182; DB 21; Length 269; 94.4%; Pred. No. 1.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
             Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human IgG1 Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96531 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA29229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96531
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Example 2A; Page 48; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                     The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)-C-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18033 represent uncleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoletic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 182; DB 21; Length 42;
Pred. No. 2.4e-15;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                      Example 2; Page 327; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96530 standard; Protein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheetham J;
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Best Local Similarity 94.4
Matches 34; Conservative
                                                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-365108/31.
WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA29225.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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was then fused in-frame to the FC region of the human IgG1 chain (see Axy96529). A compound which binds to a mpl receptor comprising a TWP dimer joined by a linker [TWP1-(L1), nWP2], is new. TWP1 and TWP2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X-2X_1-1, X-2X_1-2, X-2X_1-4, X-1-X_1-X, X-1-X_1-X, X-1-X_1-X, X-1-X_1-4, X-1-X_1-X, X-1-X_1-4, X-1-X_1-X, X-1-X_1-4, X-1-X_1-X, X-1-X_1-4, X-1-X_1-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
Overlapping oligonucleotides were used to construct a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 182; DB 21; Length 42; 94.4%; Pred. No. 2.4e-15; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anaemia, immune thrombocytopenia (ITP), human imm
associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
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99US-0428082.
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nes 34; Conservative
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22-OCT-1999;
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L)-C-F1, -(L)-C-F1-(L2)d-F2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2. P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can bave cytostatic antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention are useful for treating pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (tather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69526 and AAB18055 to AAB18003 represent invention.
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                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.8%; Score 182; DB 21; Length 42; 94.4%; Pred. No. 2.4e-15; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:338.
                Cheetham J, Boone TC;
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                                                                                                                                                                        Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
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                                                                                                                                    autoimmune diseases -
                                                     WPI; 2000-350702/30.
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                Liu C,
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                Feige U,
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The present invention describes composition of matter (1) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (1) is:

(X1)a-PI-(X2)b, where: FI = an Fc domain; XI and X2 = are each independently selected from -(L1)c-PI-(L2)d-P2.

(L1)c-PI-(L2)d-P2-(L3)e-P^3, or -(L1)c-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein and Abile95s to Aball 803 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive: EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 182; DB 21; Length 42; 94.4%; Pred. No. 2.4e-15; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
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                                                                                                                                  Disclosure; Page 313; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.48;
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Matches 34; Conservative
                                                                                                autoimmune diseases -
                WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 AA;
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                                                                                                                                                                                                                                                                           Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                  Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                        'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                           DB 21; Length 36;
                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                          Query Match 94.8%; Score 182; DB 21
Best Local Similarity 94.4%; Pred. No. 2e-15;
Matches 34; Conservative 0; Mismatches
                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                         1 IEGPTLROWLAARAGGGGGGGGEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                              Thrombopoietin mimetic peptide compound 9.
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                           AAY96528 standard; peptide; 41 AA
                                                           Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                         20..27
/label= linker
28..41
/label= TMP_2
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            Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                   04-SEP-2000 (first entry)
                        WPI; 2000-365108/31.
 (AMGE-) AMGEN INC.
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                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                       AAY96528;
                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                      Peptide
             Liu C,
                                                                                                                                                                                                                                                 RESULT 8
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Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic: thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimelic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.8%; Score 182; DB 21; Length 41; 94.4%; Pred. No. 2.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17281 standard; Peptide; 42 AA.
                                                                                                                                                                                                                            Claim 16; Page 65; 91pp; English.
                                                                          Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0105371.
99US-0428082.
23-OCT-1998; 98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 94.49 nes 34; Conservative
                                                                                                              WPI; 2000-365108/31.
                                    (AMGE-) AMGEN INC.
                                                                            Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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WPI; 2000-365108/31.
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          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an Ex domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)C-F1-(L2)d-P2.

(X1)c-F1-(L3)d-P2-(L3)e-P3, or -(L1)C-P1-(L2)d-P2.

(X1)c-F1-(L3)d-P2-(L3)e-P3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides, L1, L2, L3, and L4 = are each independently inhers; and a, b, c, d, e, and f = are each independently controlled that at least 1 of a and b is 1. The composition can each interpretation and inmunosuppressive activities. DNAs, wectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC he use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein constructions and possibly placental transfer. AAA69443 complement fixation, and possibly placental transfer. AAA69443 commonser used in the example of the manner of the example of the manner of the example of the example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemnic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optionally modified by bromoacetyl or PEG"
                                                                                                                                                                                                                                                                                                                       sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                    94.8%; Score 182; DB 21; Length 36; 94.4%; Pred. No. 2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGKGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin mimetic peptide compound 4.
             Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96523 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 34; Conserve
                                                                                                                                                                                                                                                                                                                                                     36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96523;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2 - x_{-1}, x_3 - x_3, and x_4 - p, x_2 - x_3 - x_3, x_3 - x_3, x_4 - p, x_2 - x_3, x_3 - x_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 182; DB 21; Length 36; 94.4%; Pred. No. 2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoletin mimetic peptide compound 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                               Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96525 standard; peptide; 36 AA
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/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= TMP_1
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024770-A2
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(L1)C-FI-(L2)G-F2.

(L1)C-FI-(L2)d-F2.

(L2)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F2.

(L3)d-F3.

(L3)d-F3.

(L4)f-F4.

(L4)f-F4.

(L4)f-F4.

(L3)d-F3.

(L3)d-F3.

(L4)f-F4.

(L4)f-F4.

(L3)d-F3.

(L4)f-F4.

(L4)f-F4.

(L3)d-F3.

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(L4)f-F4.

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(L4)f-F4.

(L4)f-F4.

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(L3)d-F3.

(L4)f-F4.

(L4)f-F4.

(L4)f-F4.

(L4)d-F3.

(L5)d-F3.

(L5)d-F3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VESF; almunosuppressive; EPO; TPO; CTLA4, mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.8%; Score 182; DB 21; Length 36
94.4%; Pred. No. 2e-15;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                       Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17293 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                           autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Novel composition of matter comprising an Fc domain and

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The present invention describes composition of matter (I) comprising an CC Fc domain, planmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

(L3)c-P1-(L2)d-P2.

(L3)d-P2. (L3)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4.

(C) planmacologically active peptides: L1, L2, L3, and L4 = are each independently sequences of independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and b, c, d, e, and f = are each independently linkers; and host cells from the present invention can carrivities. DRAS, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

(C) the use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein complement fixation, and possibly placental transfer. AAA69443

(C) sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin i; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloprotelnase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.8%; Score 182; DB 21; Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma; thrombosis; pharmaceutical.
                                                                                                                         Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17301 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-350702/30.
                                                          autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-P1-(X2)b, where: FI = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 192; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLROWLAARAGGGNGSGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin mimetic peptide compound 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                    Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96526 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= linker
19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.6
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000 (first entry)
                                                                         autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024770-A2
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platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                     production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                           Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VGEF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                100.0%; Score 192; DB 21; 100.0%; Pred. No. 1.2e-16;
                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
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                                                                                    Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB16963 standard; Protein; 36 AA.
  Feige U, Cheetham J;
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                                                                                                                                                                                                                                                                                                                                                      Conservative
                       WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                          36 AA;
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  Liu C,
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| Sibbilgogdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
| Sibbilgogdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
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                                                                                                                                                                     (without alignments)
247.023 Million cell updates/sec
                                                                                                                                        October 9, 2002, 08:50:51; Search time 16.1874 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
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AAY96528
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                                                                                                  OM protein - protein search, using sw model
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AAB17306 standard; Peptide; 36 AA.

AAB17306

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FG.TWP.TWP protein
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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoinmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; ascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                        TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                     98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                               99WO-US25044.
                      31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                                                                                                         synthetic.
AAB17306;
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                                                                                                                                                   -- ENZYME REGULATION: INHIBITED BY PHENYLMETHYLSULFONYL FLOURIDE.
-- PATHWAY: XYLAN DEGRADATION.
-- SUBUNIT: MONOMER.
-- SUBCELLULAR LOCATION: EXTRACELLULAR.
-- FINA: GIXCOSYLATED.
-- MASS SPECTROMETRY: MW-21806; METHOD=MALDI.
-- SIMILARITY: CONTAINS I FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
-- SIMILARITY: CONTAINS I FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
-- HSSP: P00725; 2CBH.
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-98437545; PubMed-9761918;
Makulinen N., Tenkanen M., Rouvinen J.;
"Crystallization and preliminary X-ray diffraction studies of the catalytic core of acetyl xylan esterase from Trichoderma reesei.";
Acta Crystallogr. D 54:430-432(1998).
-: FUNCTION: DEGRADEDS ACETYLATED XYLANS BY CLEAVING ACETYL SIDE GROUPS FROM THE HETERO-XYLAN BACKBONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 16; Gap's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00562; CBD_FUNGAL; FALSE_NEG.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
Cellulose degradation; Hydrolase; Serine esterase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
Wing R.A., Frisch D., Simmons J.;
Rim H., Rambo T., Henry D., Simmons J.;
Rice Genomic Sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: ACO78891: AAK52334.1: -.
Nucleocapsid; Ribonucleoprotein.
SEQUENCE 491 AA: 58271 MW; EDEEB988DBOAA3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINKER (BY SIMILARITY),
CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 3; Length 302;
                                                                                                                          -!- CATALYTIC ACTIVITY: DEACETYLATION OF XYLANS AND XYLO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 58; DB 10; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (PI
BB6EDCA2971A9F2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
PUTATIVE UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLXYLAN ESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 GPTOTHW-----GOCGGOGWTGPTOCESGTTCQVISOW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPTLRQWLAARAGGGCGGGGIEGPT-----LRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                        InterPro; IPR000254; CBD_fungal.
InterPro; IPR000734; Lipase.
Pfam: PF00734; CBD_1. 1.
ProDom: PD001821; CBD_fungal; 1.
SWART: SW00256; fCBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 N-
30754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                          OLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
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Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Adams M.D., Celniker S.E., Holt R.A., Holderson S.N., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Change M., Pfeiffer B.D., A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D., A Man K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G., A Man K.H., Doyle G., Baxendale J., Bayraktaroglu L., Basaley E.M., A Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S., A Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Botther P., Abandra I., Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I., A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., A Charly S., Dalke C., Davenport L.B., Davies P., A Charry J.M., Cawley S., Danke C., Davenport L.B., Davies P., A Bodson K., Doup L.E., Downes M., Dugan Rocha S., Punkoy B.C., Dunn P., A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Gaps , 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                    10; Gaps
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDINE-94124036; MEDINE-94124036; PubMed-8294036; Heinrich T., Erdmann V.A., Hartmann R.K.; "Sequence of the gene encoding ribosomal protein L11 from Thermus
                                                                                                                                                                                                                                             Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 134;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                           134 AA; 14336 MW; C8EB750B7B75EFFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0...MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                             PRT; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GCGGGGRSGGEGCLSTASVTGPSWRWTPTRS 125
       pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GCGGGG-----IEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                       29.4%; Score 58;
                                                8 QWLAARAGGGCGGGG-----IEGPTL 28
                                                                          36 RWLFARATAGCGSQGDDQKKTPEIEVVGPTL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                            RIBOSOMAL PROTEIN L11 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                thermophilus HBB.";
Gene 136:373-374(1993).
EMBL; L10371; AAA27503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 34.4%;
            41.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                         13; Conservative
                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Thermus thermophilus
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG13807 PROTEIN.
                                                                                                                                                                                                                                                                  NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q56434
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R. Lasko P., Lei Y., McIntosh T.C., McLeod M.P., McPherson D.,
Liu X., Mattei B., McIntosh T.C., Mcrod M.P., McPherson D.L.,
RA Merkulow G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Merkulow G., Milshina N.V., Mobarry C., Morris J., McPherson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Marzy D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
She B.C., Slden-Kamos I., Simpson M., Stwupski M.P., Smith T.,
Shue B.C., Slden-Kamos I., Simpson M., Stwupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong W., Moodage T., Worler K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Zhene Z.H., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng C.,
RA The genome sequence of Drosophila melanogaster.";
RI Science 2812.185.2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Margolles-Clark E., Tenkanen M., Soederlund H., Penttilae M.;
"Acetyl xylan esterase from Trichoderma reesei contains an active-site
serine residue and a cellulose-binding domain.";
Eur. J. Biochem. 237:553-560(1996).
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Potaranen K., Bundberg M., Korte H., Puls J.;
"Deacetylation of xylans by acetyl esterases of Trichoderma reesel.";
"Appl. Microbiol. Biotechnol. 33:506-510(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota: Fungi: Ascomycota: Pezizomycotina; Sordariomycetes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 158-186, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RUTC-30;
Sundberg M., Poutanen K.;
Furbification and properties of two acetylxylan esterases of
Trichoderma reesei.";
Biotechnol. Appl. Biochem. 13:1-11(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.4%; Score 58; DB 5; Length 170; 45.8%; Pred. No. 22; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 AA; 19099 MW: 477D79D55ADF4CE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created) . 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ACETYLXYLAN ESTERASE PRECURSOR (EC 3.1.1.72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 AA.
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NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96235218; PubMed=8647098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 EPPIVENWM----GGGGGGGGFOG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE003474; AF47627.1; -
FlyBase, FB9n0035323; CG13807.
Interpro; IPR002952; E99shell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01228; EGGSHELL.
SEQUENCE 170 AA; 19099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
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Query Match
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
                                                                                                                                                                                                                                                                                                                                                                     "Gryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:B1146B04";
Submitted (FEB-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003205; BBA645B3.1; -
SEQUENCE 158 AA: 14648 MW; 438B72F4B6C86A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 158;
                                                             Length 776;
                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AL451109; CAC18624.2; -. Hypothetical protein. SEQUENCE 776 AA; 82771 MW; C9BEA870D94A37DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmer S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; 284485; CAB06488.1; -
InterPro; IPR001487; Bromodomain.
InterPro; IPR001965; PHD.
InterPro; IPR000313; PWWP.
                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B1146B04.14 PROFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NAY-1999 (TrEMBLrel. 10, Created)
01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ554E15.1 (PEREGRIN (BR140 PROTEIN)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.7%; Score 58.5; DB 10;
Best Local Similarity 61.1%; Pred. No. 18;
Matches 11; Conservative 1; Mismatches 5;
                                                         Query Match 29.9%; Score 59; DB 3; Best Local Similarity 53.8%; Pred. No. 75; Matches 14; Conservative 3; Mismatches 5
                                                                                                                                                                                       158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 AA.
                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                              678 GGGGGGGVVDDDGEPDFAGWLAAQA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                       PRT;
                                                                                                       15 GGCGGGGI---EG-PTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00855; PWWP; 1.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 WLAARAGGG-CGGGGIEG 25
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                        B1146B04.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DJ524E15.1.
                                                                                                                                                                                                 094307;
                                                                                                                                                                                     094307
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                                                                                                                                                               RESULT 23
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Yamamoto K., Inoue N., Fujimori A., Saito T., Shinkai H., Sakiyama H.;
"Mesocricetus auratus mRNA for type XVII collagen.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, BAD27759; BAA9481.1;
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen, SEQUENCE 1431 AA; 144579 MW; 4315631FEB2C9A5C CRC64;
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                             ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58.5; DB 11; Length 1431;
Pred. No. 1.6e+02;
0; Mismatches 7; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0671B11.";
                                                                                                                                                                             DB 4; Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.4%; Score 58; DB 10; Length 117;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002746; BAB12695.1; -- SEQUENCE 117 AA; 12397 MW; A04617B3DEF9F4B3 CRC64;
                                                                                                                         90851 MW; E28C017F5C545334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                      Score 58.5; DB Pred. No. 88; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                      695 QWGAASRAPGGCSCAGAGLAGGARRRW 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                        8 QW-LAARAGGG--CGGGGIEGPTLRQW 31
SMART; SM00249; PHD; 2.
SMART; SM00293; PWMP; 1.
PROSITE; PS50014; BROMODOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 ARGGGGGGGGGGGT---WGAAPA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ARAGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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60.0%;
                                                                                                                                                                      Match 29.7%;
Local Similarity 48.1%;
les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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P0671B11.11.
                                                                                                                           805 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLLAGEN TYPE XVII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                               805
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5; Indels

ed. No. 48; Mismatches

Pred. No.

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70.6%; Pic.
                                                                                                                       6 LRQWLAARAGGGCGGGG 22
                                                           12; Conservative
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Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                 Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE 683 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998
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083436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HEA4
                                                                                                                                                                                                                                                                                                                                                                                                      ACCOOR READ BY READ BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98168839; PubMed=9510020; Wu S.C.-Y., Grindley J., Winnier G.E., Hargett L., Hogan B.L.M.; Mouse Mesenchyme forkhead 2 (Mf2): expression, DNA binding and induction by sonic hedgehog during somitogenesis."; Mech. Dev. 70:3-13(1998).
EMBL; AF023915; AAB81275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0483F08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.9%; Score 59; DB 10; Length 125; 40.5%; Pred. No. 12; ive 2; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermātophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002094; BAA96216.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 125 AA; 13396 MW; C609D8D0B07BC505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7F82440F4C435702 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                   01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 EGAAAR-WRAARSPARGGORGGHRRRGGGGGGGGGRERPRRR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EGPTLRQWLAARA------GGGCGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                       PRT; 125 AA.
                                                                         4 PTLRQW-----LAARAGGGCGGGIEGP 26
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01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00657; FORK_HEAD_1; 1. PROSITE; PS00658; FORK_HEAD_2; 1. PROSITE; PS50039; FORK_HEAD_3; 1. SEQUENCE 492 AA: 48936 MM; 7F:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001766; Fork_head. Pfam; PF00250; Fork_head; 1. PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 40.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              Q9LWC8;
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035392
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Length 492;

29.9%; Score 59; DB 11;

Query Match

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Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulte U. A. M. Wewes H.W., Moneisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        683 AA; 74518 MW; F91407FA7094AAD1 CRC64;
                                                                                                                                                                                                                                                                            Bacteria; Spirochaetales; Spirochaetaceae; Treponema NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                        (TrEMBLrel. 08, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 AA.
                                                                                                        683 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.9%; Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last and
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
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                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NICHOLS;
MEDLINE=98332770; Pubmed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Neurospora genome project;
                                                                                                                                                                                                          CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spirochete,";
Science 281:375-388(1998).
EMBL; AE001220; AAC65409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.8%;
384 LROGLKTDAGGGAGGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; TP0421; -. Interpro; IPR001258; NHL. Interpro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                    STRAIN=A3(2);
                                                                                                                                                                                                                                                STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              049843;
                        09AD76
                                        09AD76
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  RESULT 17
Q9AD76
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ش
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                        15;
                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COPROPORPHYRINOGEN OXIDASE (COPROPORPHYRIA, HARDEROPORPHYRIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.2%; Score 59.5; DB 16; Length 488; Best Local Similarity 43.3%; Pred. No. 42; Matches 13; Conservative 2; Mismatches 8: Indels 7:
                                                                                                                                                                                                                                               DB 4; Length 454;
                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                  Strausberg R.; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017210; AAH17210.1; -. SEQUENCE 454 AA; 50175 MW; CD6672F9D8FB8423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 488 AA; 52800 MW; 188918856F9774AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (FrEMBLrel. 17, Last sequence update)
01-OCT-2001 (FrEMBLrel. 18, Last annotation update)
POSSIBLE ATP/GTP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583920; CAC31378.1; -
                                                                                                                                                                                                                                                                                                             11 GPC---WLVARGGCGGPRAWSQCGGGG----LRAW 38
                                                                                                                                                                                                                                                                                              3 GPTLRQWLAARAGGG------CGGGGIEGPTLRQW 31
                        454 AA.
                                                                                                                                                                                                                                                                                                                                                                                     488 AA.
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                           Pred. No. 39;
                                                                                                                                                                                                                                               30.2%; Score 59.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLROW-----LAARAGGGCGGGGIEGP 26
                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                          PRT;
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PRINTS; PR00326; GTP1OBG.
                                                                                                                                                                                                                                                            44.48;
                                                                                                                                                                                                                                                        Local Similarity 44.4.
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=9606;
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                                    Q96AF3;
                       096AF3
                                                                                                                                                                                                                                                                                                                                                                                000060
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RESULT 15
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           096AF3
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Mol. Microbiol. 21:77-96(1996).
EMBL, AL512667; CAC21636.2; -
InterPro: IPR003838; DUF214.
Pfam; PF00587; DUF214; 1.
SEQUENCE 496 AA; 49548 MW; 54E110C4F86231A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                Seeger K.J., Harris D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: 000019; AAA17274.1; -.
SEQUENCE 518 AA: 56001 MW; 6641916cC84F374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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43.3%; Pred. No. 44;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.2%; Score 59.5; 43.8%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PILRQWL------AARAGGCGGGGIEGP 26
PRT;
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                                                                                                                                 PUTATIVE INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 43.8%;
Matches 14; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                        Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium leprae.
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Matches 13; Conserv
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RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston R.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Retchum K.A.,
RA Lasko P., Leil Y., Levitsky A.A., Li J., Liz., Liang Y., Lin X.,
RA Lasko P., Leil Y., Levitsky A.A., Li J., Liz., Liang Y., Lin X.,
RA Luu X., Mattei B., McIntosh T.C., McChed M.P., McPherson D.L.,
RA Mount S.M., Moy M., Winyby B., Murphy L., Murzhy D.M., Nelson D.L.,
RA Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinfert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rhen Reinford K., Saunders R.D.C., Scheeler F., Shen H.,
Rhen Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ray J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RR EMBL, AE003757; AAF56615.1; -.
RA MEDOS: ROA 77.1.
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"A role for amontillado, the Drosophila homolog of the neuropeptide precursor processing protease PC2, in triggering hatching behavior."; J. Neurosci. 19:6942-6954(1999).
HSSP: P04072; 1THM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%; Score 60; DB 5; Length 654; 48.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PRO073; SUBTILISIN.
PRODOM: PD000717; P_domain; 1.
PROSITE: PS00137; SUBTILASE_ASP: 1.
PROSITE: PS00137; SUBTILASE_HIS: 1.
PROSITE: PS00138; SUBTILASE_SER: 1.
SEQUENCE 654 AA; 71733 MW; 2BD57F683929D237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
AMON ONE PCZ ON CG6438.
Drosophila melanogaster (Fruit fly).
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0023179; amon.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0023179; amon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 48.0 ses 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Taketenis S., Kohno H., Terukawa T., Yoshinaga T., Tokunaga R.;
"Molecular cloning, sequencing and expression of cDNA encoding human coproporphytinogen oxidase.";
Busicchim. Biophys. Acta 1183:547-549(1994).

EMBL; 234631, CA884292.1;
EMBL; 234804; CA884292.1;
EMBL; 234804; CA884292.1;
EMBL; 234806; CA884292.1;
EMBL; 234806; CA884292.1;
FEMBL; 234806;
FEMBL;
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Coproporiphrinopen oxidase: gene organization and description of mutation leading to exon 6 skipping.";
Hum. Mol. Genet. 3:1325-1330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 454;
                                                                                                                                                                                                                                                                                                             30.5%; Score 60; DB 5; Length 654; Best Local Similarity 48.0%; Pred. No. 49; Matches 12; Conservative 3; Mismatches 0. T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50152 MW; 6EC3D15FD8FD86B5 CRC64;
                                                                                                                                                                                                                                                                               71733 MW; D021D4882293C996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) COPROPORPHYRINGEN OXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GPC---WLVARGGCGGPRAWSQCGGGG----LRAW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GPTLRQWLAARAGGG------CGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.2%; Score 59.5; B 44.4%; Pred. No. 39; Live 0; Mismatches
                                                                                                                                                                      UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01021; COPROGEN_XIDASE; 1. SEQUENCE 454 AA; 50152 MW; GEC3DL!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro, IPR001260; Coprogen_oxidas. pfam; PF01218; Coprogen_oxidas; 1. pRINTS; PR00073; COPRGNOXDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
                                                    Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PRODOM; PD000717; P_domain; 1.
PROSITE; PS00136; SUBTILASE_HSP; UN PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PLACENTA;
MEDLINE=95078835; PubMed=7987309;
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LROWLAARAGGGCG--GGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LLHWASAGAGGGAGGSGAGLSGPAV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94114558; PubMed=8286403;
                             InterPro; IPR002884; P_domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                              Protease; Neuropeptide.
SEQUENCE 654 AA; 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Query Match
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Q14060;
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"ANOVA, a putative astrocytic RNA binding protein gene that maps to
chromosome 19q13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurogenetics 1:31-36(1997).

-!- FUNCTIONS MAY REGULATE RNA SPLICING OR METABOLISM IN A SPECIFIC SUBSET OF DEVELOPING NEURONS (BY SIMILARITY).

-!- SUBSET OF DOCATION. NUCLEAR (BY SIMILARITY).

-!- TISSUE SPECIFICITY: BRAIN. EXPRESSION RESTRICTED TO ASTROCYTES.

-!- DISEASE: MAY BE A TARGET ANTIGEN IN ONE OF THE UNDEFINED HUMAN PARANEOPLASTIC SYNDKOMES.

EMBL: U70477; ABB8661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ASTROCYTIC NOVAL-LIKE RNA-BINDING PROTEIN (NEUROONCOLOGIC VENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 5
                                                                                                                                    DB 4; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 4; Length 498;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                     SMART; SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE_1; 3.
SEQUENCE 492 AA; 49008 MW; 41B63EAF6899256B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4B54196FDB6BF78 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).
BMEL; AF083989, AAC72355.1; -.
InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TYPE_1.
                                                                                                                                                              9;
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SMART; SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE_1; 3.
Nuclear protein; RNA binding; Repeat; Antigen.
                                                                                                                                                                                                                                                                                               498 AA.
                                                                                                                                                              2; Mismatches
                                                                                                                               30.5%; Score 60; DB 53.6%; Pred. No. 37;
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2; Mismatches
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POLY-GLY.
POLY-ALA.
                                                                                                                                                                                                       365 YLGAGAGGAGGG--GPLVAAAAAAGA 390
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POLY-ALA.
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                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                             PRT;
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InterPro; IPR004088; KH_TYPE_1.
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                                                        Pfam; PF00013; KH-domain; 3.
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hes 15; Conservative
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT)
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                                                                                                                                             Local Similarity
nes 15; Conserv
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498 AA;
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                                                                                                                                                                                                                                                                                                                                                                              ANTIGEN 3)
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SEQUENCE
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371 YLGAGAGGGAGGG--GPLVAAAAAAGA 396

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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandall M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
M. M. K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
A. Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A. de Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plunkov B.C., Dunn P.,
A. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Buteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%; Score 60; DB 5; Length 500; 52.2%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                       Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53946 MW; 1416327086FE7CF6 CRC64;
                                                                                       (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                      500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                  Rhabditidae; Peloderinae; Caenorhabditis.
                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
EMBL: Z78013; CAB01420.1; -
InterPro; IPR001254; Trypsin.
PROSITE, PS50240; TRYPSIN.DOM; 1.
Hydrolase; Serine protease.
SEQUENCE 500 AA, 53946 MW; 1416;
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPTLRQWLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 52.2
Matches 12; Conservative
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                         F15B9.5 PROTÈIN.
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                                                                                         01-NOV-1996
                                                                                                          01-DEC-2001
                                                                                                                                                                                                                                                                          Percy C.M.;
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                                019476
                                                                                                                                              F15B9.5
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RESULT 11
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0436E04.";
            Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0039A07.";
                                                                                                                                    Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002818: BAB16319.1; --
SEQUENCE 202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AP003235; BAB64100.1; -SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                    3; Mismatches 10; Indels
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AP000492; BAA84610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 439 AA; 47297 MW; 533EEC240CEA1BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 VVSPSCRRQTAGR-HGGCGGGRWMAAAGGRDGGGCRRWWAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGCGG-----GGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                               , Match 31.5%; Score 62; DB 10; Local Similarity 51.94; Pred. No. 11; hes 14; Conservative 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                     80 GPTVGVRVAYRAGAGGGGGGPRGFALK 106
                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                     3 GPTLRQWLAARAGGGCGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                               P0436E04.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
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                                                                                                                                       Query Match
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                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=9900731; pubmed=9789075; Yang Y.Y., Yin G.L., Darnell R.B.; "The neuronal RN-binding protein Nova-2 is implicated as the autoantigen targeted in POMA patients with dementia.";
                                    14;
Score 61; DB 10; Length 439;
Pred. No. 25;
2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%; Score 60; DB 4; Length 464; 53.6%; Pred. No. 35; tive 2; Mismatches 9; Indels
                                                                    1 IEGPTLRQWLAARAGGGCGGGG-----IEGPTLRQWLAARA 36
                                                                                                     39 LHAPLLRLWPLGGGGGGGGGGGGGGGGERVGAVGGAVRGEEARSQRAAEA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006540; AAD13116.1; -.
InterPro; IPR004089; KH. TYPE_1.
InterPro; IPR004088; KH. TYPE_1.
InterPro; IPR001859; Ribosomal_P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 464 AA; 45901 MW; 0B16BAE99C271CC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                         464 AA.
                                                                                                                                                                                                                                                                             RNA-BINDING PROTEIN NOVA-2 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00013; KH-domain; 3.
PRINTS; PR00456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 53.6%;
15; Conservative
      31.0%;
32.0%;
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                                      Conservative
                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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37368 MW; 5105598D7E1C77B2 CRC64;

360 AA;

SEQUENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-MUSCLE;
Kuribayashi T., Ohashi K.;
"Chicken Formin binding protein 11-related protein interacted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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Saraki T., Matsumoto T., Yamamoto K.;
Saraki T., Matsumoto T., Yamamoto K.;
Saraki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
"Lone: P04622408 T.
InterPro; IPP00051; 2f-CCCH.
Pfam; PF00042; 2f-CCCH; 4.
SMART; SM00356; ZnF_C3H1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.5%; Score 66; DB 13; Length 1070; Best Local Similarity 48.1%; Pred. No. 17;
                                                                                   Score 67; DB 2; Length 865;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1070 AA; 119556 MW; A4FA68B7D946BEDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO57590; BAB68206.1; -.
NON_TER 1
PRINTS; FRUCES, PRD; 1.

SWART; SM0089; PRD; 1.

PROSITE; PS50093; PRD; 1.

PROSITE; PS500142; ZINC_PROTEASE; UNKNOWN_1.

PROSITE; PS60142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FORMIN BINDING PROTEIN 11-RELATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9LGC9;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TEMBLrel. 18, Last annotation update)
PUTATIVE ZINC FINGER PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                      PRT; 1070 AA.
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                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLROWLAARAGGGGGGGGGTEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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0
                                                                                      34.0%;
66.7%;
                                                                                                                                                                   651 WLAACAAGNCGGGGTNPP 668
                                                                                                                                                9 WLAARAGGGCGGGGIEGP 26
                                                                             Ouery Match
Best Local Similarity 66.79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
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                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                               Gallus.
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Q9LGC9
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 431;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Liu Y., Xue J.X., Zhang W., Fu D.C., He R.Q., Xue Z.G.;
Liu Y., Xue J.X., Zhang W., Fu D.C., He R.Q., Xue Z.G.;
Superain-Z. a POU-Dox gene expressed in quail embryos.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULARITY: WITH OTHER HOMEOBOX PROTEINS.
EMBL; AR091043; AAF00040.1; -.
RISSP; P14859; 10CT.
RICEPTO; IPRO01356; Homeobox.
RICEPTO; IPRO01357; POU.
READ: PF000457; POU.
READ: PF000457; POU.
Score 65; DB 10; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 431 AA; 43722 MW; 1DC47E53F9ACC7D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QWLAARA-----GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 OWIAALSHGGPGGGGGGGGGGGGGGGGGGGTAP----WAAAAA 95
                              10;
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                                                                                                                                                                   431 AA
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40.5%; Pred. No. 10;
iive 2; Mismatches
                              2; Mismatches
                 Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                                                                                                                    PRT;
                                                                               1 IEGPTLRQWLAARAGGGCGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
 33.0%;
52.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00035; POU_1; 1. PROSITE; PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                               13; Conservative
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                                                                                                                                                                                                                                               POU-BOX PROTEIN BRAIN-2.
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01-DEC-2001 (TrEMBL
P0039A07,6 PROTEIN.
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   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
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                                                                                                                                                                                      09PVG9
                                                                                                                                                                    O9PVG9
                                  Matches
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(without alignments)
482.803 Million cell updates/sec
                                                                                                      October 9, 2002, 08:52:16; Search time 12.8993 Seconds
                                                                                                                                                                                                                                                                                                                                        562222
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGCGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
sp_bacteriap:*
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sp_human:*
sp_invertebrate:*
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sp_vertebrate:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp_rodent: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10:
                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                  Scoring table:
                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O54108 streptomyce	Q90yb6 qallus qall	Q91qc9 oryza sativ	Q9pvg9 coturnix co	Q943k0 oryza sativ	Q9ftz5 oryza sativ	Q9sdk6 oryza sativ	Q9ueal homo sapien	Q9unw9 homo sapien	O43267 homo sapien	Q19476 caenorhabdi	Q9vbc7 drosophila	Q9uae7 drosophila	Q14060 homo sapien	Q96af3 homo sapien	Q9ccc0 mycobacteri
SUMMARIES	OI	054108	Q90YB6	09LGC9	09PVG9	Q943K0	Q9FT25	Q9SDK6	90EA1	6MND60	043267	19476	9VBC7	9UAE7	14060	296AF3	022260
		7	13	10	13	10	10	10	4	4	4	2	s	s	4	4	16
	Query Match Length DB	865	1070	360	431	253	202	439	464	492	498	200	654	654	454	454	488
a	Query	34.0	33.5	33.0	32.7	31.5	31.2	31.0	30.5	30.5	30.5	30.5	30.5	30.5	30.2	30.2	30.2
	Score	67	99	65	64.5	62	61.5	61	9	9	9	9	9	09	59.5	59.5	59.5
	Result No.	1	~	m	4	Ŋ	φ	7	æ	σ	10	11	12	13	14	15	16

Q9ad76 streptomyce Q4943 mycobacteri Q91wc8 oryza sativ Q33392 mus musculu Q8436 treponema p Q9he4 neurospora Q94307 oryza sativ Q95404 mesocricetu Q9fu16 oryza sativ Q56434 thermus the Q9w033 drosophila Q99034 trichoderma Q94D10 foryza sativ	Q94810 can may Cubago Q95596 myxococcus Q95596 myxococcus Q95700 mycobacteri Q95700 petromycon Q9700 petromycon Q9700 petromycon Q91804 polyangium Q92805 oryza sativ Q91804 polyangium Q9270 homo sapien Q91804 polyangium Q91805 oryza sativ Q91805 oryza sativ Q91805 oryza sativ Q91805 oryza sativ Q94109 oryza sativ
30.2 496 2 Q9AD76 30.2 518 2 Q9B43 29.9 125 10 Q91WC8 29.9 683 16 Q9843 29.9 683 16 Q9843 29.9 7 158 10 Q9430 29.7 1431 11 Q97MH4 29.7 1431 11 Q97MH4 29.4 117 10 Q5F026 29.4 117 10 Q5F026 29.4 134 2 Q56434 29.4 130 3 Q99033 29.4 491 10 Q94LP1	246 10 246 10 302 2 495 16 377 13 414 3 524 4 607 2 607 2 612 4 651 4 130 4
7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
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ALIGNMENTS

Db 96 QWLSPTAAAGGGSNGGG 112

Search completed: October 9, 2002, 09:00:19 Job time: 5.3831 secs

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PROSITE; PS50039; FORK_HEAD_3; 1.

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-i- SUBCELLULAR LOCATION: Nuclear
-i- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein D3 (HNF3/FH transcription factor genesis) (Winged
helix protein CWH-3).
                                                                                                                                                                                                                    VA -> WP (IN REF. 1).
PSGMRSLABPECCPHTGASESPTASPTTSVSSLTERADTG
TSILGSVTSSDSECDV -> ERDALPGRARLPHARLSRVTVH
GGQPDHQCVQPDGARGHRHFDPLGNLQRLGM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.; "Aberrant cell growth induced by avian winged helix proteins."; Cancer Res. 57:123-129(1997).
                                                                                                                                          POLY-ALA.
LQHQAIGPSGMRSLAE -> SVAGTAARPPQA (IN
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                          Developmental protein; Homeobox; DNA-binding; Nuclear protein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                 26.4%; Score 52; DB 1; Length 333; 62.5%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                      ISOFORM SIX3A).
MISSING (IN ISOFORM SIX3A).
G -> GG (IN REF. 1).
                                                                                                                                                                                                                                                                                                   1AD7D3C4388043B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 55;
0; Mismatches
                                            PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                            GLY-RICH.
                                                                                                                             HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDLINE=97141794; Pubmed=8988052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00250; FOTK_head; 1.
PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; 1.
PROSITE; PS00657; FORK HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rkansfac; 102493; -.
InterPro; IPR001766; Fork_head.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                   333 AA; 35592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U37274; AAC60066.1; -. HSSP; Q63245; 2HFH.
             Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                 62.5%;
                                                                                                                                                                                                                                                                                                                                              Local Similarity 62.5
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               11 AARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           59 AGGAGGGSGGGSRAP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T02495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                               33
                                                                                                                                          264
271
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P79772;
                                                                                                                             DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                        CONFLICT
                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLONE MONTAIN BIOL. 36:417-425(1998).

-!- FUNCTION: MAY HAVE A ROLE TO PLAY IN FORMATIVE EVENTS IN OVULE AND EMBRYO MORPHGENESIS.

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- SUBCELLULAR SPECIFICITY: UBIQUITOUSLY EXPRESSED IN THE MATURE PLANT.

-!- SIMILARITY: BELONGS TO THE TALE/KNOX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. VFNT CHERRY;
MEDILINE-98145476; PubMed-9484482;
Janssen B.J., Williams A., Chen J.J., Mathern J., Hake S., Sinha N.;
"Isolation and characterization of two knotted-like homeobox genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum (Tomato).

Bubrayophy, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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0
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                                                                                                            DB 1; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 426;
                                                                                                                                         3; Indels
DNA-binding, Nuclear protein; Transcription regulation.
DOMAIN 67 70 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5B52B9E0A34A86BC CRC64;
                                                                            40995 MW; 324A4B36B9E31899 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homeobox protein knotted-1 like LET12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 1
Pred. No. 68;
1; Mismatches
                                                                                                          Query Match 26.4%; Score 52; DB Best Local Similarity 76.9%; Pred. No. 64; Matches 10; Conservative 0; Mismatches
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELK DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF000142; AAC49918.1; -.
InterPro; IPR001356; Homeobox.
SMART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                             FORK-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ALA.
POLY-ASN.
                                                POLY - ALA
                              POLY-GLY
                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
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64.7%;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
76
152
287
348
                              91
                                                                                                                                                                        13 RAGGGCGGGGIEG 25
                                                                                                                                                                                                       82 RGGGGGGGGEEG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
325
349
426 AA;
                                                                             394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from tomato.
                                                                                                                                                                                                                                                                                 HKLB_LYCES
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SEQUENCE
                                                               DNA_BIND
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AB001902; I AB001903; I AB001904; I AB001905; 1 AB001914; 1 AB001901; AB001904; AB001908; AB001914; AB001901; AB001908; AB001902; AB001914; AB001901; AB001902; AB001903; AB001904; AB001905; AB001906; AB001908; AB001910; AB001911; AB001912; AB001913; AB001914; AB001898; AB001901; AB001898; AB001902; AB001903; AB001905; AB001906; AB001907; AB001904; AB001907; AB001903; AB001908; AB001898; AB001900; AB001900; AB001909; AB001905; AB001900; AB001906; AB001898, EMBL;

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  -!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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AB001898; BAA21620.1;
AB001900; BAA21620.1;
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BAA21621.1;
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                                                                                                                                                                                                                                                                                      BAA21620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAA21621.1;
                                                                                                                                                                                                                                                                                                                                                                                                             BAA21621.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA21621.1;
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                                                                                                                                                                                                         EMBL; M80482; AAA59998.1;
                                                                                                                                                                                                                                                                                                                                                                                          BAA21621.
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AB001903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SIX/SINE OCULIS FAMILY OF HOMEODOMAIN
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Six3, a murine homologue of the sine oculis gene, demarcates the most anterior border of the developing neural plate and is expressed director development."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                7;
                                                                                                                                          Score 52.5; DB 1; Length 969;
pred. No. 1.2e+02;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver G., Mailhos A., Wehr R., Copeland N.G., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD, PRT; 333 AA.
062233; P70176; P70177;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Homeobox protein SIX3 (Sine oculis homeobox homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TISSUE-Embryonic brain; MEDLINE-96125147; PubMed-8575305;
                                                                                                                                                                                                                                              11 AARAGGCGGGGIEGPTLR-----QWL 32
                                                                                                                                                                                                                                                                               EMBL; X90871; CAA62379.1; ALT_INIT.
EMBL; D83144; BAA11822.1; -.
EMBL; AB001904; BAA21625.1; JOINED. EMBL; AB001905; BAA21625.1; JOINED. EMBL; AB001906; BAA21625.1; JOINED. EMBL; AB001907; BAA21625.1; JOINED. EMBL; AB001908; BAA21625.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/C;
MEDLINE=96409319; PubMed=8814301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during eye development.";
Development 121:4045-4055(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D83144; BAA11822.1; -. EMBL; D83145; BAA11823.1; -.
                                                                                                                                                  26.68;
                                                                                                                                                                           44.88;
                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:102764; Six3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T03263; -.
TRANSFAC; T03270; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P40427; 1B8I.
                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS.
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                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
SIX3_MOUSE
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIX3.
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Gaps
                                                                                                                                                                                                                                                       PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; 015099; 005100; 09VEJJ; 09VEJJ; 09UEJJ; 09UEJ9; 09VEGJ; 095099; 005100; 09V4H1; 09VEGJ; 09VEGJ; 09VEGJ9; 00VAH0; 09VAH1; 01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
Focy-2001 (Rel. 40, Last annotation update)
Paired basic amino acid cleaving enzyme 4 precursor (EC 3.4.21.-) (Subtilisin/kexin-like protease PACE4) (Subtilisin-like proprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a second human subtilisin-like protease gene in
the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of novel cDNAs encoding human kexin-like protease,
      FlyBase, FBg00016978; snRNP70K.
InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS00030; RRM_II.
PROSITE; PS00030; RRM_RNP_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A., Matsuda Y.,
                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B).
TISSUE-Hepatoma, and Kidney;
MEDIINE-920705167; Pubmed-1741956;
Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                       Score 52.5; DB 1; Length 448;
                                                                                    RNA-BINDING (RRM).
ARG/GLU-RICH (MIXED CHARGE).
N - S (IN REF. 1).
ODDFB5A39CA72AEB CRC64;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5] SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a novel PACE4 isoform, PACE4E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                 Pred. No. 63;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94235049; Pubmed-8179631;
                                                                                                                                                             5;
                                                                                                                                                                                                      182 TVKGWLPRRLGGGLGGTRRGG 202
                                                                                                       278 N
52900 MW;
                                                                                                                                                                                  5 TLRQWLAARAGGGCGG---GG 22
                                                                                                                                       26.6%;
                                                                                                                                                 Best Local Similarity 52.43
Matches 11; Conservative
                                                                                    180
                                                                                                                                                                                                                                                                                                                                               convertase 4) (SPC4).
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                102
254
3
278
248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PACE4 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE*Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PACE4 isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuda Y.;
                                                                                                        CONFLICT
                                                                                                                 SEQUENCE
                                                                                                                                       Query Match
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                                                                                    DOMAIN
                                                                                               DOMAIN
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PAC4_HUMAN
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-!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; PACE4A-I/PACE4 (SHOWN HERE),
PACE4A-II, PACE4B/PACE41, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
PACE4A-II, PACE4B/PACE41, PACE4B/PACE4CS, PACE4D, PACE4E-I AND
PACE4E-II; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
-!- TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A-I IS EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, PANOREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA, PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
EXPRESSED IN PLACENTA. PACE4E-I IS EXPRESSED IN CERRBELLUM,
PLACENTA AND PITUITARY. PACE4E-II IS AT LEAST PRESENT IN
                                            MEDLINE=97335942; PubMed=9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACRA isoform, PACR4E is an active processing protease
containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
MEDLINE=98021085; PubMed=9378725;
TSUJi A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S.,
Bando M., Sakai E., Mori K., Akamatsu T., Matsuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4),
Kexin-like processing endoprotease.";
J. Biochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM. ISOFORM PACEAU LACKS THE PROPEPTIDE DOMAIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Endopritease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Blochem. J. 339:639-647(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.; "Functional analysis of human PACE4-A and PACE4-C isoforms:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification of a new PACE4-CS isoform.";
FEBS Lett. 396:31-36(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE SPLICING (ISOFORM PACE4CS).
MEDLINE=97064242; PubMed=8906861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99233559; PubMed=10215603;
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TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
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Wed Oct

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DDR
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                                                                                                                                                                                                                                                                                                          MOL. PHYLOGENET. EVOL. 15:157-164(2000).

-I-FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-I-COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-I-SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000179; Cyt.b.b6.
Pfam; PF00032; cytochrome_b_c; 1.
Pfam; PF00033; cytochrome_b_n; 1.
PROSTIE; PS00193; cytochrome_b_n; 0.
PROSTIE; PS00192; CYTOCHROME_B_HEME; FALSE_NEG.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         Slowinski J.B., Keogh J.S.;
"Phylogenetic relationships of elapid snakes based on cytochrome b
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels . 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 75 IRON 1 (HEME B562 AXIAL LIGAND).

89 89 IRON 2 (HEME B566 AXIAL LIGAND).

174 174 IRON 2 (HEME B562 AXIAL LIGAND).

188 188 IRON 1 (HEME B566 AXIAL LIGAND).

370 AA; 42083 MW; CCDE45269CAB2B9D CRC64;
                                                                                                                                                                                                      Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroides,
Elapidae, Notechinae, Micropechis.
NCBL_TAXID=66188,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 370;
                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                  PRT; 370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52.5;
Pred. No. 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 GPTLTTWL-----WGGFSINDPTLTRFFA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPTLRQWLAARAGGGCGGGGIEGPTLRQWLA 33
4 PTLRQWLAARAGGG---CGGGGIEGPTLR 29
             27 PIARQRRCSAAGGNWYPVGGGGIQDPMCR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20229584; PubMed=10764543;
                                                                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RU17_DROME STANDARD; F
P17133; Q9VM56;
01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF217826; AAF37245.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.68;
41.98;
                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                        MTCYB OR COB OR CYTB.
                                                                                                                                                                     Micropechis ikaheka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  mtDNA sequences.";
                                                                                                                                                                               Mitochondrion.
                                                                                                                                              Cytochrome B.
                                                                                 CYB_MICIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RU17_DROME
                                                         RESULT 25
                                                                    CYB_MICIK
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RC STRAIN=Berkeley;

RA Manatides F.G. Scherer S.E. Li P.W., Boskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Barli J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

RA Ballaw R.M. Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,

RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,

RA Ballaw R.C., Bucham N.R., Bouck J., Brokkein D., Bolshakov S.,

RA Burtis K.C., Bucham N.R., Bouck J., Brokkein D., Bolshakov S.,

RA Burtis K.C., Bucham D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Burtis K.C., Bucham D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Burtis K.C., Bucham D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Durbin K.J., Cavley S., Dahlke C., Davaneport L.B., Davies P.,

RA Burtis K.J., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,

RA Burtis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvey D., Helman T.J., Hernandez J.R., Moltek J.,

Alasko P., Lel Y., Everitsky A.A., Li J., Li Z., Linn Y. V., Reise M.

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Bittman G.S., Pan S., Pollard J., Weisenbach J. M.,

Spier E., Spradiling A.C., Stapleton M., Stupski M.P., Sainth T.,

Spier B., Spradiling A.C., Stapleton M., Stupski M.P., Sainth H.,

RA Beng X.R., Moodage T., Worley K.C., Wu Weissenbach J.,

RA Beng X.R., Moodage T., Worley C., Nu D., Yang S., Zhu X., Smith H.,

Ra Beng X.R., Moodage T., Worley C., Nu D., Stupski M., Sainth M.,

Ra Beng X.R., Rodiec of Drosevala M., Stupski M., Sain B.,

Schoec 287; Saider-Kampson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ul small nuclear ribonucleoprotein 70 kDa (Ul snRNP 70 kDa) (snRNP70).
SNRNP70K OR SNRNP27D OR CG8749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: MEDIATES THE SPLICING OF PRE-MRNA BY BINDING TO THE STEM LOOP I REGION OF U1-SNRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90258833; PubMed-1692955; Mancebo R., Lo P.C.H., Mount S.M.; "Structure and expression of the Drosophila melanogaster gene for the Ul small nuclear ribonucleoprotein particle 70K protein."; Mol. Cell. Biol. 10:2492-2502(1990).
                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOUR I REGION OF OI SMRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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EMBL; AE003615; AAF52471.1; -.

PIR; A36311; A36311.

us-09-422-838c-31.rsp

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                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
Zeistra-Ryalls J.H., Kaplan S.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR REPLICATION OF THE CHROMOSOME. IT IS ALSO INVOLVED IN DNA RECOMBINATION AND REPAIR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  Biochim. Biophys. Acta 1307:318-324(1996).
                                                                                                                                                                2-BOUND GDP FOR GTP.
SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
                                                                                                                                                                                                       DELTA AND EPSILON.
-i- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein).
                                         Flowers K.M., Mellor H., Matts R.L., Kimball S.R., Jefferson L.S.; "Cloning and characterization of complementary and genomic DNAs encoding the epsilon-subunit of rat translation initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.9%; Score 53; DB 1; Length 716; Best Local Similarity 43.3%; Pred. No. 83; Maches 13; Conservative 3; Mismatches R: TnAple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 716 AA; 80240 MW; C6E4BFCE060AF6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00132; hexapep; 3.
Pfam; PF00202; W2: 1.
Pfam; SW00515; erF5C; 1.
Amino-acid biosynthesis; Translation regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE SSB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AARAGGGGGGGGIEG-----PTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U19511; AAB17691 1; -.
InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003307; eIF5C.
                               MEDLINE=96305355; PubMed=8688467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U19516; AAB17690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
               STRAIN-SPRAGUE-DAWLEY;
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodobacter.
                                                                                                                                                                                       -i- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSB_RHOSH
                                                                                                            factor-2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSB_RHOSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93389435; PubMed-8376960;
Dall D., Sriskantha A., Vera A., Lai-Fook J., Symonds T.;
"A gene encoding a highly expressed spindle body protein of Heliothis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choristoneura biennis entomopoxvirus (CbEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             armigera entomopoxvirus.";
J. Gen. Virol. 74:1811-1818(1993).
-!- FUNCTION: THIS PROTEIN IS A SPINDLE BODY PROTEIN.
-!- SUBUNIT: HOMODIMER; DISGUEIDE-LINKED.
-!- SIMILARITY: WITH HAEPV SPINDOLIN AND ACMNPV SPINDOLIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A SPHEROIDIN.
                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 26.8; Score 52.5; DB 1; Length 341; 1 Similarity 44.8%; Pred. No. 50; 13; Conservative . 2; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                                       Score 52.5; DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90223988; PubMed-2327073;
Yuen L., Dionne J., Arif B., Richardson C.;
"Identification and sequencing of the spheroidin gene of
Choristoneura biennis entomopoxvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E84EF9BCD901E72F CRC64;
                                                                                                                                                                                            DNA replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA.
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                           Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 21-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPINDOLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004302; Chitin_bind_3. Pfam; PF03067; Chitin_bind_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                          Pfam; PF00436; SSB. 1.
PROSTTE; PS00735; SSB_1; FALSE_NEG.
PROSTTE; PS00735; SSB_1; FALSE_NEG.
PNA-binding; DNA repair; DNA replic
SEQUENCE 174 AA; 18496 MW; DBF5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spindolin precursor (Spheroidin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 341 AA; 38709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M34140; AAA42887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.6%;
Best Local Similarity 44.8%;
                                                                                                                                                                                                                                                                                                                           66.78;
                   EMBL; U82280; AAD00529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 AGAGGGMGGGGYEDRGGP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 175:427-433(1990).
                                                                                                                                                                                                                                                                                                 26.68;
                                                                                                                                                                                                                                                                                                                                                                                                                      12 ARAGGGCGGGGIE---GP 26
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISION TO FUNCTION.
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                                                                                                                                                                                                                                                                                                                       Local Similarity
es 12; Conserva
                                                   HSSP; P02339; 1EYG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPIN_CBEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P50 OR SPH
                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    PARASIVE GENE GECAY IN the leprosy bacillus.";

Nature 409:1007-1011(2001).

-! FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED GLU-TRNA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINIL-TRNA SYNTHETASE. THE REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH AND ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).

-! CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE = ADP + PHOSPHATE + L-GLUTAMINL-TRNA(GLN) + L-GLUTAMATE.

-! SUBUNIT: HETEROTRIMER OF A, B AND C SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                   STRAIN-TN;
MEDLINE-21128732; PubMed=11234002;
MEDLINE-21128732; PubMed=11234002;
Wheeler P. R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares S.,
Barrell B.G.;
                   Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) (Glu-ADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 53; DB 1; Length 497; 52.6%; Préd. No. 61; tive 0; Mismatches 9; Indels
                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00571; AMIDASES; 1.
Protein biosynthesis; Ligase; Complete proteome.
SEQUENCE 497 AA; 51536 MW; D3723D871518BDC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                       subunit A).
GATA OR ML1702 OR MLCB637.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leproma; ML1702; -.
InterPro; IPR000120; Amidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL583923; CAC30655.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GPTRNPWNVDRVPGGSGGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPTLRQWLAARAGGGCGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 299263; CAB16428.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01425; Amidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                           Mycobacterium leprae.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
                                                                                                                                   NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchange factor).
EIF2B5 OR EIF2BE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2BE_RAT 064350:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2BE_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- CATALYIIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
             17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin.no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Jin.no K., Pukui S., Naqai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000058; BAA79072.1; -
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR001904; tRNA-synt_Is_1.
InterPro; IPR00191; tRNA-synt_If; I.
PR05ITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + L-1ysyl-trna(Lys)
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lysyl-trna synthetase (EC 6.1.1.6) (Lysine--trna ligase) (LYSRS).
                                                                                                                                                                                                                                                                                                                  Archāea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 562;
           12; Indels
                                   6 LRQWLAARAGGG--CGGGGIEGPTLR-------QWLAARA 36
                                                                       33 LRSWLLSRQGPAETGGGGOPOGPGLRTRLLITGLFGAGLGGAWLALRA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA; 65114 MW; 753664E2937FBF27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                           562 AA
       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "HIGH" REGION.
"KMSKS" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.2%; Score 53.5; 39.3%; Pred. No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 QWLAARAGG---GCGGGGIEGPTLRQWL 32
                                                                                                                                                                                                          Created)
Matches 17; Conservative
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                 16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                  Aeropyrum pernix.
                                                                                                                                                                     SYK_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATA_MYCLE
033105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                               SYK_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
GATA_MYCLE
                                                                                                                                                                                   δ
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8 QWLAARAGGGGGGGGGEGPTLRQ 30

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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J. Doup L.E., Downers M., Dugan-Rocha S., Dunkov B.C.,

BA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Garrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattel B., McIntcsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Kimmel B.E., Kodira C.D., Kraft C., McIncis J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter F., Shan H.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA Zhone Salcance 2872186-10870000.

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RE Science 2872188-1956(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way used in an order of the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 - FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY RECITEYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- TISSUB SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST
EXPRESSION IN WUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- MISCELLANEOUS: INHIBITED BY BARIUM.
-I- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POT)
W; 09AE1A3669072E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PORE-FORMING 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING 1 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 54; DB 52.2%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U55321; AAC69250.1; --
EMBL, AE003484; AAF47972.1; --
F1VBBASS; F8070017561; Ork1.
InterPro; IPR003280; 2porek_channel.
InterPro; IPR001622; Channel_pore_K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN LARVA AND EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 22
244 26
244 26
265 100
58 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS REVERSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
-:- TISSUE SPECIFICITY: UBJUQUITOUS.
-:- DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE
-:- CAUSE OF PATAL INFANTILE
-:- CAUSTOENCEPHALOWOOPATHY WITH COX DEFICIENCY. THIS DISEASE IS
CHARACTERIZED BY HYPERTROPHIC CARRICOMYOPATHY, LACTIC ACIDOSIS,
GLIOSIS. HEART AND SKELETAL MUSCLE SHOW REDUCTIONS IN COX
ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
                                                                                                                                                                                                                                                                                                                                                                                         SECURICE FROM N.A., AND VARIANTS FIC LYS-140 AND PHE-225.

MEDLINE-20014747; PubMed-1054552;

MEDLINE-20014747; PubMed-1054552;

MEDLINE-20014747; PubMed-1054552;

MEDLINE-20014747; PubMed-1054552;

Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M., Sannske S., Van Coster K., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S., Dev Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.;

"Fatal infantile cardioencephalomyopathy with Cox deficiency and mutations in SCO2, a Cox assembly gene.";

Nat. Genet. 23:333-337(1999).

"I FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION COPPER CONCURSION."
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion; Transit peptide; Disease mutation; Polymorphism. TRANSIT 1 41 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCO2 PROTEIN HOMOLOG.
R -> P (IN DBSNP:140523).
/FTIG=VAR_011738.
E -> K (IN FIC).
/FTIG=VAR_008874.
S -> F (IN FIC).
/FTIG=VAR_008875.
                                                                                                                                                                                                                                                                                                                                                    Smink L.J., Burton J.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                          SCO2_HUMAN STANDARD; PRT; 266 AA. 043819; Q9UK87; STANDARD; SO-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) SCO2_protein homolog, mitochondrial precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53.5; [
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003782; SC01_SenC. Pfam; PF02630; SC01-SenC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AA; 29810 MW;
761 OQQAAAAGGAAGGGGISRGSRKQ 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%;
35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225
                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFICIENCIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                              TISSUE=Monocytes;
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604377;
MIM; 220110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                  SCO2_HUMAN
                                                                  RESULT 19
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.; 0

Gaps

; 0

9; Indels

2; Mismatches

Conservative

Best Local Similarity

Query Match

12;

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-9637999; PubMed=8688087;
MEDLINE-9637999; PubMed=8688087;
MEDLINE-9637999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen NS.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                   Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: TO COENTYME F420 HYDROGENASE BETA SUBUNIT.
-i- SIMILARITY: TO M.JANNASCHII MJ1349, MJ0725 AND MJ0551.
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-45/SIROHEME DOMAIN FOUND IN MITRITE REDUCTASES (EC 1.6.6, 4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 1; Length 201;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                            Rott M.E., Tremaine J.H., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA-2.";
J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
9038506E18D7B450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
Hypothetical 20.2 kDa protein in RNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 RAGGGCGGGIE----GPTLRQWLAA 34
                                                                                                                              MEDLINE=91311402; PubMed=1856689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20194 MW;
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D12477; BAA02044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.48;
57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last a
Hypothetical protein MJ0870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 57.7 les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                                                                                                                      PIR; JQ1094; JQ1094.
HSSP; P04002; IWFA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AA;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=12281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y870_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Open rectifier potassium channel protein 1 (Two pore domain potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20196006, PubMed=10731132, Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Besson K.Y., Benos P.V., Bareman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.; "ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomyces
                                                                                                                                                                                                                                                                                                             protein; Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                              IRON-SULEUR (4FE-4S) (POTENTIAL)
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) AND SIROHEME
                                                                                                                                                                                                                                                                                                                                                    IRON-SULFUR (4FE-4S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.4%; Score 54; DB 1; Length 620; 43.5%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 58;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
9D71D2580D7D0BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1001 AA.
                                                                                                                                                                                                             PRINTS; PRO0397; NIR SIR; 1.
PRINTS; PRO0397; SIROHABM.
PROSITE; PS000198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00365; NIR_SIR; 1.
COMPLACT
                                                                                                                                                                            InterPro; IPR001450; 4Fe45_ferredoxin.
InterPro; IPR000660; Nir_Sir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97075152; PubMed=8917578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 EGPLVRATLACPGGGNCSSGLVD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EGPTLRQWLAARAGGGCGGGGIE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                         620 AA; 69793 MW;
                                                                                                                           EMBL; U67531; AAB98876.1; -. HSSP; Q45560; 1BQX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 43.59
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                428
                                                                                                                                                                                                                                                                                                                                                                 434
468
472
                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                  428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORK1 OR CG1615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel Orkl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Larva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORK1 DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294526;
                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORK1_DROME
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QΩ
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us-09-422-838c-31.rsp

Wed Oct

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91293102; PubMed=1712294;
MEDLINE=91293102: PubMed=1712294;
Mavel-Ninio M.T.M., Terracol R., Kafatos F.C.;
Mavel-Ninio M.T.M., Terracol R., Kafatos F.C.;
Mavel-Ninio M.T.M., Terracol R., Kafatos F.C.;
Menel gene of Drosophila encodes a zinc finger protein required for female gene of Drosophila encodes a zinc finger protein required for Emblo J. 0:2259-2266(1991).
-INDECELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity."; Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                Hedstrom R., Culpepper J., Schinski V., Agabian N., Newport G., "Schistosome heat-shock proteins are immunologically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 11;
Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%; Score 54.5; DB 1; Length 198; ilarity 41.4%; Pred. No. 19; Conservative 3; Mismatches 3; Indels 11
                                                                                                                                                                                           Biochem. Parasitol. 29:275-282(1988).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 AA; 21845 MW; 800F8586046D5313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVO_DROME STANDARD; PRT; 1028 AA. P51521; 09XZU4; P1621; 09XZU4; 01-0CT-1996 (Rel. 34, Last sequence update) 116-0CT-2001 (Rel. 40, Last annotation update) OVO PROTEIN (Shaven baby protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 RAGG-----GCGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTEFPC: IPRO01023; HSP70.
PROSITE: PS00297; HSP70_1; PRRTIAL.
PROSITE: PS00329; HSP70_2; PRRTIAL.
PROSITE: PS01036; HSP70_3; PARTIAL.
ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ovary;
MEDLINE-95021209; PubMed-7935398;
                                                                                                                    MEDLINE-88318804; PubMed-2457805;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M21011; AAA29897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          A54507.
                                                                                                                                                                               host-like antigens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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tes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            P08109; 1CKR
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                 NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                          A54507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                 IN THE EGG,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000822; Znf-C2H2.
PRIM: F00096; Z1C2H2; 4.
SMART; SM00355; ZnF_C2H2; 4.
SMART; SS00028 ZINC_FINGER.
SMOSTIE; PS00028 ZINC_FINGER_C2H2_1; 3.
PROSTIE; PS00028 ZINC_FINGER_C2H2_1; 3.
Zinc_finger; Metal_binding; DNA-binding; Repeat; Nuclear protein;
SUBCELLULAR LOCATION: Nuclear (Potential).
DEVELOPMENTAL STACE: FIRST APPEARS IN THE GERNARIUM AND
ACCUMILATES IN NURSE CELLS DURING OOGENESIS. STORED IN THE E
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> R (IN REF. 2).
: D7068BB2BC0F6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
C2H2-TYPE.
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POLY-ALA.
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POLY-ALA.
POLY-SER.
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                                                                                                                                                                                                                                                                                                                                   EMBL; U11383; AAB60216.1; -.
EMBL; X59772; CAB36921.1; ALT_SEQ.
HSSP; P25490; 1ZNM.
Flybase; FBgn0003028; ovo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110620 MW;
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01-MAY-1992 (Rel. 22, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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P25245;
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CONFLICT
SEQUENCE
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              SO THE PROPERTY OF THE PROPERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- CAFALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01411; tRNA-synt_2c; 1.
PRIATS; PR00980; TRNASYNTHALA.
PROSITE; PS00179; AA_TRNA_LIGASE_LIL_1; FALSE_NEG.
PROSITE; PS000379; AA_TRNA_LIGASE_LIL_2; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Gaps
                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
ALAS OR TC0125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.9%; Score 55; DB 1; Length 875; 28.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGCGGGGIE------GPTLRQWLAAR 35
                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches 16; Indels
                                                                                            607 GKTLESWRSLCTRCCWASKGAAVGGGAGATAAGGGGGGGGGGGG 652
                                                          -----LAARAGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      875 AA; 98185 MW; A75F8977A23DC41D CRC64;
                                                                                                                                                                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                        875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 112 AA.
   Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO INTERPOSA A TRNA_ligase_II.
INTERPRO; IPRO03156; DHHA1.
INTERPRO; IPRO02318; tRNA-synt_2c.
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MOPN / NIGG;
MEDLINE-20150255; Pubmed-10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE002279; AAF39003.1; -
32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 28.6%;
Matches 14; Conservative
 Best Local Similarity 32.6
Matches 15; Conservative
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02272; DHHA1; 1
                                                        3 GPTLRQW-----
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Completé proteomé.
SEQUENCE 875 AA;
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83560;
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006285;
                                                                                                                                                                                    SYA_CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                    SYA_CHLMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haff D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcook K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Genelles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skellon S., Squares S., Squares R., Sellon S., Squares S., Squares R., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the blology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0T-1993 (Rel. 26, Last annotation update)
01-JUL-1993 (Rel. 26, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Fragment).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DOMINDAT T-CELL ANTIGEN AND STIMULATES
LYMPHOPROLIFERATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 112 AA; 12098 MW; A4B32E478CBAC3E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; Immune response; Signal; Complete proteome.
SIGNAL 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 LKQWVAAGRRVGGRRRGRSGSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LRQWLAA------RAGGGCGGGGI---EGPTLRQW 31
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                      LSR2 protein precursor.
LSR2 OR RV3597C OR MT3704 OR MTCY07H7B.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%; Score 54.5; 33.3%; Pred. No. 12
                                                                                                                                                                                                                        MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z95557; CAB08947.1; -. EMBL; AE007170; AAK48061.1; -
                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculist; Rv3597c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
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                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MT3704; -
                                                                                                                                                                                                     STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS70_SCHJA
P12795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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us-09-422-838c-31.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishvelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular cloning and characterization of human Frizzled-8 gene on
            "Structure of a Numb PTB domain-peptide complex suggests a basis for
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PFU0640; r.r., SMART; SMO0462; PTB; 1. PROSITE; PS01179; PID; 1. Nuclear protein; ATP-binding; Alternative initiation; 3D-structure. Nuclear protein; ATP-binding; NUMB PROTEIN, ZYGOTIC ISOFORM. TSG NUMB PROTEIN, MATERNAL ISOFORM
                                                               DURING
                              diverse binding specificity.";

"Nat. Struct. Biol. 5:1075-1083(1998).

"AL. Struct. Biol. 5:1075-1083(1998).

"AL. STRUCTION: NUMB IS REQUIRED IN DETERMINATION OF CELL FATE DURING SENSORY ORGAN FORMATION IN DROSOPHILA EMBRYOS. IT FUNCTIONS IN NUCLEIC AND SEEMS TO INTERACT WITH NUCLEIC ACIDS.

-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: CONTAINS 1 PID DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 1; Length 556; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4FECAAE9C98FEE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR MATERNAL ISOFORM.
ATP (POTENTIAL).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Frizzled 8 precursor (Frizzled-8) (Fr-8) (hFz8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | : | | | | | | 486 QTLASGTGAAVGGGGPDDPFDAEWVA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-21192958; PubMed-11295046; Saitch T., Hirai M., Katch M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 QWLAARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                           PIR; A32466; A32466.
PDB; 2NMB; 04-NOV-98.
FlyBase; FBgn0002973; numb.
InterPro; IPR000050; PID_domain.
Pf00640; PID; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Int. J. Oncol. 18:991-996(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%;
                                                                                                                                                                                                                                                                                                           EMBL; M27815; AAA28730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.99
Best Local Similarity 42.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
29
57
208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 10p11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
Forman-Kay J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F2D8_HUMAN
Q9H461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
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DOMAIN
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FZD8_HUMAN
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Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Mnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                      --- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/Deta-catenin signaling pathway (By similarity).
---- DOMAIN: The fz domain is involved in binding with Wnt ligands (by
                                                                                                                                               -i-SUBCELLULAR LOCATION: Integral membrane protein.
-i-TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by brain and lung. In adult tissues, expressed in kidney, heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                             similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SMUJUUS, ..... PROSITE; PSS0038; FZ; 1. PROSITE; PSS0038; FZ; 1. Multigene family; G-PROTEIN_RECEP_F2_4; 1. Multigene family; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal. 27 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
Pfam; PF01534; Frizzled; 1.
Pfam; PF01392; Fz; 1.
SMRNTS; PR00489; FRIZZLED.
                                                                                                                                                                                                 pancreas and skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR000539; Frizzled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB043703; BAB41064.1; -. EMBL; AL121749; CAC10185.1; -.
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505
533
553
5554
5554
606
606
108
1198
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                                                                                                                                                                                                                                                                                              RECEPTORS.
                                                                                                                                        tissues
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TRANSMEM
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Length 694;

DB 1;

Score 55;

27.9%;

Query Match

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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AARAGGCCGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                               68120 MW;
                                    EMBL; M18334; AAA33592.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                             63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 64-210.
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                          49
606
619
207
373
566
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189
191
477
480
                                                                                                                     Glycoprotein; Repeat.
SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 58:349-360(1989).
                                                                                                                                                                                                                                                                                                                                                                                              619 AA;
                                                                                                                                         22
50
607
84
216
                                                                                                                                                                                                                                    Numb protein.
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CARBOHYD
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                                                                                                                                                   CHAIN
PROPEP
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METAL
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NUMB_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88087214; PubMed-2961749; Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Characterization of two allelic forms of Neurospora crassa laccase. Amino- and carboxyl-terminal processing of a precursor."; J. Biol. Chem. 263:885-866(1988).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                           Gaps
    PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
COPPER (TYPE 3) (PROBABLE).
POPER (TYPE 1) (PROBABLE).
POPER (TYPE 1) (PROBABLE).
POPER (TYPE 1) (PROBABLE).
TRED (GLUNAC...) (POTENTIAL).
KED (GLUNAC...) (POTENTIAL).
KED (GLUNAC...) (POTENTIAL).
TRED (GLUNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (Rel. 1.0.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele TS)
                                                                                                                                                                                                          N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLERR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION. Secreted (POtential).

-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes;
                                                                                                                                                                                                                                                                                    DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT
                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                              FDED6D78B65048E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 619 AA
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                 28.4%; Score 56; 63.6%; Pred. No.
   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                         11 AARAGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                     44 AERYGG-GGGCNSPINRQCW 64
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                                                                                                                                                                                                                                                              68198
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             619
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Local S.
14;
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P10574;
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                                                                                                                                                                                                                                                             SEQUENCE
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                                        DOMAIN
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                     CHAIN
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(See http://www.isb-sib.ch/announce/
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pyerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99061335; PubMed-9846878;
Li S.-C., Zwahlen C., Vincent S.J., McGlade C.J., Kay L.E., Pawson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                    Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uemura T., Shepherd S., Ackerman L., Jan L.Y., Jan Y.N.;
"Numb, a gene required in determination of cell fate during sensory
organ formation in Drosophila embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.4%; Score 56; DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBB6CCDE18841145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                          PIR; B28523; KSNCLT.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
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MEDLINE=89324081; PubMed=2752427;
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13; Conservative
                                                                                                                                                                                                      STANDARD;
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                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                              Neurospora crassa.
                                                                                                                                                                                                       LAC1_NEUCR
         DISULFID
                                                              Query Match
DISULFID
                                     SEQUENCE
                                                                                                                                                                                           LAC1_NEUCR
                                                                                        Matches
                                                                             Best
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FFFS
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                                                                                                                                                                                                                                                                                                                MEDLINE-94280518; PubMed-8011164; MEDLINE-94280518; PubMed-8011164; Ohlsen S.M., Lugenbeel K.A., Wong E.A.; "Characterization of the linked ovine insulin and insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 27 22.

SEQUENCE OF 27 22.

SEQUENCE OF 27.

PREDIINE-7258016

PRECENSON J.D., Nehrlich S., Oyer P.E., Steiner D.F.;

Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.;

Procedure...

J. Blol. Chem. 247:4866-4871(1972)

J. ROLO. THE PERPOSERS BLOOD GLUCOSE CONCENTRATION. IT

INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND

INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND

CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

J. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
               Gaps
                                                                                                                                                                                                                            Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted. -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin family; Hormone; Glucose metabolism; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULIN B CHAIN.
                                                                                                                                                             11-001-1986 (Rel. 01, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Blochem. J. 60:556-565(1955).
                                                                                                                                    105 AA
    50.0%; Pred. No. 6.8;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01315; 9INS.
Interpro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C PEPTIDE
                                                                                                                                     PRT;
                                          1 IEGPTLRQWLAARAGGGCGGGGIEGP 26
                                                         DNA Cell Biol. 13:377-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-54 AND 85-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U00659; AAB60625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
                   13; Conservative
                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Ovis.
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S16430; INSH.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                     Insulin precursor.
                                                                                                                                                                                                                                                                               NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                               factor-II genes
                                                                                                                                     INS_SHEEP
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CHAIN
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                      Matches
                                                                                                                          INS_SHEEP
                                                                                                               RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
-!- FUNCTION. LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
-!- FUNCTION: (PROBABLE).
-!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88087214; PubMed=2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
Germann G.A., Mueller G., Hunziker P.E., Lerch K.;
Amaracterization of two allelic forms of Neurospora crassa laccase.
Amino- and carboxyl-terminal processing of a precursor.";
J. Biol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germann U.A., Lerch K.; "Isolation and partial nucleotide sequence of the laccase gene from Neurospora crassa: amino acid sequence homology of the protein to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF60394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
(Urishiol oxidase) (Laccase allele OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                    3;
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-i- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-i- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariaceae; Neurospora.
NCBL_TaxID=5141;
                                                                                                                                                  Score 56.5; DB 1; Length 105;
Pred. No. 6.8;
2; Mismatches 8; Indels
31 91 IMTERCHAIN.
43 104 INTERCHAIN.
90 95
105 AA; 11235 MW; 8B27C7FB9922BC7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                   1 IEGPTLROWLAARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                       58 VEGP---QVGALELAGGPGAGGLEGP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87067412; PubMed=2947240;
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EMBL; M18333; AAA3591.1; ··
PIR; A28523; KSNCLO.
PIR; A29762; A29762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 379-619 FROM N.A.
                                                                                                                                                                            28.7%;
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SEQUENCE
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 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger F., Tuppy H.;
"The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates."; blochem. J. 49:481-490(1951).
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization of proinsulin C-peptide from bovine
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 85-105.
Sanger F., Thompson E.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.";
                                                                                                                                                                                                                                                                                                                                                              D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                     .;
8
                   Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=71116409; PubMed=5545080;
Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D.,
Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                                                "Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid for bovine preproinsulin."; Mol. Endocrinol. 1:327-331(1987).
                                                                                                 28.9%; Score 57; DB 1; Length 339;
                                                                                                                     Indels
                                                                             370DC47C6929F7E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-105.
MEDLINE=71166442; PubMed-4928892;
Nolan C., Margoliash E., Peterson J.D., Steiner D.F.;
"The structure of bovine proinsulin.";
J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=71257721; PubMed=5105368;
Salokangas A., Smyth D.G., Markussen J., Sundby F.;
                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                            105 AA
                                                                                                                     2; Mismatches
                                                  POLY-GLY.
SER/THR-RICH.
                                                                                                          Pred. No. 16;
                                                                                                                                                    3 GPTLRQWL-----AARAGGGCGGGIEGP 26
                                       GLY-RICH.
                                                                    HOMEOBOX.
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreas.";
J. Biol. Chem. 246:1365-1374(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biochem. 20:183-189(1971).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88288209; PubMed=2456452;
PS00027; HOMEOBOX_1; 1. PS50071; HOMEOBOX_2; 1.
                                                                              34992 MW;
                                                                                                           40.68;
                                                                                                          Best Local Similarity 40.6
Matches 13; Conservative
                                                                                                                                                                                                            STANDARD;
                                                131
                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                 taurus (Bovine).
                                                                             339 AA;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 57-82.
                                                                                                                                                                                                                                                             Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-54
           PROSITE; PS50071;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from pancreas.";
                                                                                                                                                                                                                                                                                                                                                                         Frazier M.L.
                                                                                                                                                                                                         INS_BOVIN
P01317;
                                                                    DNA_BIND
                                                                               SEQUENCE
 PROSITE;
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                                                 DOMAIN
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                                                                                                                                                                                                 INS_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97285914; PUDMEd-9141131;
Brange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L.;
Brange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L.;
A model of insulin fibrills derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin).";
Proteins 27:507-516(1997).
-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://www.expasy.org/spotlight/articles/spt1t009.html".
                                                                                                                                                 X-RAY CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
Reynolds C.D.;
                                      AMIDES, SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS. RYLP A.P., Sanger F., Smith L.F., Kitai R.; "The disulphide bonds of insulin."; Biochem. J. 60:541-556(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY:
-!- DATABASE: NAME-Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75307CF78E61C06A CRC64;
                                                                                                                                                                                                              "The structure of des-Phe bl bovine insulin.";
Acta Crystallogr. B 38:3028-3032(1982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C PEPTIDE.
INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE-Issue 9 of April 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
11393 MW;
Biochem. J. 53:366-374(1953).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M54979; AAA30722.1; -.
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82
1005
1005
1004
468
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1011
1033
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A40909; A40909.
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105 AA;
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STRAND
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DB 1; Length 105;

Score 56.5;

28.7%;

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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- CATALYTIC ACTIVITY: AFP + L-alanine + tRNA(Ala) = AMP +
diphosphate + L-alany1-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 1; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ALA.
EAAF498D216BE019 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002106; AA_tRNA_ligase_II.
Interpro; IPR003156; DHHAI.
Interpro; IPR002318; tRNA-synt_2c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
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                                                                                                                                                                                               InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRUTS; PR00033; FORKHEAD.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00657; FORK_HEAD_2; 1.
PROSITE; PS00659; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=D/UW-3/CX;
MEDLINE=99000809; Pubmed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
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                                                                      EMBL; AF042832; AAC15421.1; -. HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PT--LRQWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49007 MW;
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66.7%;
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250
306
409
426
                                                                                                                                             FRANSFAC; T02485; -.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=813;
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                                                                                                                                                                          MIM; 602211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis R.W.;
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084754;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02272; DHHA1; 1.
Prim; PF0411; tRNA-Synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
AMINOACY1-KRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
GCMPLete Proteome.
875 AA; 97671 MW; 81C2DA7B29A5D11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-89356622; PubMed-2569970;
Dolle P., Duboule D.;
"Two gene members of the murine HOX-5 complex show regional and cell-
                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renucci A.G.P., Zappavigna V., Zakany J., Izpisua-Belmonte J.-C., Buerki K., Douboule D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparison of mouse and human HOX-4 complexes defines conserved sequences involved in the regulation of Hox-4.4."; EMEO J. 11:1459-1468(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGCGGGIE------GPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                        5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.1-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
HOMDeobox protein Hox-D9 (Hox-4.4) (Hox-5.2).
HOXD9 OR HOXD-9 OR HOX-4.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AA
                                                                                                                                                                                                                                                                                   Query Match

29.4%; Score 58; DB

Best Local Similarity 30.6%; Pred. No. 29;

Matches 15; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92224884; Pubmed=1348690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X62669; CAA44542.1; -.
EMBL; X14714; CAB57813.1; -.
PIR; S09398; S09398.
PIR; S09569; S09569.
PIR; S20880; S20880.
HSSP; P02834; 1B81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01755; ...
MGD; MGI:96210; HOXG4
InterPro; 1PR001365; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 272-331 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HXD9_MOUSE
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DDT T

DDT D

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SIGNAL
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                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92212967; PubMed-1313578;
Ip N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92075279; PubMed=1742028; Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
MEDLINE-2005885; Dubmed-10631974;
Robinson R.C., Radziejewski C., Spraggon G., Greenwald J.,
Kostura M.R., Burtnick L.D., Stuart D.I., Choe S., Jones E.Y.;
"The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk-binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: HIGHEST LEVELS IN PROSTATE, LOWER LEVELS IN THYMUS, PLACENTA, AND SKELETAL MUSCLE. EXPRESSED IN EMBRYONIC AND ADULT TISSUES.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein Sci. 8:2589-2597(1999).
-!- FUNCTION: TARGET-DERIVED SURVIVAL FACTOR FOR PERIPHERAL SENSORY
SYMPATHETIC NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                            . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian neurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                        6
                                                                                                                                                              32.2%; Score 63.5; DB 1; Length 209; 37.5%; Pred. No. 2.2;
                                                                                                                                                                                        Indels
                                                                                                             N-LINKED (GLCNAC. . .) (PC
R -> P (IN REF. 2).
DF5112C05C5D5B85 CRC64;
                                                                                                                                                                           Pred. No. 2.2;
2; Mismatches 14;
                                                                                                                                                                                                                                          128 GSPLRQYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue distribution, and receptor specificity."; Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                                                                                                                                                  3 GPTLRQWL------AARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                             NEUROTROPHIN-5.
                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                          210 AA.
                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
                                                                                                                                        22332 MW;
                                                                                                                                                                                                                                                                                                                                                                                    (NT-4) (Neutrophic factor 4).
PROSITE; PS50248; NGF_1; 1. PROSITE; PS50270; NGF_2; 1.
                                                                                                                                                            Query Match
Best Local Similarity 37.59
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 7:857-866(1991).
                         Growth factor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                        209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A.
                                                                                                                                                                                                                                                                                                         NT5_HUMAN
P34130;
                                                                                                                            CONFLICT
                                                                          DISULFID
                                                                                                    DISULFID
                                                                                                               CARBOHYD
                                                                                        DISULFID
                                                 PROPEP
                                      SIGNAL
                                                                                                                                                                                                                                                                                              NT5_HUMAN
                                                                                                                                                                                                                                                                               RESULT 2
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhaed box protein D2 (Forkhead-related protein FKHL17) (Forkhead-related transcription factor 9) (FREAC-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98066765; PubMed=9403061;
Ernstsson S., Betz R., Lagercrantz S., Larsson C., Ericksson S.,
Cacherbera A., Carlsson P., Enerbaeck S.;
"Cloning and characterization of freac-9 (FKHL17), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34.";
Genomics 46:78-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 N-LINKED (GLCNAC. . .) (POTENTIAL)
22426 MW; DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GSPLROYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQWL-----AARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
-i - SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROTROPHIN-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.7%; Score 60.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal; 3D-structure,
                                                                                                                                                               EMBL; M86528; AAA60154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00248; NGF_1; 1. PROSITE; PS50270; NGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002052; NGF; 1.
                                                                                                                                                                                                                                                                                                                         InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00140; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
170
199
                                                                                                                                                                                                                                         1B8M; 09-FEB-99.
1B98; 26-FEB-99.
162662; -.
                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00268; NGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                   A42687; A42687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FXD2_HUMAN
060548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:51:41; Search time 4.29977 Seconds Run on:

(without alignments) 324.181 Million cell updates/sec

US-09-422-838C-31 Perfect score:

1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rattus	30 ношо	3 homo 8	54 chlam	22	P01317 bos taurus	P01318 ovis aries	P06811 neurospora					006285 mycobacteri			P25245 tomato ring		_		_	033105 mycobacteri							_	_			_	
SUMMARIES	ΙΙ		NT5_HUMAN	FXD2_HUMAN	SYA_CHLTR	HXD9_MOUSE	INS_BOVIN	INS_SHEEP	LAC1_NEUCR	LAC2_NEUCR	NUMB_DROME	FZD8_HUMAN	SYA_CHLMU	LSR2_MYCTU	HS70_SCHJA	OVO_DROME	YR21_TRSVR	Y870_METJA	ORK1_DROME	SCO2_HUMAN	SYK_AERPE	GATA_MYCLE	E2BE_RAT	SSB_RHOSH	SPIN_CBEPV	CYB_MICIK	RU17_DROME	PAC4_HUMAN	SIX3_MOUSE	FXD3_CHICK	HKLB_LYCES	OC3N_HUMAN		SRF_XENLA
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PIR; JH0504; JH0504. PIR; B42687; B42667. HSSP; P34130; 1B8M. InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1. PRINTS; PR00268; NGF. ProDom; PD00252; NGF. SMART; SM00140; NGF; 1.

008580 mus musculu			P12252 drosophila							
ERRI_MOUSE	CG12_YEAST	CG11_YEAST	CNA1_DROME	K1CJ_HUMAN	MYSC_ACACA	NIR_NEUCR	PHYB_SORBI	RU17_MOUSE	RU17_HUMAN	FXGA_CHICK
٦,	-	, -	Н	Н	Н	Н	Н	Н	Н	П
462	545	546	584	593	1168	1176	1178	378	437	440
26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.1	26.1	26.1
52	52	52	52	52	52	52	52	51.5	51.5	51.5
34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92212967; PubMed=1313578;
ID N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.;
"Mammalian neurotrophin-4: structure, chromosomal localization,
tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992).
                                                                                             01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurotrophin-5 precursor (NT-5) (Neutrophic factor 5) (Neurotrophin-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92075279; PubMed-1742028;
Berkemeier L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                          Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A.; "Neurotrophic factor that activates trk and "Neurotrophin-5: a novel neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 7:857-866(1991).
-!- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR SENSORY AND SYMPATHETIC NEURONS.
-!- TISSUE SPECIFICITY: EXPRESSED IN THYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                      209 AA.
                                                                           01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                      (NT-4) (Neutrophic factor 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M86742; AAA41728.1; -. EMBL; S69323; AAB20548.1; -.
                                      STANDARD;
                                                                                                                                                                            NTF5 OR NTF4 OR NT4.
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                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
RESULT 1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Moclecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: EMBL:277655; PIDN:CAB01137.1; GSPDB:GN00023; CESP:C56A3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C56A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20268
                                                                                                                                                                                                              hypothetical protein Y41C4A.4b - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C.Accession: T26808
  Gaps
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A;Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%; Score 55; DB 2; Length 393; 45.5%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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5;
                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-333 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CESS:Y41c4A.4b
A;Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C;Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                           R;Steward, C. submitted to the EMBL Data Library, October 1998 A;Reference number: 220269 A;Accession: T26808
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, July 1996
A;Reference number: Z19244
A;Accession: T20268
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5;
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A; Introns: 51/3; 91/1; 121/1; 331/3
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Best Local Similarity 69.20
The second of Conservative
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  Conservative
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                                             15 GGGGGGGIEGPT 27
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Matches 10; Conserv
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6
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nypothetical protein At2945420 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accord C 84890
R; Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A. Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487
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A;Residues: 1-257 <STO>
A;Cross-references: GB:AE002093; NID:92583113; PIDN:AAB82622.1; GSPDB:GN00139
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
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A; Accession: T26807
A; Accession: T26807
A; Molecule type: DNA
A; Molecule type: DNA
A; Mosidues: 1-331 < WILL>
A; Residues: 1-331 < WILL>
A; Cross-references: EMBL:AL032627; PIDN:CAB54381.1; CESP:Y41C4A.4a
A; Experimental source: clone Y41C4A
                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <SCCH>
A;CESidues: 1-201 <SCCH>
A;Cross-references: EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.290
A;Experimental source: BAC clone B9J10; strain OR74A
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Pred. No. 34;
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submitted to the Protein Sequence Database, May 2000
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Pred. No. 52;
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A;Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C;Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Steward, C. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                     Mismatches
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81.8%; Pred. No. 4
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                                                                                                                                                                                                                                                                                     27.98;
52.48;
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69.28;
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Best Local Similarity 52.49
Matches 11; Conservative
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                      A; Reference number: 225022
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Best Local Similarity
'-has 9; Conserve
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Best Local Similarity
                                                                                                                                                                                                         A;Gene: NCSP:B9J10.290
A;Map position: 6
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                                          A; Accession: T49792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: C84890
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A;Map position: 2
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uppouncettest lything their process in vivory in your centrum curetourous (strain n3/RV) (Species Mycobacterium tuberculosis (Species Mycobacterium tuberculosis (Species Mycobacterium tuberculosis (Species Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Nov-1999 C;Accession: E70895 C;Accession: E70895 C;Accession: E70895 C;Arris Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987 A;Accession: E70895 A;Accession: E70895 A;Accession: E70895 A;Accession: E7087 CCU.>
A;Molecule type: DNA B;Molecule type: DNA B
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C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49792
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49530
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                 hypothetical glycine-rich protein Rv1087 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related to glycine-rich cell wall structural protein [imported] - Neurospora crassa N;Alternate names: protein B21J21.90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.4%; Score 56; DB 2; Length 767; 46.7%; Pred. No. 85;
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Pred. No. 31;
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C;Superfamily: unassigned collagens
11 AARAGGGGGGGGIEGPTLRQ-W 31
                                                                44 AERYGGG-GGGGCNSPTNRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain H37Rv
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73.3%;
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Best Local Similarity 46.73
Matches 14; Conservative
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Matches 11; Conservative
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A, Accession: T49530
A, Status: preliminary
A, Molecule type: DNA
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T49792
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A; Realdues: 379-619 (GE2>
A; Realdues: 379-619 (GE2>
C; Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
                                          A.Accession: A28523
A.Molecule type: DNA
A.Rosidues: 1-619 <a href="https://docs.org/learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning-learning
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Pred. No. 70;
0; Mismatches 6; Indels
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0; Mismatches
     A; Reference number: A28523; MUID:88087214
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Matches 14; Conservative
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Best Local Similarity 63.6
Matches 14; Conservative
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cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chryso C;Species: Phanerochaete chrysosporium C;Species: Phanerochaete chrysosporium C;Date: 20-oct-1994 **sequence_revision 10-Nov-1995 **text_change 21-Jul-2000 C;Accession: S44716; S33165 **
R;Sims, P.F.G.; Soares-Felipe, M.S.; Wang, Q.; Gent, M.E.; Tempelaars, C.; Broda, P. Mol. Microbiol. 12, 209-216, 1994 **
A;Title: Differential expression of multiple exo-cellobiohydrolase I-like genes in th A;Reference number: S44714; MUID:94335641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-540 cS12>
A; Cross-references: EMBL:229653; NID:9453222; PIDN:CAA82761.1; PID:9453223
C; Superfamily: cellulose 1,4-beta-cellobiosidase 1; fungal cellulose-binding domain h
C; Keywords: 91ycosidase; hydrolase; polysaccharide degradation
F;479-510/Domain: fungal cellulose-binding domain homology <FCB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chryso C; Species: Phanerochaete chrysosporium C; Date: 20-May-1994 * sequence_revision 10-Nov-1995 * text_change 22-Jun-1999 C; Accession: S4714; S4194 * S4194 * Sims, P.F.G.; Soares-Fellpe, M.S.; Wang, Q.; Gent, M.E.; Tempelaars, C.; Broda, P. Mol. Microbiol. 12, 209-216, 1994
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R;Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
L. Biol. Chem. 263, 885-896, 1988
A;Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Differential expression of multiple exo-cellobiohydrolase I-like genes in th A; Reference number: S44714; MUID:94335641
A; Accession: S44714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Superfamily: cellulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;480-511/Domain: fungal cellulose-binding domain homology <FCB>
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-511 <SIM>
A; Cross-references: EMBL:222527; NID:9296028; PIDN:CAA80252.1; PID:93980202
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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48.0%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.4%; Score 56; DB 2; Length 511; 48.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laccase (EC 1.10.3.2) precursor - Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
. 9
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1; Mismatches
Mismatches
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                                                                                                                    473 GPTVPQW-----GQCGGIGYSGST 491
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                                                             3 GPTLRQWLAARAGGGCGGGGIEGPT
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Matches 12; Conservative
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12; Conservative
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Les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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   Matches
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Hitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Introns: 505/1
C.Superfamily: callulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain homd
C.Keywords: glycosidase; hydrolase; polysaccharide degradation
F:479-510/Domain: fungal cellulose-binding domain homology <FCB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysospo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Differential expression of multiple exo-cellobiohydrolase I-like genes in the A;Reference number: $44714; WUID:94335641 A;Accession: $44715
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C;Species: Phanerochaete chrysosporium
C;Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: 544715; 541943
C;Accession: 544715; 541944
Mol. Microbiol. 12, 209-216, 1994
                         A;Cross-references: EMBL:AF067609; PIDN:AAC17537.1; GSPDB:GN00022; CESP:C23H5.9
A;Experimental source: strain Bristol N2; clone C23H5
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A:Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F13K9.10 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: E86405
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A;Cross-references: EMBL:Z29653; NID:g453222; PIDN:CAA82762.1; PID:g453224
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                                                                                                                                                                                                                                                      Length 163;
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22;
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59;
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                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pred. No. 4
                                                                                                                                                                                                                                                      Score 56;
Pred. No.
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Pred. No.
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48.0%;
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Best Local Similarity 75.0%;
Matches 12; Conservative
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                                                                                                                                                           A;Map position: 4
A;Introns: 1/3; 101/3; 126/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <STO>
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Best Local Similarity
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   A; Residues: 1-163 < LAM>
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                                                                                                                       A; Gene: CESP:C23H5.9
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Matches

RESULT 19

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C; Genetics:

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9 WLAARAGG--GCGGGGIEGPTLRQW 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: translated from GB/EMBL/DDBJ
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nes 11; Conserv
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A; Residues: 1-56 <KUN>
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A; Residues: 1-56 <LAZ>
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: B72698
C;Accession: B72698
C;Accession: B72698
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339
A;Reference number: A72450; MUID:99310339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-176 < KAN>
A;Residues: 1-176 < KAN>
A;Residues: 1-176 < KAN>
A;Residues: DNA
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A99343
A;Contents: annotation; amides; disulfides
R;Wenzel, T.; Eckerskorn, C.; Lottspelch, F.; Baumeister, W.
FEBS Lett. 349, 205-209, 1994
A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degradath A;Reference number: $46258; MUID: 94326921
A; Molecule type: protein
A; Residues: 25-54 <ARN.
A; Residues: 25-54 <ARN.
R; Cheng, R.; Kawakishi, S.
Eur. J. Blochem. 223, 759-764, 1994
A; Title: Site-specific oxidation of histidine residues in glycated insulin mediated by
A; Reference number: S48184; MUID: 94333378
A; Accession: S48184
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A; Status: preliminary
A; Mocession: 546298
A; Status: preliminary
A; Mocession: 52-54
A; Molecule type: protein
A; Residues: 25-54
A; Mexno
C; Superfamily: insulin
C; Keywords: hormone; pancreas
F; 1-24/Domain: signal sequence #status predicted <SIG>F; 1-24/Domain: insulin chain B #status experimental <BCH>F; 25-54, 85-105/Product: insulin #status experimental <MAT>F; 25-54, 27/Domain: connecting peptide #status experimental <APEP>F; 55-105/Domain: insulin chain A #status experimental <APEP>F; 85-105/Domain: insulin chain A #status experimental <APEP>F; 31-91, 43-104, 90-95/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-30, X',32-42, X',44-54 <CH2>
R;Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai, R.
Blochem J. 60, 541-556, 1955
A;Title: The disulphide bonds of insulin.
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Pred. No. 21;
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ilarity 34.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain K1
C; Genetics:
A; Gene: APE1002
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 85-105 <CHE>
A; Accession: S48185
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es 15; Conserv
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R; Kunst, ettereuces: Expoi.exvio.is; NID:93023478; FID:9302347; FIDN:ARCIZVYZ.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Brron, S.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Nature 390, 249-256, 1997.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997.
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Kroßh, S.; Kumano, M.; Kurita, K.; Lapdua, S.; Hullo, M. Koetter, P.; Koningstein, G.; Kroßh, S.; Kumano, M.; Kurita, K.; Lapdua, S.; Mau Y, M.; Ogawa, K.; Oguwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanla, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sedfone, V.; Toppini, A.; Tosato, V.; Uchiya A; Authors: Yoshkawa, H.; Zanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
                                                                                                                                                C, Accession: T12783; H69719
C, Accession: T12783; H69719
R; Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A; Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 pro
A; Reference number: 217583
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A)Experimental source: strain 168
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F;33-48 Disulfide bonds: #status predicted
F;33-Modified site: dehydroalanine (Ser) #status experimental
F;38-41/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status predicted
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sublancin 168 precursor - Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
C;Date: 13-Aug-1999 *sequence_revision 13-Aug-1999 *text_change 24-Sep-1999
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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C;Superfamily: unassigned lanthionine-containing peptides
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R; Lamar, E.; Kramer, J.
submitted to the EMBL Data Library, May 1998
A; Description: The sequence of C. elegans cosmid C23H5.
A; Reference number: Z21286
A; Accession: T33130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: antiblotic; lanthionine
F;1-19/Domain: propeptide #status predicted <PRO>
F;20-56/Product: sublancin 168 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C23H5.9 - Caenorhabditis elegans
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1 IEGPTLRQWLAARAGGGCGGGGIEGP 26
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50.0%;
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Best Local Similarity 50.09
Matches 13; Conservative
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                                                                                                                                                     A; Accession: S16431
A; Molecule type: protein
A; Residues: 31-56 <PET>
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A; Residues: 85-105 <SAN>
                                                                                                                                                                                                                                         C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A92074
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R; Duboule, D.; Dolle, P.
EMBO J. 8, 1497-1505, 1989
A; Title: The structural and functional organization of the murine HOX gene family resemb A; Reference number: S09569; MUID:89356621
A; Accession: S09569
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Dolle, P.; Duboule, D.
EMBO J. 8, 1507-1515, 1989
A;Title: Two gene members of the murine HOX-5 complex show regional and cell-type specif A;Reference number: S09398; MUID:89356622
A;Accession: S09398
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
C;Accession: $20880; $509569; $509398
R;Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboule, EMBO J. 11, 1459-1468, 1992
A;Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences involA;Reference number: $20879; MUID:92224884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:X14714; GB:M21040; NID:951427; PIDN:CAB57813.1; PID:96015583
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A;Residues: 272-331 cOUB>
A;Cross-references: EMBL:X14714; NID:g51427; PIDN:CAB57813.1; PID:g6015583
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
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A,Cross-references: GB:BA000019; PIDN:BAB73303.1; PID:g17130693; GSPDB:GN00179
A,Experimental source: strain PCC 7120
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: S16430, S16431
B;Brown, H; Sanger, F; Kitai, R.
Biochem. J. 60, 556-565, 1955
A;Title: The structure of pig and sheep insulins.
A;Reference number: A90344
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                                                                                                                                     Length 327;
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Pred. No.
                                                                                                                                     28.9%; Score '57; 50.0%; Pred. No.
                                                                                                                                                                                                                                            10 LAARAGGGGGGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                          Query Match 28.9%;
Best Local Similarity 40.6%;
Matches 13; Conservative
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                                                                                                                                                                                         Conservative
                                                                                                          Query Match
Best Local Similarity
' has 11; Conserve
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A; Residues: 272-331 < DOL>
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A; Residues: 1-339 <REN>
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                                                                                    A; Gene: alr1346
                                                           C; Genetics
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insulin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: 24-Apr-1984 **sequence_revision 22-Apr-1995 **text_change 16-Jul-1999
C;Accession: A40909; A92080; A92074; A91185; A99341; S48184; S48185; S46258;
R;D'Agostino, J; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.
Mol. Endocrinol: 1, 337-331, 1987
A;Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic a A;Reference number: A40909; MUID:88288209
A;Molecule type: protein
A;Residues: 1-30;57-77 <BRO>
Y;Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4871, 1972
A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proin A;Reference number: A92111; MUID:72258016
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A,Residues: 57-82 <SAL>
R:Sanger, F.: Thompson, E.O.P.
Birthen J. 53, 366-374, 1953
A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation
A;Reference number: A90342
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Biochem. J. 49, 481-490, 1951
A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A92080
A,Molecule type: protein
A,Roblecule type: protein
A;Residues: 25-105 <NOL>
R;Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
J. Balol. Chem. 246, 1365-1374, 1374, 1374
A;Fitle: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A;Reference number: A92074; MUID:71116409
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A;Residues: 1-105 <DAA>
A;Residues: 1-105 <DAA>
A;Cross-references: GB:M54979; NID:g163578; PIDN:AAA30722.1; PID:g163579
A;Cross-references: GB:M54979; NID:g163579
A;Experimental source:
B;Nolan, C.; Margoliash, E.; Peterson, J.D.; Steiner, D.F.
J. Biol. Chem. 246, 2780-2795, 1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fj1-30,57-77/Product: insulin #status experimental <MAT>
Fj31-56/Domain: connecting peptide #status experimental <CIF;57-77/Domain: insulin chain A #status experimental <ACH>
F;77-63,19-76,62-67/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: hormone; pancreas F;1-30/Domain: insulin chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Œ,
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Eur. J. Biochem. 20, 183-189, 1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56.5; Pred. No. 10;
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Gaps

14;

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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A;Reference number: A71570; MUID:99000809
A;Reference number: B71476
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <ARN>
A;Cross-references: GB:AE001346; GB:AE001273; NID:93329203; PIDN:AAC68344.1; PID:9332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: D70505
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-495 <COL>
A;Cross-references: GB:Z98209; GB:AL123456; NID:93261838; PIDN:CAB10901.1; PID:e33228
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C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable Hflx - Mycobacterium tuberculosis (strain H37RV)
C;Species: Wycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
C;Accession: D70505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein alr1346 [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: alas
C;Superfamily: alanine--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 57.5; DB 2; Length 495; 43.3%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874 VQAHTLLAELLAPYGGRCGGKAISAQGSSAELPQIEFLNKTLRQWISTQ 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 58; DB 2; Length 924 llarity 30.6%; Pred. No. 60; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PTLRQW-----LAARAGGGGGGGIEGP 26
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Best Local Similarity 43.3%
Watches 13; Conservative
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es 15; Conserva
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A; Residues: 1-327 <KUR>
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Matches
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C;Decies: Trichoderma reesei
C;Decies: Trichoderma reesei
C;Decies: Trichoderma reesei
C;Decies: Trichoderma reesei
C;Decession: S71334
R;Margolles-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.
R;Margolles-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.
R;Margolles-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.
R;Title: Acctyl xylan esterase from Trichoderma reesei contains an active-site serine re
A;Reference number: S71334
M;Molecule type: MRNA
A;Residues: 1-302 < MAR>
A;Residues: 1-302 < MAR>
A;Residues: 1-302 < MAR>
A;Genetics:
C;Genetics: RBL: Z69256; NID: g1431619; PID: e220701; PID: g1431620
C;Genetics: A;Genetics: EMBL: Z69256; NID: g1431619; PID: e220701; PID: g1431620
C;Genetics: A;Genetics: B;Genetics: A;Genetics: A;Genetic
                                                                                                                                                                                                                                                 RESULT 7
B71325
conserved hypothetical protein TP0421 - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24 Jul-1998 #sequence_revision 24 Jul-1998 #text_change 05-Nov-1999
C; Accession: B71325
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDC
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID: 98332770
A; Accession: B71325
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-683 < COL>
A; Cross-references: GB: AEO01220; GB: AEO00520; NID: 93322705; PIDN: AAC65409.1; PID: 93322705
A; Genetics:
A; Genetics:
A; Genetics:
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alanine--tRNA ligase (EC 6.1.1.7) - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
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Pred. No. 36;
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               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl xylan esterase precursor - fungus (Trichoderma reesei)
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8
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           2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 35
                                                                                                                                4 PTLROW-----LAARAGGGCGGGGIEGP 26
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           Conservative
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Best Local Similarity
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           13;
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           Matches
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C; Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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                                                                 A;Cross-references: EMBL:278013; PIDN:CAB01420.1; GSPDB:GN00023; CESP:F15B9.5
A;Experimental source: clone F15B9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $72938
hflx protein - Mycobacterium leprae
N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL:U00019; NID:9467079; PIDN:AAA17274.1; PID:9467091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 518;
                                                                                                                                                                                                                                                                              Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                          A;Map position: 5
A;Introns: 46/3; 63/3; 125/2; 162/2; 283/3; 391/1; 446/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.5; DB 2;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-500 <WIL>
                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993 A; Description: Mycobacterium leprae cosmid B2235. A; Reference number: $72587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59.5;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 | | | | : | | | | 189 PRLRGWGESMSRQVGRAGGSGGVGLRGP 218
                                                                                                                                                                                                                                                                                   Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PTLRQW------LAARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                       429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                                                                                                                                                                                                                                                                                                                                      3 GPTLRQWLAARAGGGCGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%;
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                                                                                                                                                                                                                                                                                   30.5%;
52.2%;
                                                                                                                                                                                                                                                                                 Query Match 30.34
Best Local Similarity 52.28
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S72938
R; Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-518 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-488 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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                                                                                                                                                                              A; Gene: CESP: F15B9.5
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A; Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: ML0997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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                        C.Comment: This protein is a targed-derived, diffusible neurotrophic factor.

C.Comment: The neurotrophins stimulate autophosphorylation and transduce signals through
C.Comment: The neurotrophins stimulate autophosphorylation and transduce signals through
C.Superfamily: nerve growth factor beta chain
C.Keywords: glycoprotein
F.1-20/Domain: signal sequence #status predicted <SIG>
F.1-20/Domain: propeptide #status predicted <NIG>
F.80-209/Product: neurotrophin-5 #status predicted <NIG>
F.80-709/Product: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Dec-1993 #text_change 16-Jul-1999
C; Accession: A42687; JH0503
R; Ip, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L. Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A; Title: Mammalian neurotrophin 4: structure, chromosomal localization, tissue distribut A; Reference number: A42687; MUID:92212967
A; Accession: A42687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-210 <BER>
C;Comment: The neurotrophins stimulate autophosphorylation and transduce signals through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M86528; NID:g190264; PIDN:AAA60154.1; PID:g190265
A;Note: sequence extracted from NCBI backbone (NCBIN:93810, NCBIP:93811)
R;Berkemeier, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenthal, Neuron 7, 857-866, 1991
A;Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB. A;Reference number: JH0503; MUID:92075279
A;Accession: JH0503
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20961
  A;Cross-references: GB:S69323; NID:g240025; PIDN:AAB20548.1; PID:g240026 .
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F;1-54/Domain: propeptide #status predicted <PRO>
F;81-210/Product: neurotrophin-4 #status predicted <NEU>
F;76/Painding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 210;
                                                                                                                                                                                                                                                        Score 63.5; DB 2; Length 209;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                                                                                                                                                                                                                                                                                                                                                                            128 GSPLRQYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                    2; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQWL------AARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F15B9.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                        3 GPTLRQWL-----AARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1996
A; Reference number: 219351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.7%; Score 60.5; 35.0%; Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 19pter-19qter
C;Superfamily: nerve growth factor beta chain
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:134723; OMIM:162662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                      32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: neurotrophin-5
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotrophin-4 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-210 <IP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: NTF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps

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5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2002
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OM protein - protein search, using sw model

9, 2002, 08:54:17; Search time 8.09368 Seconds (without alignments) 427.397 Million cell updates/sec October Run on:

US-09-422-838C-31 197

Perfect score:

1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	probal	α		н		hflx protein - Myc		acetyl xylan ester	ď		cal p	homeotic protein H	insulin precursor		hypothetical prote	æ	Ω.	cal	4	1,4	٦		laccase (EC 1.10.3	hypothetical glyci	_	Lice	_		П
SUMMALES	αī	T34584	B42687	A42687	T20961	G87033	572938	B71325	571334	E71476	D70505	AG1974	S20880	INSH	IPBO	B72698	T12783	T33130	E86405	S41943	S44716	S41942	KSNCLO	KSNCLT	E70895	T49530	T49792	C84890	T26807	T26808
	DB		(7												•	~	•		7										7	
	Query Match Length		209	210	200	488	518	683	302	924	495	327	339	77	105	176	26	163	349	510	511	540	619	619	767	180	201	257	331	333
æ	Query	34.0	32.2	30.7	30.5	30.2	30.2	σ	σ	σ	σ	28.9	₩.	28.7	28.7	28.7	28.4	œ	28.4	28.4	æ	28.4	28.4	28.4	28.4	27.9	27.9	27.9	27.9	27.9
	Score	9	63.5	ö	09	59.5	œ.	53	28	ഗ	57.5	57	in	56.5			26	26	26	26	26	26	26	26	26	52	52	55	52	55
	Result No.	1	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A; Status: preliminary

A; Molecule type: mRNA A; Residues: 1-176,'P',178-209 <BER1>

A;Molecule type: DNA A;Residues: 1-209 <BER> A;Accession: JH0505

C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R;IP, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A;Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distrinance number: A42687; MUID:92212967
A;Accession: B42687

neurotrophin-4 precursor - rat

RESULT 2

hypothetical prote	MYB transcription	numb protein - fru	alanyl-tRNA synthe	probable lsr2 prot	dnaK-type molecula	U1-snRNP binding p	DNA-binding protei	ovo protein - frui	hypothetical 20.2K	transcription fact	phosphatidylinosit	probable amidase -	coenzyme F420 hydr	potassium channel	3-deoxy-D-manno-oc
T20268	T47712	A32466	H81739	F70954	A54507	G02371	A56038	S16356	JQ1094	A49447	T09084	E70948	F64408	T13807	E87286
7	~	7	7	7	7	7	7	7	7	П	7	7	7	~	7
393	399	556	875	112	198	246	1028	1213	201	445	490	495	620	1001	416
6.	6.	6.	6.	۲.	٠.	۲.	۲.	. 7	4.	7.	₹.	4.	₹.	7.	7
27.9	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
25	22	22	52	54.5	54.5	54.5	54.5	54.5	54	54	54	54	54	54	53.5
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ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-865 <MORS>
A; Cross-references: EMBL:AL021529; PIDN:CAA16449.1; GSPDB:GN00070; SCOEDB:SC10A5.17
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC10A5.17
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probable secreted proteinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                             C; Accession: T34584
R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1998
A; Reference number: 221548
A; Accession: T34584
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%; Score 67; DB 2; Length 865; 66.7%; Pred. No. 5.9; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    651 WLAACAAGNCGGGGTNPP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 WLAARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.0°
Best Local Similarity 66.7°
Matches 12; Conservative
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.1%; Score 73; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 14; Conservative 0; Mismatches 0; Indels
                                 37.1%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                       NEGAL INFORMATION:
APPLICANT: Dower, William J.
CWILTA Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                     100.0%; Pred. ...
1... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK3281 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 9, 2002, 09:06:34 Job time : 6.98595 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                             Sequence 194, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IEGPTLRQWLAARA 15
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                                                                                                                            1 IEGPTLROWLAARA 14
                                                                                                                                                       COUNTRY: USA
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                                                                Best Local Similarity
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US-09-516-704-18
                                              Query Match
                                                                                      Matches
                                                                                                                                                                                                                                          RESULT 30
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                                                                                                                                     δλ
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Hendren, Richard W.
Deprince, Randh B.
Podduturi, Surekha
FOGGULURI, SUREKHA
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                  37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/516,704
FILING DATE: 01 Mar - 2000
CLASSIFICATION: «Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
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NAME: Hrubiec, Robert T.
REGISTRATION UNDRER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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ADDRESSEE: Glaxo Wellcome
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               REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J. Barrett, Ronald W. Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
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                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                            LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-232
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                                                                                                                                                amino acid
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                                                                                                                                                                  STRANDEDNESS:
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US-09-244-298A-232
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APPLICANT:
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APPLICANT:
COUNTRY:
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APPLICANT:
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       APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: H-ubiec, Robert T.
RESISTRATION NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                      STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: 15 COTHER INFORMATION: /product= "Beta-ala" US-09-244-298A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Podduturi, Surekha
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Podduturi, Surekha
                                                                                                        Glaxo Wellcome
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LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wel
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                             STATE:
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ZIF: 27709

ZIF: 27709

COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRETWARET APPLICATION DATA:
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Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Peprince, Randolph B.
                                                                                                                 11-DEC-1996
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                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REPRENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
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STREET: Five Moore Drive, P.
CIIY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-09-244-298A-194
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ADDRESSEE: Glaxo Wel
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                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                        FILING DATE: 11 CLASSIFICATION:
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us-09-422-838c-31.rai

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Matches
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                 37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.016; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 16;
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COMPUTER: IBM PC Compatible
SERVING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                     OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.1%; Score 73; DB 3;
100.0%; Pred. No. 0.016;
tive 0; Mismatches 0
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APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY AGENT INFORMATION:

NAME: HICUDIC, RODERT T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET WINBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               Sequence 194, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWILLA, Steven E.
Duffin, David J.
Gates, Christian
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Mattheakis, Larry C.
Schatz, Peter J.
                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
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                                                                                                                                                     Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                   1 IEGPTLROWLAARA 14
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                NAME/KEY:
                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF
                                                                                                                                                                                                                                                                                                                               US-08-973-225-194
FEATURE:
                                                                                              US-08-973-225-18
                                                                                                                                     Query Match
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Gaps
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                              THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirls, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balsaubramnian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-973-225-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                    ; Sequence 220, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                                                   Haselden, Sherril S.
                                                                                                                                                                                                                                        Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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                                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 220: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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ZIP: 27709
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US-08-973-225-220
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APPLICATION NUMBER: US/08/764,640
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Waddren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.1%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                  ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: HTUDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK32E
TELECHMUNICATION INFORMATION:
TELEPHONE: 919-248-100.
INFORMATION FOR SEQ ID NO: 194:
                                                          Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IEGPTLROWLAARA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                     USA
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APPLICANT:
                                                                                                     COUNTRY:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                               Length 16;
                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 37.1%; Score 73; DB 2; Length 16; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSES: Glazow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION: INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagstrom, Christopher R.
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Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 18, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                               NAME: Hrubiec, Robert I
REGISTRATION UNDRER: 36,392
REPERENCE/DOCKET UNDRER:
FELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18:
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11-DEC-1996
N: 514
                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                           16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                              amino acid
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FILING DATE: 11 CLASSIFICATION:
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US-08-973-225-18
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PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR 244
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764.640
                                                                                                                                                                                                     E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: /product= "Beta-ala" US-08-764-640-18
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APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W. APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha
                 Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 194, Application US/08764640
Patent No. 5869451
Patent No. 5869451
GENERAL INFORMATION:
                                                         Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                               Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PX.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
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                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARA 14
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11 CLASSIFICATION:
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US-08-764-640-194
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                                                                                                                                                                                                       ADDRESSEE:
                                                         APPLICANT:
APPLICANT:
APPLICANT:
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                                        APPLICANT:
                     APPLICANT:
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                                                                                                                                                                                                                                                                                                             Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSES: Glaxow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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*ive 0; Mismatches
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Balasubramanian, Palaniappan
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08764640 Patent No. 5869451 Patent No. 5869451
                                                                                                      ; Sequence 185, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                  APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schatz, Peter J.
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 14; Conservative
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        1 IEGPTLROWLAARA 14
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Best Local Similarity
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                                                                                     US-09-516-704-185
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US-08-764-640-18
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APPLICANT:
APPLICANT:
                                                                    RESULT 19
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Podduturi, Sureskha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.1%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                          Query Match 37.1%; Score 73; DB 3; Length 15; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <u >Unknown></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,392
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCES: 244
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Best Local Similarity 100.
Matches 14; Conservative
                       15 amino acids
SEQUENCE CHARACTERISTICS:
                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-244-298A-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARA 14
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ZIP: 27709
                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NC
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US-09-516-704-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                      OPERATING SYSTEM: C-DOS/MS-DOS
SOFTWARE PETCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDICC, ROBERT T.
REGISTRICATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 9K3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,392
          IBM PC compatible
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NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                OPERATING SYSTEM:
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APPLICANT:
            COMPUTER:
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APPLICANT:
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us-09-422-838c-31.rai

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Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                      SEQUENCES: 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.1'
Best Local Similarity 100.
Matches 14; Conservative
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COMPUTER READABLE FORM:
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ZIP: 27709
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APPLICANT:
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                                                                                                                                                                                                                                         Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSES: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PR3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-973-225-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 185, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWITIA, Steven E.
Duffin, David J.
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                            APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
              Sequence 17, Application US/08973225A Sequent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-973-225-185
US-08-973-225-17
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Wagstrom, Christopher R. Wrighton, Nicholas C. TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                        STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DUMBER: US/08/973,225A
ATTORNEY/AGENT INFORMATION:
NAME: HINDIGG, RODERT T
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELEPHONE: PS-21000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yin, Qun TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                        THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Five Moore Drive, P.O. Box 13398
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APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                         CITY: Research Triangle Park
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; Patent No. 6121238
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Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Triangle Park
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Gaps

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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
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                                                                                               37.1%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schatz, Peter J.
APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
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; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,392
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Garla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glaxo Wellcome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hrubiec, Robert T
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 15 amino acids
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Matches 14; Conservative
                                                                                                           Query Match
Best Local Similarity 100.C
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IEGPTLRQWLAARA 15
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                                 TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                    Yin, Qun
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TYPE: amino acid
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           STRANDEDNESS:
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                   ; STRANDEDNES;
; TOPOLOGY:
; MOLECULE TYPI
US-08-764-640-17
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APPLICANT:
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                                                                                                                                                                                                                                                                           RESULT 13
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                          37.1%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764.640
                                                         ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 98,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SED ID NO: 193:
SEQUENCE CHARACTERISTICS:
         APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz, Peter J.
Balasubramanian, Palaniappan
Magstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-1996
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                             FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 17, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                  LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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COUNTRY:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                        APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.1%; Score 73; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERRNCE/DOCKET NUMBER: PR3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: CWITLA, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                     Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                   Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match . 37.1%; Score 73; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: HTUDLEC, Robert T.
REGISTRATION NUMBER: 96,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 193, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids
NUMBER OF SEQUENCES: 244
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                                                                                                                                                       ZIP: 27709
                                                                                                             STATE: NC
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ZIP: 27709
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                                                                                                                                    COUNTRY:
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27709
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US-08-973-225-193
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APPLICANT:
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APPLICANT:
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                                     Query Match
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                                                                                                                                                                                                                                                                                                                               Length 14;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 0.014;
tive 0; Mismatches 0
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APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
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                     ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research Triangle Park
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 193, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 amino acids
       FILING DATE: 04-Dec-1997
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
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COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
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Best Local Similarity 100.0
Matches 14; Conservative
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US-08-973-225-193
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
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37.1%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      ; Sequence 13, Application US/09244298A ; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Five Moore Drive, P.C
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                    Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36, 3
REFERENCE/DOCKET NUMBER:
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Best Local Similarity 100.
Matches 14; Conservative
                             Best Local Similarity 100.
Matches 14; Conservative
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APPLICANT: DOWER,
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                   ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                  Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                          Wagstrom, Christopher R.
Hendren, Richard W.
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                             Deprince, Randolph B. Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                      Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING EVENEY.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION POR SEQ ID NO: 13:
Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hrublec, Robert T.
REGISTRATION NUMBER: 36,392
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Cwirla, Steven E.
Gates, Christian
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APPLICANT: Dower, William J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 14; Conservative
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MEDIUM TYPE: Floppy of
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
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US-08-764-640-193
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APPLICANT:
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APPLICANT:
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                                                                    APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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-...DER: US/08/764,640
11-DEC-1996
7N: 514
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                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
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Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                          Research Triangle Park
                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: peptide US-08-764-640-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARA 14
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                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                          FILING DATE: 11 CLASSIFICATION:
                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                   27709
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                                                                                                                                                                                                                                SOFTWARE:
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US-08-973-225-13
                                                                                                                   COUNTRY:
                                                                                              STATE:
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APPLICATION NUMBER: US/08/973,225A

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RESULT 3
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                                                                                                                              Gaps
                                                                                     38.8%; Score 76.5; DB 2; Length 25; 40.6%; Pred. No. 0.0098; tive 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ch 38.8%; Score 76.5; DB 3; Length 25; l Similarity 40.6%; Pred. No. 0.0098; l3; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Five Moore Drive, P.O. Box 13398
Research Triangle Park
                                                                                                                                                        2 EGPTLRQWLAARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                            2 DGPTLREWISFXA-----DGPTLREWIS 24
                                                                                                                                                                                                                                                                                                                                                                                                         Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
TORNEY APPENDED
                               OTHER INFORMATION: /product= "Ava"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : LOCATION: 13
; OTHER INFORMATION: /product= "Ava"
US-09-244-298A-231
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                              Sequence 231, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PK3281
                                                                                                                                                                                                                                                                                                                                  Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glaxo Wellcome
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Modified-site
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REGISTRATION NUMBER: 36
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                                                                                                                      Conservative
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CORRESPONDENCE ADDRESS:
                                                                Query Match
Best Local Similarity
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Best Local Similarity
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                                   ; OTHER INFORUS-08-764-640-231
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NAME/KEY:
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                LOCATION:
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APPLICANT:
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Gaps

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2 EGPTLRQWLAARAGGGCGGGGGEGPTLRQWLA 33

Matches

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Gaps
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%; Score 76.5; DB 4; Length 25; 40.6%; Pred. No. 0.0098; Live 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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0.0098;
2;
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                                                                                                                                                                Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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                                                                                                                                                                                                       Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                              Research Triangle Park
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                   ; Sequence 231, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                       STREET: Five Moore Drive,
                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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; Patent No. 5869451
; Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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Best Local Similarity 40.69
Watches 13; Conservative
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US-09-516-704-231
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US-08-764-640-231
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                      October 9, 2002, 08:55:27; Search time 5.98595 Seconds (without alignments) 146.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 18, Sequence 194,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-973-225-185
US-09-244-298A-17
US-09-244-298A-185
US-09-516-704-18
US-09-516-40-18
US-08-764-640-194
US-08-764-640-194
US-08-764-640-194
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US-08-973-225-194
US-08-973-225-120
US-09-244-298A-18
US-09-244-298A-194
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US-08-764-640-17
US-08-764-640-185
US-08-973-225-17
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US-09-244-298A-193
US-09-516-704-13
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                                                                                                                                                                                                                                                                                                                 231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                                                                                           US-09-422-838C-31
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Match Length DB
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                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                  Sequence:
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                                                                                                                       Run on:
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Sequence 195,
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Sequence 200,
Sequence 209,
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Sequence 196,
Sequence 200,
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
        US-09-516-704-18
US-09-516-704-194
US-09-516-704-194
US-08-764-640-195
US-08-773-225-195
US-08-973-225-199
US-08-973-225-199
US-09-244-298A-195
US-09-516-704-199
US-09-516-704-199
US-09-516-704-199
US-08-764-640-209
US-08-764-640-209
US-08-764-640-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Five Moore Drive, P.O. Box 13398
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US,08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PK3281
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 231, Application US/08764640 Patent No. 5869451 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: DOWEr,
337.1
337.1
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The present invention describes composition of matter (I) comprising an (XI)a-FI-(X2)b, where FI = an FC domain; XI and X2 = are each independently selected from -(LI)c-PI-(LI)c-PI-(LI)d-P2.

(LI)c-PI-(LI)d-P2-(LI)e-P2, or -(LI)c-PI-(LI)d-P2-(LI)e-P3-(L4)f-P4 where PI, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities: DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TRF: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytocoxic T cell lymphocyte antigen 4; tumour neorosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                      1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 320-321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                          AAB17299 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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                                                                                                                                                                                            31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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1 IEGPTLRQCLAARAGGGGGGGGGFEGPTLRQCLAARA 36
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Job time : 17.1874 secs

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80.7%; Score 159; DB 21; Length 36; 91.7%; Pred. No. 6.1e-12; Live 0; Mismatches 3; Indels 1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36

33; Conservative

Matches

Query Match Best Local Similarity

0; Gaps

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The present invention describes composition of matter (I) comprising an Fr domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a=F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)C-P1-(L2)d-P2.

(L0)c-P1-(L2)d-P2-(L3)d-P3, or -(L1)C-P1-(L2)d-P2-(L3)d-P3-(L3)d-P3-(L4)f-P4 are each independently sequences of the peptides: L1, L2, L3, and L4 = are each independently active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and host cells from the present invention can carriage of a producing pharmaceutical compositions. The compositions are be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein composition composition composition complement fixation, and possibly placental transfer. AAA69443 complement seemplification of the present invention.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autolmmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                         2;
86.8%; Score 171; DB 21; Length 34; 94.4%; Pred. No. 2.3e-13; ive 0; Mismatches 0; Indels
                                                                                                                                                  1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                AAB17290 standard; Peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                       Query Match
Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                      RESULT 28
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83.5%; Score 164.5; DB 21; Length 33;

Query Match

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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

EC (XI)a-FI-(X2)b, where: FI = an FC domain; XI and X2 = are each independently selected from -(L1)C-PI-(L2)d-P2.

Independently Selected from -(L1)C-PI-(L2)d-P2-(L3)d-P2.

CC (L1)C-PI-(L2)d-P2-(L3)d-P3, or -(L1)C-PI-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently interestive antiasthmatic, thrombolytic and immunosuppressive continuities. DNAS, vectors and host cells from the present invention can extivities DNAS, vectors and host cells from the present invention can cell for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions, or autoimmune diseases.

CC be used for producing pharmaceutical compositions are used in FC domain (rather than a Fab domain) can provide a longer to Alf-life or incorporate functions such as FC receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443

CC sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; LL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.7%; Score 159; DB 21;
91.7%; Pred. No. 6.1e-12;
Live 0; Mismatches 3;
91.7%; Pred. No. 1.3e-12;
ive 0; Mismatches 0;
                                                        1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                             TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                            AAB17298 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                        Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                              Matches
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Sequence
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(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1-(L2)d-P2.

(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of parmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b 1s1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein and particles and Amble955 and Amble955 and Amble955 and Amble955 and Amble955 and pacental transfer. Amade9443 sequences used in the exemplification of the present invention.
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiathmatic; thrombolytic; VEGF; immunosuppresalve; EPO; TPO; CTLA4; mimetic; IL-1; TPF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour neorosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                               3;
                                                                                                        DB 21; Length 39;
                                                                                                                                               Indels
                                                                                                 Score 173.5; DB 21;
Pred. No. 1.3e-13;
0; Mismatches 1;
                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGKPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                      1 IEGPTLRQWLAARAGGG----CGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boone IC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                   AAB17296 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feige U, Liu C, Cheetham J,
                                                                                                        88.18;
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                                                                                                                         Local Similarity 89.7 nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                              39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                            AAB17296;
                                                                   Sequence
                                                                                                          Query Match
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                              RESULT 26
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The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L3)e-P3. (L4)e-P2-(L3)e-P3. (L4)e-P2-(L3)e-P3. (L4)e-P2-(L3)e-P3. (L4)e-P3. (L4)e-P3. (L4)e-P3. (L4)e-P3. (L4)e-P4. (L5)e-P4. (L5)e-P3. (L4)e-P3. (L4)e-P4. (L5)e-P4. (L5)e-P3. (L4)e-P4. (L5)e-P4. (L5
                                                                                                                                                                                          ï
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                          ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                             Score 172; DB 21; Length 42;
Pred. No. 2.1e-13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARA-----GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17291 standard; Peptide; 34 AA
                                                                                             87.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first.entry)
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
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                                                                                             Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17291;
     Sequence
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34 AA;

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8888888888

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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2, (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L3)d-P3, or -(L3)e-P3, or 
useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB18035 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; exythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.6%; Score 174.5; DB 21
94.6%; Pred. No. 9.6e-14;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARA-GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLROWLAARAGGGGGGGGGGTEGPTLROWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 319; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17295 standard; Peptide; 38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases
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Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                     37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-P1 -(L2)C-P2-(L3)-P2.

(L1)C-P1-(L2)d-P2.

(L1)C-P1-(L2)d-P2.

(L2)d-P2.

(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently inkers; and a, b, c, d, e, and f = are each independently inkers; and a, b, c, d, e, and f = are each independently have explosible that at least 1 of a and b is 1. The composition can have explosible triasthmatic, thrombolytic and immunosuppressive cutivities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are used for producing cancer, asthma, thrombosis, or autoimmune diseases.

The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443
                                                                                                                                                                                              ή:
half-life or incorporate functions such as Fc receptor binding, protein
                     A binding, complement fixation, and possibly placental transfer. AAA69442 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; AMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytocxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                              2;
                                                                                                                                                    Length 38;
                                                                                                                                                                                              Indels
                                                                                                                                                    88.3%; Score 174; DB 21; 92.1%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                         1 IEGPTLRQWLAARA--GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGGGGGGGGGIEGPTLRQWLAARA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                          AAB17304 standard; Peptide; 39 AA.
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                                                                                                                                                                          92.1%;
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000 (first entry)
                                                                                                                                                                                                    35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                              Best Local Similarity
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                                                                                                                 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17304;
                                                                                                                   Seguence
                                                                                                                                                           Ouery Match
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                RESULT 25
                                                                                                                                                                                                                                                                                                                                                                        AAB17304
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or E; \chi_{-9} = W, Y or E; \chi_{-1} = L, I, \dot{V}, \dot{A}, \dot{F}, \dot{M}, or K; \chi_{-1} = A, I, \dot{V}, \dot{K}, \dot{K}, \dot{M}, or \dot{M}, \dot{M}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an (X1)a-F1-(X2)b, where F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2.
-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; fumuosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       90.9%; Score 179; DB 21; Length 36; 94.4%; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 317-318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17292 standard; Peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 94.49 nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                          36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17292;
                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 22
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             8555555555<del>x</del>8
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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, (L3)e-P2, (L4)e-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptidess: L1, L2, L3, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently independently at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; vyctocxaic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                / Match 90.1%; Score 177.5; DB 21; Length 35; Local Similarity 97.2%; Pred. No. 4.1e-14;
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                      Pred. No. 4.1e-14;
                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17294 standard; Peptide; 37 AA.
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                                                                                                                                                                                                                                                                            35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases -
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                                                                                                                                                                                          35 AA;
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17294;
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                          91.9%; Score 181; DB 21; Length 268; 97.1%; Pred. No. 1.2e-13; Live 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                  134 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAAR 268
                                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17306 standard; Peptide; 36 AA
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.1
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                        268 AA;
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                                                                                                                                                                                                                                                                          Sequence
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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                    90.9%; Score 179; DB 21; Length 36; 94.4%; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGNGSGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin mimetic peptide compound 7.
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/label= linker
19..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= TMP_1
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/label= TMP_2
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                                                                                                                                                                                                                                                                                                               Query Match 90.99
Best Local Similarity 94.43
Matches 34; Conservative
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                                                                                                                                                                                                                                                             36 AA;
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                                                                                                                                                                                                                                                                   Sednence
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Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain: X1 and X2 = are each independently selected from -(L1)c-P1, (L1)c-P1-(L2)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P2, (L3)d-P3, or (L1)c-P1-(L2)d-P2-(L3)d-P3, or (L1)c-P1-(L2)d-P2-(L3)d-P3, or (L3)d-P3, or (L3)d-
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin; IgGl; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ō
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.98; Score 185; DB 21; Length 269; 97.28; Pred. No. 4.1e-14; Live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2A; Page 49-50; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96531 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human IgGl Fc TMP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 97.28
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365108/31.
N-PSDB; AAA29229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY9653.
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from (Li)c-P1, -(Li)c-P1-(L2)d-P2, (L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                              ..
                                                                                                                                                                                 93.9%; Score 185; DB 21; Length 269; 97.2%; Pred. No. 4.1e-14;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                         234 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 269
                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 182-183; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                          AAB16959 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                              35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases
                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                       Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                      AAB16959;
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                              RESULT 19
AAB16959
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                                                                                                                                                                       for increasing the production of platelets or platelet megakaryocytes) in a mammal, which is useful for
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                    precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; YRF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic TMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                                                                          Score 185; DB 21; Length 42;
Pred. No. 6.5e-15;
                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                          7 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 42
                                                                                                                                                                                                                                                                                                                            1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                          93.9%; Score 185; 97.2%; Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 331; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB17311 standard; Peptide; 60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                          Query Match 93.9
Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                  42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17311;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
AAB17311
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                                                                                                                                                                                                                                                                                                                                  useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (Xl)a-F1-(X2)b, where: F1 = an Fc domain; Xl and X2 = are each independently selected from -(L1)c-P1-(L1)d-P2-(L3)d-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-(L3)q-P2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.9%; Score 185; DB 21; Length 60; 97.2%; Pred. No. 9.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IEGPTLRQWLAARAGGGGGGGGGEGFTLRQWLAARA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMP-TMP-Fc protein sequence SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 185-186; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB16960 standard; Protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA69446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB16960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16960
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AAA69443
                                                                                          The present invention describes composition of matter (1) comprising an (X1)a-F1-(X2)b, where F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-F^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-F^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-F^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently necessaries or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                     useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.9%; Score 185; DB 21; Length 42; 97.2%; Pred. No. 6.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic TMP-TMP gene construction peptide SEQ ID NO:374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
                                                    Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17308 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J,
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 97.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
                     autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17308;
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binding, protein
transfer, AAA69443
                                                                                                                                    Fc domain, pharmacologically active peptides, and linkers. Where [1] is: (K1)a-r1-(K2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L3)d-P2, -(L3)d-P3, -(L3)d-P2, -(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A binding, complement fixation, and possibly placental transfer. AAA69445 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; 1961; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                            The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overlapping oligonucleotides were used to construct a synthetic gene encoding a thrombopoietin mimetic peptide (TMP), which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 185; DB 21;
Pred. No. 6.5e-15;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IEGPTLRQWLAARAGGGGGGGGGTEGPTLRQWLAARA 42
                                                         Example 2; Page 327; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2A; Page 48; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96530 standard; Protein; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 97.2
Matches 35; Conservative
autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA29225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                             A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP] (L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 \cdot X_1 = 0, X_2 \cdot X_1 = 0, X_1 \cdot X_1
                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MNP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 185; DB 21;
Pred. No. 6.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17281 standard; Peptide; 42 AA.
                                                                                                                                                                           Claim 16; Page 65; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%;
97.2%;
Feige U, Cheetham J;
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99US-0428082
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                                          WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17281;
    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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Ec domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)=T-(XZD), where: FI = an FC domain; XI and X2 = are each

(XI)=T-(XZD), where: FI = an FC domain; XI and X2 = are each

(C) independently selected from -(LI)-FI - (LI)-FPI-(LZD)-FP.

(C) redependently selected from -(LI)-FI - (LI)-FPI-(LZD)-FP.

(C) pharmacologically active peptides; LI, L2, L3, and L4 = are each

(C) pharmacologically active peptides; LI, L2, L3, and L4 = are each

(C) cor I, provided that at least I of a and b is I. The composition can

(C) or I, provided that at least I of a and b is I. The composition can

(C) cor i, provided that at least I of a cor and immosuppressive

(C) or I, provided that at least I of a cor and invention can

(C) cor i, provided that at least I of a cor and invention can

(C) cor i, provided that at least I of a cor and invention can

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(C) cor i, provided that at least I of a cor and invention can

(C) cor i, provided that at least I of a cor and invention can

(C) cor i, provided that at least I of a cor and invention can

(C) cor i, corporate functions such as FC receptor binding, protein

(C) The use of an FC domain (rather than a Fab domain) can provide a longer

(C) C) cor incorporate functions such as FC receptor binding, protein

(C) Abinding, complement fixation, and possibly placental transfer. AbA69443

(C) sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease, cytostatic, antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoiethin; thrombopoiethin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%; Score 185; DB 21; Length 42; 97.2%; Pred. No. 6.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IEGPILROWLAARAGGGGGGGGGEGPTLROWLAARA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO-mimetic peptide sequence SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC;
                                                                                                                                                                    Disclosure; Page 313; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17282 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044.
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99US-0428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                          autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
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Local Sim
35;
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                                                                                                                                                                               A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TWP) dimer joined by a linker [TWP_1-(L_1)_DTWP_2], is new. TWP_1 and TWP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2 - x_{-1} - 0, x_2 - x_{-1} - 1, x_3 - x_3 - x_3 - 1, or E; x_2 - x_3 - 
                                                                                                                                                                                                                                                                                                                                                                                                                                    platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                     Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TRN: antagonist; MMP; inhibitor; erythropiciein; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.9%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 5.6e-15; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGGGGGGGGGFTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17302 standard; Peptide; 40 AA.
                                                                                                                                                   Claim 16; Page 62; 91pp; English.
Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
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                                    WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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The present invention describes composition of matter (I) comprising an (X1) a F1-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from (L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2, (L1)c-P1-(L2)d-P2, (L2)d-P2, (L3)c-P3, or (L1)c-P1-(L2)d-P2-(L3)e-P3, or (L1)c-P1-(L2)d-P2-(L3)e-P3, ord P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fe domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fe receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69442 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 185; DB 21; Length 40;
Pred. No. 6.2e-15;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGG----CGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin mimetic peptide compound 9.
                                                                                                                            Example 1; Page 322; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96528 standard; peptide; 41 AA.
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/label= linker
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90.0%;
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/label= TMP 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US24834.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Conservative
                                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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The present invention describes composition of matter (I) comprising an Cr domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-F1. (L1)c-F1-(L2)d-F2.

(L1)c-F1-(L2)d-F2.

(L3)d-F2. F3, and P4 = are each independently sequences of where P1, P2. P3, and P4 = are each independently active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and bass 1 of a and b is 1. The composition can carriage expressive and sequences of corrections of the compositions are cactivities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC be used for producing pharmaceutical compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC half-life or incorporate functions such as Fc receptor binding, protein and possibly placental transfer. AAA69443

CC sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "optionally modified by bromoacetyl or PEG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                         93.9%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 5.6e-15; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGCGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin mimetic peptide compound 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96523 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5..22
label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.9%
Best Local Similarity 97.2%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365108/31.
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                                                                                                                                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                     Query Match 93.9%; Score 185; DB 21; Length 36; Best Local Similarity 97.2%; Pred. No. 5.6e-15; Matches 35; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                  Thrombopoietin mimetic peptide compound 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     AAY96525 standard; peptide; 36 AA.
                                      Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= TMP_1
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                                                                                                                                                                                                                                                                                                                                                      04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                            36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                       AAY96525;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                       RESULT 9
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The present invention describes composition of matter (1) comprising an (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(11)c-P1, -(12)d-P2-(13)d-P2-(13)e-P3-(14)f-P4 (11)c-P1-(12)d-P2-(13)e-P3-(14)f-P4 (11)c-P1-(12)d-P2-(13)e-P3-(14)f-P4 (14)f-P4-(12)d-P2-(13)e-P3-(14)f-P4 (14)f-P4-(12)d-P2-(13)e-P3-(14)f-P4 (14)f-P4-(12)d-P3-(14)f-P4-(12)d-P3-(14)f-P4-(12)d-P3-(14)f-P4-(12)d-P3-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4-(14)f-P4
                                                                                                                                            present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNR: antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%; Score 185; DB 21; Length 36; 97.2%; Pred. No. 5.6e-15; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLROWLAARAGGGGGGGGGGTEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:349.
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                                                                                  Disclosure; Page 190; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17293 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US25044.
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA69526 and AAB18055 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; evythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                            Score 185; DB 21; Length 36;
Pred. No. 5.6e-15;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLROWLAARAGGGGGGGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:357.
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC;
            Example 1; Page 318; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17301 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                              Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                           93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                                                                                                                   Seguence
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                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                       Matches
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RESULT 5
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                                 production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                     0; Gaps
                           Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive: EPO: TPO: CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour neorosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                        100.0%; Score 197; DB 21; Length 36; 100.0%; Pred. No. 2.2e-16; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGGGGGGGGFEGPTLRQWLAARA 36
                                                                                                                                                                                                                                    1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feige U, Liu C, Cheetham J, Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                 asthma; thrombosis; pharmaceutical.
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                                                       Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                   AAB17305 standard; Peptide; 39
  Cheetham J;
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                                                                                                                                                                                                                       36; Conservative
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               WPI; 2000-365108/31.
                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                             36 AA;
  Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                           WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         04 - MAY - 2000
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                AAB17305;
                                                                                                                                                                                                           Query Match
  Liu C,
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                      RESULT 4
                                                                                                                                                                                                                                                                             AAB17305
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                                                                                                                                                                                                                                                   d
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the present invention describes composition of macter (1) compared to the present invention describes compositions, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 (L3)d-P2-(L3)e-P3-(L4)f-P4 (L3)d-P3-(L4)f-P4 (L3)d-P3-(L4)d-P3-(L3)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(L4)d-P3-(
                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease, cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGGC---GGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | IEGPTLRQWLAARAGGGCPEGGGGGIEGPTLRQWLAARA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide TMP-TMP SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boone TC;
                                                                                                                                                                                                  Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16963 standard; Protein; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0105371.
99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 92.3
Matches 36; Conservative
                                                                                                           autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB16963;
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ij

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Fe domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fe domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
the pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
to or 1, provided that at least 1 of a and b is 1. The composition can
have eytostatic, antiasthmatic, thrombolytic and immunosupressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fe domain (rather than a Feb domain) can provide a longer
half-life or incorporate functions such as Fe receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
centuances used in the evamalification effective and amino acid
                                                                                                                                The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive: EPO; TPO; CTLA4: mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 197; DB 21;
Pred. No. 2.2e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGCGGGGTEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Cheetham J, Boone TC;
                                                                                            Example 1; Page 322; 608pp; English.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044
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                                                        autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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Novel composition of matter comprising an Fc domain and

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C domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3-(L4)f-P4

(L1)c-P1-(L2)d-P2-(L3)e-P3-yr -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
independently linkers; and a, b, c, d, e, and f = are each independently
c) or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiathmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443

to AAA69526 and AAB16955 to AAB18013 represent unvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                    The present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 197; DB 21;
100.0%; Pred. No. 2.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin mimetic peptide compound 5.
                                                Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96524 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9..31
/note= "optional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15..22
/label= linker
23..36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..14
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US24834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0105348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0
Best Local Similarity 100.0
Matches 36; Conservative
                  autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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δλ
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein – protein search, using sw model

October 9, 2002, 08:50:51; Search time 16.1874 Seconds (without alignments) 247.023 Million cell updates/sec Run on:

US-09-422-838C-31 Perfect score: Title:

1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAARA 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

A_Geneseq_032802:* Database :

. , subal, yequata, noturgeneseqp = embl, AAL1981. Jupit: *
. , SIDS1/gcgdata/hold geneseqy geneseqp = embl, AAL1981. DAT: *
. , SIDS1/gcgdata/hold geneseqy geneseqp = embl, AAL1981. DAT: *
. , SIDS1/gcgdata/hold geneseqy = embl, AAL1981. DAT: *
. , SIDS1/gcgdata/hold geneseqy = embl, AAL1981. DAT: *
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. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1981. DAT: *
. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: *
. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: *
. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: *
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. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: *
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. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: *
. , SIDS1/gcgdata/hold -geneseqy/geneseqp = embl, AAL1991. DAT: * /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TPO-mimetic peptid	TPO-mimetic peptid	Thrombopoietin mim	TPO-mimetic peptid	TPO-mimetic peptid	TPO-mimetic peptid	TPO-mimetic peptid	Thrombopoietin mim	Thrombopoietin mim	TPO-mimetic peptid	Thrombopoietin mim
	QI	AAB17303	AAB17307	AAY96524	AAB17305	AAB16963	AAB17293	AAB17301	AAY96523	AAY96525	AAB17302	AAY96528
		21	21	21	21	21	21	21	21	21	21	21
	Query Match Length DB	36	36	36	39	36	36	36	36	36	40	41
P	Query Match	100.0	100.0	100.0	94.2	93.8	93.9	93.9	93.9	93.9	93.9	93.9
	Score	197	197	197	185.5	185	185	185	185	185	185	185
	Result No.	н	7	٣	4	S	9	7	00	6	10	11

OOE OF	لد بي يو			TPO-mimetic peptid TPO-mimetic peptid TPO-mimetic peptid Thrombopoletin mim Thrombopoletin mim TPO-mimetic peptid
AAB17281 AAB17282 AAB17308 AAY96530 AAB17311 AAB16960				AAB17288 AAB17287 AAS17297 AAY96520 AAB17286 AAB17286 AAB16970 AAB16973 AAB16973 AAB16974
			212212212212212212212212212212212212212	
44446 24446 2000	269 269 36 36 36	37 38 39 34	33333333333333333333333333333333333333	31 32 32 33 33 34 34 31 31 31 31
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		88.6 88.3 88.1 87.3 86.8	83.5 80.7 80.7 80.7 80.2 79.7	76.9 73.1 73.1 73.1 73.1 70.3 67.0 66.8 65.7
185 185 185 185 185	185 181 179 179	174.5 174 173.5 172 172	വവവവവ	151.5 145 144 144 138.5 132.5 129.5 129.5 125.5
12 13 14 15 16	118 20 22 22	23 24 25 27	9 9 9 9 9 9 8 9 8 9 9 9 9 9 9 9 9 9 9 9	2 8 8 8 8 8 9 9 8 9 8 9 9 9 9 9 9 9 9 9

ALIGNMENTS

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotxxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothella1 growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. TPO-mimetic peptide sequence SEQ ID NO:359. AAB17303 standard; Peptide; 36 AA. 31-OCT-2000 (first entry) Synthetic. AAB17303; RESULT 1 AAB17303

WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999; 98US-0105371. 99US-0428082. 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

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0;
 0;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-BRAIN;
MEDLINE-98403880; PubMed=9734811;
MEDLINE-98403880; PubMed=9734811;
Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
EMBL: AB014600; BAA31675.1;
-InterPro; IPR003822; PAH.
Pfam: PF02671; PAH: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
 0; Gaps
                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.1%; Score 58; DB 4; Length 1130; Best Local Similarity 54.2%; Pred. No. 1.2e+02; Matches 13; Conservative 0; Mismatches 11; Indels
 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1130 AA; 129359 MW; B767339317ECC96D CRC64;
                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KIRAD/700 PROTEIN (FRAGMENT).
                                                                                                                                            PRT; 1130 AA.
 1; Mismatches
                                               10 PSLSLSERERAGGGGGGGGGG 31
                              4 PTLRQWLAARAGGGKGGGGIEG 25
13; Conservative
                                                                                                                                            PRELIMINARY;
                                                                                                                                           075182
Matches
                                                                                                          RESULT 30
075182
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Search completed: October 9, 2002, 09:03:13 Job time : 14.9826 secs

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Best Local Similarity
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Query Match
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                                                                                                                          O9ASE5
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                                                                                                   RESULT 28
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0
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related, Kurebayashi S., Jetten A.M.;
related, Kurepel-like protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325914; AAK00954.1; -
HSSP; POB151; ZGLI.
InterPro: IPR000922; Zif-CZH2.
Ffam; PF00096; Zif-CZH2.5.
SWART; SW00355; ZnF_CZH2.5.
PROSITE; PS00128; ZINC_FINGER_CZH2_1; 4.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 4.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 524 AA; 55704 MW; 3EZCZ7243DE5ABSE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                           Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                       Wu S.C.-Y., Grindley J., Winnier G.B., Hargett L., Hogan B.L.M.; "Mouse Mesenchyme forkhead 2 (Mf2): expression, DNA binding and induction by sonic hedgehog during somitogenesis."; Mech. Dev. 70:3-13(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                     30.1%; Score 58; DB 11; Length 492; 70.6%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00659; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
SEQUENCE 492 AA; 48936 MW; 7F82440F4C435702 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 10-DEC-2001 (TrEMBLrel. 19, Last annotation update) RRUPPEL-LIKE ZINC FINGER PROTEIN GLISZ. HOMO Sapiens (Human).
                                                                      Last sequence update)
Last annotation update)
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                                    492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                           Created)
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                                                                                                                                                                                    TISSUE-MESENCHYME;
MEDLINE-98168839; Pubmed-9510020;
                                                                                                                                                                                                                                                                             TRANSFAC; T02492; --
MGD; MGD:1347471; Foxd2.
InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                             Mech. Dev. 70:3-13(1998).
EMBL; AF023915; AAB81275.1; -.
                                                       1-JAN-1998 (TrEMBLrel. 05,
1-JAN-1998 (TrEMBLrel. 05,
1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                         PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 LROGLKTDAGGGAGGGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRQWLAARAGGGKGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                   063245;
                                                                                                        FOXD2 OR MF2.
                                                            01-JAN-1998
                                                                       01-JAN-1998
                                                                                             FORKHEAD 2
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                                     035392
               RESULT 26
035392
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EMBL; AB040891; BAA95982.1; -.
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0456F08."
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002901: BAB39414.1;
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR00205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.1%; Score 58; DB 10; Length 529; 63.2%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 612;
DB 4; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pram; PF01593; Amino_oxidase; 1.
SEQUENCE 529 AA; 55981 MW; 0A5DA55CDD076D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
KIAA1458 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                (TrEWBLrel. 17, Created)
(TrEWBLrel. 17, Last sequence update)
(TrEWBLrel. 18, Last annotation update)
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67;
                                                                                                                                                                                                                                                          529 AA.
30.1%; Score 58; DB 53.8%; Pred. No. 57; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 58;
2; Mismatches
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                                                                                                                         PRT;
                                                                                            3 GPTLRQWLAARAGGGKGGGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 63.2
Matches 12; Conservative
                          Best_Local Similarity 53.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                       P0456F08.14 PROTEIN.
P0456F08.14.
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                         01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001
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156 AA

PRT;

PRELIMINARY;

408 PTLQAQLGGGAGGGGGGGGGGGGGGGGP 439

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003144; BAB44127.1; --
SEQUENCE 156 AA; 17366 MW; C71A84810571D102 CRC64;
                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                              STRAIN=CV. NIPPONBARE;
                                                                                                                                                                          Oryza sativa (Rice)
                                                                                                                                                P0507H06.1 PROTEIN.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      clone: P0507H06."
                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                              P0507H06.1
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                          094EA0;
                                                                           Q94EA0
                                                RESULT 24
                                                            Q94EA0
       q
                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares S., Squares R., Shelton S., Squares S., Squares R., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:337-544(1998).

EMBL: 298209; CAB10901.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                 30.3%; Score 58.5; DB 16; Length 495; 43.3%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seeger K.J., Harris D., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      Tuberculist; Rv2725c; -.
Hypothetical protein; Complete proteome.
SEQUENCE 495 AA; 53327 MW; F82BA93092945121 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL: AL512667; CAC21636.2; -.

InterPro. 11:77-98 (1994).

Pfam: PF02687; DUF214.

SEQUENCE 496 AA; 49548 MW; 54E110C4F86231A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE INTEGRAL MEMBRANE PROFEIN.
                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AA
                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.3%; Score 58.5; 143.8%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                    199 PRLRGWGESMSRQAGGRAGGSGGGVGLRGP 228
                                                                                                                                                                                                                                                                                                                                                         4 PTLRQW-----LAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                      MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor,
                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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3; Indels

1; Mismatches

6 LRQWLAARAGGGKGG 20

30.1%; Score 58; DB 10; Length 156; 73.3%; Pred. No. 17;

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                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
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44.4%; Pred. No. 41;
tive 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 377 AA; 37998 MW; C2DBC19402D3A172 CRC64;
                                                                                                                                                                  01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Biol. 0:0-0(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBLEARITY: WITH OTHER HOMEOBOX PROTEINS.
EMBL, AF099746; AAC82470.1;
-HSSP; P06601; IPUL.
                                                                                                                                                                                                                                                                                                                          Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
                                                                                                                             377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 QGYTAASYYGVECGGGGGGGGGGFYL 291
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EGPTLRQWLAARAGGGKGGGGIEGPTL 28
                                                                                                                                                                                                                                                                             Petromyzon marinus (Sea lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.48
Matches 12; Conservative
                                                                                                                           PRELIMINARY;
15 LRPWLFAFAGGGRGG 29
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                           Q9YHD0
                                                                         RESULT 25
                                                                                                   Q9YHD0
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Gaps

6

6; Indels

3; Mismatches

14; Conservative

Matches

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4 PTLROWL-----AARAGGGKGGGGIEGP 26

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P0436E04.1
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                                                                                                                                                                                                                                                                                                                 Q9FTZ5;
                                                                                                                                                                                                                                                                                                       Q9FT25
                                                                                                                                                                                                              Matches
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TISSUE-BRAIN;
MEDLINE-99365357; PubMed-10436051;
Siekhaus D.E., Fuller R.S.;
"A role for amontillado, the Drosophila homolog of the neuropeptide precursor processing professe PC2, in triggering hatching behavior.";
J. Neurosci. 19:6942-6954(1999).
                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                               5;
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           DB 5; Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71733 MW; D021D4882293C996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PROCHORMONE AND NEUROPEPTIDE PROCESSING PROTEASE.

AMON OR PC2 OR CG6438.
                                                                                                                                                                                                                                                                                                                                                          Flydase; 200.03; Flydase; Flydase; Flydase; Flydase; InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
Pfam; PF01483; P; P; P domain.
Prom; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00137; SUBTILASE_ASP; PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                    Pred. No. 55;
3; Mismatches
           Score 59; Pred. No. 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 59; 48.0%; Pred. No.
                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LRQWLAARAGGGKG--GGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NICHOLS;
MEDLINE-98332770; Pubmed=9665876;
                                                                15 LLHWASAGAGGGAGGSGAGLSGPAV 39
                                                   6 LRQWLAARAGGGKG--GGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                              EMBL; AF033117; AAD49105.1; -. HSSP; P04072; 1THM.
MEROPS; SO8.073; -.
            30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 48.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                Conservative
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; Neuropeptide.
SEQUENCE 654 AA; 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                        Similarity
                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=160;
                                 12;
              Query Match
                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            083436
                                                                                                                                     Q9UAE7
                                                                                                                            Q9UAE7
                                                                                                       RESULT 19
Q9UAE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
                                  Matches
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Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0436E04.",
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002818; BAB16119.1;
                                                                                                                                                                                    Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818; BAB10319.1; -.
202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             683 AA; 74518 MW; F91407FA7094AAD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 53.3 KDA PROTEIN
HFLX OR RV2725C OR MTCX154.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 VVSPSCRRQTAGRHGGCGGGRWMAAAGGRDGGGCRRWWAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLRQWLAARAGGGKGG-----GGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.6%; Pred. No. 1.,
tive 5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.3%; Score 58.5; I
36.6%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PTLROWLAARAGGGKGGGGIEGPTLROWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6%;
                                                                                                                                                                                                                                                              EMBL; AE001220; AAC65409.1;
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Best Local Similarity 36.65
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 43.8 nes 14; Conservative
                                                                                                                                                                                                                              spirochete.";
Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                       InterPro; IPR001258; NHL. InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01436; NHL; 4.
Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P0436E04.1 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
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371 YLGAGAGGGAGGGG--GPLVAAAAAAGA 396

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STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosnids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOI. Microbiol. 21:77-96(1996).
EMBL; AL022268; CAA18333.1; -.
Hypothetical protein.
SEOUENCE 497 AA; 54506 MW; FB3646D4D6E54028 CRC64;
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurogenetics 1:31-36(1997).

-!- FUNCTION: MAY REGULATE RNA SPLICING OR METABOLISM IN A SPECIFIC SUBSET OF DEVELOPING NEURONS (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: WUCLEAR (BY SIMILARITY).

-!- TISSUE SPECIFICITY: BRAIN. EXPRESSION RESTRICTED TO ASTROCYTES.

-!- DISEASE: MAY BE A TARGET ANTIGEN IN ONE OF THE UNDEFINED HUMAN PARANEOPLASTIC SYNDROMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joki K., Ramaswamy S., Billings S.J., Mohrenweiser H.W., Louis D.N., annova, a putative astrocytic RNA binding protein gene that maps to chromosome 1973 3 ".
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ASTROCYTIC NOVAL-LIKE RNA-BINDING PROTEIN (NEUROONCOLOGIC VENTRAL ANTIGEN 3) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                                   Score 59; DB 2; Length 497;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 498;
                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4B54196FDB6BF78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50084; KH_TYPE_1; 3.
Nuclear protein; RNA-binding; Repeat; Antigen.
                                                                                                                                                                                                                                                                                                                                                           498 AA.
                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                          206 PRLRGWGQSLSRQMGGGKGGGLATRGP 232
                                                                                                                                                                                                                                           4 PTLRQW---LAARAGGGKGGG-GIEGP 26
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20197319; PubMed=10735272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U70477; AAB88661.1;
InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TYPE_1.
                                                                                                                                                                                 30.6%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00013; KH-domain; 3.
SMART; SM00322; KH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.6%;
53.6%;
                                                                                                                                                                            Query Match 30.6%
Best Local Similarity 51.9%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   West Local Similaria
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 19q13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANOVA OR NOVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                      043267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                       RESULT 17
043267
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9 WLAARAGGGKGGGIEGPTLRQWLAARA 36

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RX MEDLINE—20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basul A., Baxendale J., Rapraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basul A., Baxendale J., Rapraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basul A., Baxendale J., Rapraktaroglu L., Beasley E.M.,
RA Berkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chun P. RA Burtis K.C., Barngelista C.C., Ferraz C., Gubrinkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasset K.,
A Gostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mettei B., McIntosh T.C., Morbin R., Mout S.M., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy E., Mussern D.R., Pacleb J.M.,
Rabarkluo G., Milshina N.V., Mobarry C., Morris J., Weigh T.,
Rabarcolo M., Fittenna G.S., Pan S., Pollard J., Paul W., Rese M.,
Reinert K., Remington K.A., Nixon K., Mussernan D.R., Pacleb J.M.,
Rabarcolo M., Fittennan G.S., Pan S., Pollard J., Wang X.,
Reinert K., Remington K.A., Worley R., Wang X.,
Reinert K., Remington K.A., Worley R., Wang X.,
Reinert K., Remington R., Strong G., Zheo Q., Zheng L.,
Ray Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,
Ray Wassarman D.A., Weinstook G., Wu D., Yung S., Zhao Q., Zhene S., Zhan R., Weiner S., Whyers E.W., Rubin G.,
R., Phence R., Wassarman D.A.
                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2BD57F683929D237 CRC64;
                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                          654 AA.
                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00136; SUBTILASE ASP; 1. PROSITE; PS00137; SUBTILASE_HIS; 1. PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
EMBL; AE003757; AAF56615.1; -.
HSSP; P04072; 1THM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0023179; amon.
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 AA;
                                                                                                                                                                                                                                                                                                                                        STRAIN-BERKELEY;
                                                                                                                                                                  AMON OR CG6438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; PO4072; 17
MEROPS; S08.073;
                                                                                                                                            AMON PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                        Q9VBC7
RESULT 18
                    Q9VBC7
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.E., Howlend T.J., Wel M.H., Tbegwam C.,
RA Jalali M., Ralush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei X., Levitsky A.A., Li Z., Kulp D., Lai Z.,
RA Lasko P., Lei X., Levitsky A.A., Li Z., Liang Y., Lin X.,
RA Mattei B., McIntosh T.C., McIeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Melson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pollard J., Shen H.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Suith T.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Suith T.,
RA Spier E., Spradling A.C., Stapleron M., Strong R., Suith T.,
RA Williams S.M., Woodage T., Weinstook G.M., Weissenbach J.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter E., Wang A.H.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA FIYBBse; FB90003523; CG13807.
BR RINTS; PR01228; EGSHELL.
SEQUENCE 170 AA, 19099 WW, 477D79D55ADF4CE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stllwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Liu S., Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., Arellaro S., Luccas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.6%; Score 59; DB 5; Length 170; 45.8%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AC006540; AAD13116.1; ... InterPro; IPR004087; KH. TYPE_1. InterPro; IPR004088; KH. TYPE_1. InterPro; IPR004088; KH. TYPE_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RNA BINDING PROTEIN NOVA-2 (FRRGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EGPTLRQWLAARAGGGKGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 EPPIVENWM----GGGGGGGGFQG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50084; KH_TYPE_1; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00013; KH-domain; 3.
PRINTS; PR00456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.8%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00322; KH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29UEA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9UEA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UEA1
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Gaps
                                                                 Gaps
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                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                               5;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99007301; PubMed=9789075;
MEDLINE=99007301; Darnell R.B.;
"The neuronal RNA-binding protein Nova-2 is implicated as the autoantigen targeted in PoMA partients with dementia."; Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Score 59; DB 4; Length 492; 53.6%; Pred. No. 41;
                              DB 4; Length 464;
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00013; KH-domain; 3.
SMART: SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE_1; 3.
SEQUENCE 492 AA; 49008 MW; 41B63EAF6899256B CRC64;
1 1 464 AA; 45901 MW; 0B16BAE99C271CC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-UUN-2000 (TrEMBLrel. 14, Last annotation update) HYPOTHETICAL 54.5 KDA PROTEIN.
                                                                                                                                                                                                                                       (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 497 AA
                                                                                                                                                                                                492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                  2; Mismatches
                                     Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 YLGAGAGGAGGGG--GPLVAAAAAAGA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 WLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                          337 YLGAGAGGGAGGGG--GPLVAAAAAAA 362
                                                                                               9 WLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004087; KH.
InterPro; IPR004088; KH_TYPE_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.6%;
                                       30.6%;
53.6%;
                                                                                                                                                                                                                                                                         RNA-BINDING PROTEIN NOVA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.6°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                    15; Conservative
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeger K.J., Harris D.;
                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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01-DEC-2001
   NON_TER
SEQUENCE
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                                           Query Match
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                                                                                                                                                                                                                    :6MND6C
                                                                                                                                                                                                    6MND60
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                                                                        Matches
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Query Match
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                                                         Matches
                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                     Q9JMH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                        Score 60; DB 10; Length 113;
Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 60; DB 10; Length 125; 40.5%; Pred. No. 7.9; tive 2; Mismatches 9; Indels
                                                                                                                    3; Indels
OSJNBa0068A07, from Chromosome 10, complete sequence."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC091734; ARA98762.1; ... Hypothetical protein.
SEQUENCE 113 AA: 12154 MW; CIEGE87E9B00D577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002094; BAA96216.1; -.
Hypothetical protein.
SEQUENCE 125 AA; 13396 MW; C609D8D0B07BC505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL451109; CAC18624.2; -.
Hypothetical protein.
SEQUENCE 776 AA: 82771 MW; C9BEA870D94A37DE CRC64;
                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 EGAAAR-WRAARSPARGGORGGHRRRGGGGGGGGGRERPRRRR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EGPTLRQWLAARA-------GGGKGGGGIEGPTLRQ 30
                                                                           31.1%; Scor
56.5%; Pred. No. / ..,
57 Mismatches
                                                                                                                                                                                                                                               125 AA.
                                                                                                                                                                                                                                             PRT;
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                                                                                                                                          14 AGGGKGGGIEGPTLRQWLAARA 36
                                                                                                                                                        :||:||||| | ::| :||||| 26 SGGEGGGG--GRRMQQRMAARA 46
                                                                                                 Local Similarity 56.59
les 13; Conservative
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                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
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                                                                                     Query Match
                                                                                                                                                                                                                                                      Q9LWC8;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Ann K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Ballew R.W., Bernos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Broxstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto K., Inoue N., Fujimori A., Saito T., Shinkai H., Sakiyama H.; Mesocricetus auratus mRNA for type XVII collagen."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB027759; BAA94381.1.
InterPro: IPRO00897; Collagen.
Pfam: PF01391; Collagen.
SEQUENCE 1431 AA; 144579 MW; 4315631FEB2C9A5C CRC64;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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31.1%; Score 60; DB 3; Length 776; 53.8%; Pred. No. 50;
                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.8%; Score 59.5; DB 11; Length J
60 0%; Pred. No. 1.1e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144579 MW; 4315631FEB2C9A5C CRC64;
                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
COLLAGEN TYPE XVII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                   PRT; 1431 AA
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                                             3; Mismatches
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                                                                                                                               678 GGGGGGGVVDDDGEPDFAGWLAAQA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                         15 GGGKGGGGI---EG-PTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 ARGGGGGGGGGGT---WGAAPA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 ARAGGGKGGGGIEGPTLRQWLAARA 36
                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.0 tes 15; Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
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                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus.
NCBI_TaxID=10036;
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Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome."; mol. Microbiol. 21:77-96(1996).
EMBL, AL163003; CAB86095.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.3%; Score 60.5; DB 2; Length 407; 58.3%; Pred. No. 23;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                       Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 407 AA; 42643 MW; 7E4C266610E051FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
POSSIBLE ATP/GTP-BINDING PROTEIN.
                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) PUTATIVE SUGAR HYDROLASE (FRAGMENT).
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                                                                            407 AA
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                                                                             PRT;
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                                                                               PRELIMINARY;
                                                                                                                                                                                                        Streptomyces coelicolor.
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ses 14; Conserv
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                                                                                                                   L-OCT-2000
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                            Score 60.5; DB 16; Length 488;
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43.3%; Pred. No. 29;
iive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00019; AAA17274.1; '.
SEQUENCE 518 AA; 56001 MW; 6641916CC84F374B CRC64;
                                                                                                                                                                                                                                                                                     Indels
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Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                 488 AA; 52800 MW; 188918856F9774AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 12.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; ALS83920; CAC31378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA.
                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                  Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 PRLRGWGESMSROVGGRAGGSGGGVGLRGP 248
                                                                                                                                                                                                                                                                                                                                                                     189 PRLKGWGESMSRQVGGRAGGSGGGVGLKGP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLROW-----LAARAGGGKGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                          4 PTLRQW-----LAARAGGGKGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                 InterPro; IPR000765; GTP1_OBG
                                                                                                                                                                                                                                            31.3%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.3%;
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                           PRINTS; PR00326; GTP10BG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
STRAIN-NIPPONBARE;
                                                                                                                                                                                                                                                               Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                    Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1769;
                                                                                        Leproma; ML0997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                  Query Match
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1;

80 GPTVGVRVAYRAGAGGGGGGGPRGFALK 106

qq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                 Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65.5; DB 13; Length 431;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%; Score 63; DB 10; Length 253; 51.9%; Pred. No. 7.3; tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AP003235; BAB64100.1; -. SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                     Liu Y., Xue J X., Zhang W., Fu D.C., He R.Q., Xue Z.G.; "qBrain-2, a POU-box gene expressed in quail embryos."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).-: SIMILARITY: WITH OTHER HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Homeobox; Nuclear protein.
431 AA; 43722 MW; 1DC47E53F9ACC7D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 QWLAARA-----GGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 OWINALSHGGPGGGGGGGGGGGGGGGGAP----WAAAAA 95
      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
POU-BOX PROTEIN BRAIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
PROSITE; PS00027; HOMEOBOX_1: 1.
PROSITE; PS50071; HOMEOBOX_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF091043; AAF00040.1; -...
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00035; POU_1; 1
PROSITE; PS00465; POU_2; 1
DNA-binding; Homeobox; Nuc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P0039A07.6 PROTEIN. P0039A07.6.
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone: P0039A07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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3 GPTLRQWLAARAGGGKGGGGIEGPTLR 29

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                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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0
                                                                                                                                                                                                                                                                                                                                                                2; Mismatches 18; Indels 14;
                                                                                                                                                                                                                              "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0705D01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 5; Length 500;
Pred. No. 25;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                        Length 439;
                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGKGGGG------IEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                           39 LHAPLLRLWPLGGGGGGGGGGGGGGFRVGAVGGAVRGEEARSQRAAEA 88
                                                                                                                                                                                                                                                               Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AP000492: BAA84610.1; -. Hypothetical protein. SEQUENCE 439 AA; 47297 MW; 533EEC240CEA1BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53946 MW; 1416327086FE7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                        32.1%; Score 62; DB 10; 32.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 500 AA
                       439 AA.
                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(198).
Science 278013; CAB01420.1: -
Interpro; IPR001254; Trypsin.
PROSITE: PS50240; TRYPSIN.DOM; 1.
Hydrolase; Scrine protease.
SEQUENCE 500 AA, 53946 MW; 1416
                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GPTLRQWLAARAGGGKGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                 32.1%
Query Match
Best Local Similarity 32.0%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                          PRELIMINARY;
                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                            Oryza sativa (Rice)
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F15B9.5 PROTEIN.
                                                                                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percy C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q19476
Q19476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F15B9.5
                                         09SDK6;
                           09SDK6
RESULT 4
               09SDK6
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Q9pyg9 coturnix co
Q943k0 oryza sativ
Q95dk6 oryza sativ
Q19476 caenorhabdi
Q910b6 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 049843 mycobacteri
0947t7 oryza sativ
091wc8 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oghea4 neurospora
Ogjmh4 mesocricetu
Ogw033 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091gc9 oryza sativ
                                                                                                                               October 9, 2002, 08:52:16; Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ogueal homo sapien
Ogunw9 homo sapien
O69972 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                               562222
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGKGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q943K0
Q9SDK6
Q19476
Q9L0B6
Q9CCC0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LWC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 049843
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Q69972
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sp_human:*
sp_invertebrate:*
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Score Match Length DB ID
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sp_phage:*
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Maximum DB seq length: 2000000000
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Sp_bacteria:*
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sp_rodent:*
sp_virus:*
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                                                                                                                                                                                                                                             Perfect score:
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63.5
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62
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                               Run on:
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043267 homo sapien 09vbc7 drosophila 083436 treponema p 09ftz5 oryza sativ 033320 mycobacteri 09ad76 streptomyce 094ea0 oryza sativ 094ea0 oryza sativ 095780 musculu 09bze0 homo sapien 075182 homo sapien 075184 drosophila 09184 drosophila 09184 drosophila 09184 mus musculu 09458 musculu 09458 musculu 09458 musculu 09458 musculu 09484 mus musculu 09484 mus musculu 094854 arabidopsis 094011 caenorhabdi	ALIGNMENTS	360 AA.	Created) Last sequence update) Last annotation update)	Oryza sativa (Rice). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	; c DNA, chromosome 1, PAC	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002525; BAB07996.1; InterPro; IPR00571; Zf-CCCH. InterPro; IPR00642; Zf-CCCH. SMATY; SM00356; ZnF_C3H1; 4. SEQUENCE 360 AA: 37388 MW; 5105598D7E1C77B2 CRC64.	re 66; DB 10; Length 360; d. No. 4.7; Mismatches 10; Indels 0; Gaps 0;
043267 099867 083436 083436 098725 094EA0 094EA0 094EA0 0958ES 0998ES 0998ES 0998ES 0975182 097866 075182 097866 075182 097866 075182 097866 075182 097866 075182 097866 075182 097866	ALIG	PRT;	Created) Last seq Last ann	eptoph Lilio	moto K. genomi	MBL/Ger 51055	Score 66; Pred. No. 2; Mismatc
5 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			15, C 15, L 18, L	Str yta; ryza	Уата: 3A3)	he Ell; - CCH. 4.	s; s
698 654 654 663 663 663 663 663 663 613 613 613 613		PRELIMINARY;	Lrel. 1 Lrel. 1 Lrel. 1 ER PROT). lantae; nolioph zeae; O	ARE; to T., ? onbare(0) to tl 307996.] L; Zf-CC CCH; 4. -C3H1;	34.2%; 52.0%; ative
30.06 30.06 30.06 30.01			(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.	a (Rice Viridip La; Magi ae; Ory:	N N.A. WIPPONBA Matsumota n nippo	100. / 10N-200(125; BAE 12; Zf-C 156; ZnE 160 AA;	h Similarity 52. 13; Conservative
59 59 59 59 59 59 59 59 50 50 50 50 50 50 50 50 50 50		600	01-0CT-2000 (TrEMBLrel. 15, C 01-0CT-2000 (TrEMBLrel. 15, L 01-0CT-2001 (TrEMBLrel. 18, L PUTATIVE ZINC FINGER PROTEIN.	a sativi ryota; matophy: artoidea	[1] SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE; Sasaki T., Matsumoto T "Oryza sativa nipponba	itted (c); AP002E rPro; IF PF0064 r; SM003	/ Match Local Simi es 13;
117 220 220 220 220 220 230 244 244 240 240 240 240 240 240 240 24		5 3			SEQU STRA Sasa "Ory	Subm Subm EMBL Inter Pfam SMAR' SEQUI	Query Match Best Local Matches 1
		RE 1D	GN DI	8000x3	RR RA RT RA	RL DR DR DR	OMX

431 AA.

PRT;

PRELIMINARY;

RESULT 2 Q9PVG9 ID Q9PVG9

1 IEGPTLRQWLAARAGGGKGGGIEG 25 :||| | | | | | | | | | | 26 26 LEGPMWRMGLGGGGGGGGGGGG 50

Qy Db us-09-422-838c-27.rspt

δ q

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MEDLINE=2027482; PubMed=10819331; Magase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.; Nadases T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.; Prediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; EMBL; AB040891; BAA95982.1; -.
                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PTLRQCLAARAGGGGGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 PSLSLSLRERAGGGGGGGGG 31
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                                                                   KIAA1458 PROTEIN (FRAGMENT).
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 54.59
Watches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 63.6 es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=46242;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=G2;
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                                                                                      KIAA1458
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Obermaler B., Ottenwaelder B., Duchemin D., Zeitler K., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
MISTAZ sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0039A07.";
                                                                                                                                                                                                                                                                                                                                                                          37.4%; Score 71; DB 10; Length 253; 55.6%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%; Score 68; DB 10; Length 199;
                                                                                                                                  Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AP003235; BAB64100.1; SEQUENCE 253 AA; 25568 MW; A963166CE5F97B2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ALIG3816; CAB87755.1; --
INTERPTO; IPR000345; Cytc. heme_bind.
InterPro; IPR00245; Kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein.
199 AA; 21539 MW; E5D28AC167B3FBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EGPTLRQC------LAARAGGGGGGGGGGFEGPTLRQC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 21.5 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00334; KININOGEN.
PROSITE; PS00190; CYTOCHROME_C; UNKNOMN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQCLAARAGGGGGGGGGIEGPTLR 29
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16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                 P0039A07.6.
Oryza sativa (Rice).
                                                                  P0039A07.6 PROTEIN.
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                         NCBI_TaxID=4530;
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Q9P270
ID Q9P27
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0
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0
                                           35.8%; Score 68; DB 4; Length 612; 63.6%; Pred. No. 4.4;
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                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu J., Wang L., Hu X., Pang Y.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF325155; AAL01786.1; -..
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence Analysis of the Spodoptera litura Multicapsid
612 AA; 65593 MW; 9AA4061D21E1E9FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Spodoptera litura nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C5626A8FFA9C9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 7.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 AA.
                                                                                                                                                                                                                                                                                                   66 AA
                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21425398; PubMed=11531416;
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612 AA

PRT;

PRELIMINARY;

Q9P270

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GenCore version 5.1.3,
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2002, 08:52:16 : Search time 12.8993 Seconds (without alignments) 482.803 Million cell updates/sec Run on:

US-09-422-838C-27 190 Title: Perfect score:

1 IEGPTLRQCLAARAGGGGGGGGGIEGPTLRQCLAARA 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:*

1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_archeap:* sp_mammal:* sp_mhc:* sp_human:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q91gc9 oryza sativ	Q943kO oryza sativ	Q9lyb2 arabidopsis	Q9p270 homo sapien	Q91bc5 spodoptera	Q9m6al catharanthu	Q9m699 catharanthu	Q9xe89 sorghum bic	Q9li26 oryza sativ	Q96sq2 homo sapien	Q9ad76 streptomyce	Q19476 caenorhabdi	Q9byd8 homo sapien	Q96jg7 homo sapien	Q61869 mus musculu	Q96134 homo sapien
	ID	629760	Q943K0	Q9LYB2	Q9P270	Q91BC5	Q9M6A1		Q9XE89	Q9L126	096502	Q9AD76	019476	Q9BYD8	096JG7	061869	096L34
	DB	10	10	10	4	12	10	10	10	10	4	7	S	4	4	11	4
	Query Match Length DB	360	253	199	612	99	137	160	369	413	474	496	200	688	689	707	752
æ	Query Match	38.4	37.4	35.8	35.8	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7
	Score	73	71	89	68	99	99	99	99	99	99	99	99	99	99	99	99
	Result No.		7	ო	4	ស	9	7	80	σ	10	11	12	13	14	15	16

ö

253 AA.

PRT;

PRELIMINARY;

RESULT 2 O Q943K0 ID Q943K0 Q943K0

Q9y648 homo sapien	Q9gnp1 ciona savig				Q9afi5 mycobacteri			Q9u2i0 caenorhabdi	096755 branchiosto	Q9ase5 oryza sativ	Q9f7t9 streptomyce	Q9s0r8 streptomyce	Q942u6 oryza sativ	Q9mli8 arabidopsis	09cle7 schizophyll	Q942r8 oryza sativ	Q9ccc0 mycobacteri	Q49843 mycobacteri	Q27258 drosophila	Q9v7u9 drosophila	096828 drosophila	Q9sxi9 oryza sativ	O61080 acanthamoeb	Q9sz70 arabidopsis	Q9c0il homo sapien	Q9w149 drosophila	oryza	Q9ftk4 oryza sativ
29Y648	Q9GNP1	Q9LD54	Q9VJK4	Q9VP99	29AFI5	29VV01	290211	090210	096755	Q9ASE5	Q9F7T9	Q9S0R8	0942U6	Q9M1 I 8	Q9C1E7	Q942R8	000060	049843	027258	60V7U9	096828	61XS60	061080	098270	Q9C011	Q9W149	Q9LWC8	Q9FTK4
4	N.			_	-	_				10				10				2								'n	10	10
355	770	381	452	150	165	309	331	333	422	529	3626	3972	113	434	146	186	488	518	296	797	806	841	1186	339	775	867	125	168
34.5		•		æ,	33.9	Э.		33.7	3	m.	33.7	33.7	33.4	3.	33.2					ω,		3.	Э.		ζ.	ς.	ά.	2
65.5	65.5	65	65	4	64.5	64	64	64	64	64	64	64	63.5	63.5	9	63	63	63	63	63	63	63	63	ζ.	62.5	ď	62	62
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35						41	42		44	45

ALIGNMENTS

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Gaps
                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                           STRAIN—CV. NIPPONDARE;
Sasal T., Matsumoto K.;
Sasal T., Matsumoto T., Yamamoto K.;
Sasal T., Matsumoto T., Yamamoto K.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR003525; BAR07096.1;
InterPro; IPR000571; Zf-CCCH.
Fram, PF00642; Zf-CCCH; 4.
SEQUENCE 360 AA; 37368 MW; 5105598D7E1C77B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.4%; Score 73; DB 10; Length 360; Best Local Similarity 56.0%; Pred. No. 0.72; Matches 14; Conservative 2; Mismatches 9; Indels
                                              01-0CT_2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE ZINC FINGER PROTEIN.
                             360 AA.
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 LEGPMWRMGLGGGGGGGGGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQCLAARAGGGGGGGGIEG 25
                             PRELIMINARY;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=4530;
                                           Q9LGC9;
                             O9LGC9
RESULT 1
                609T60
                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
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